

From: Bunner, Bridget
Sent: Wednesday, April 06, 2005 2:00 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/810,796:

1. the nucleic acid sequence of SEQ ID NO: 2
2. the nucleic acid sequence of SEQ ID NO: 3

CRFE

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:27:56 ; Search time 426.638 Seconds
(without alignments)
10332.249 Million cell updates/sec

Title: US-09-810-796-2
Perfect score: 2694
Sequence: 1 atgaaggatgtggagtcggg.....ctcatgtcaactgaataa 2694

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2689.2	99.8	3137	4	US-09-590-304-1
2	2681.2	99.5	3074	4	US-09-813-148-1
3	2625.2	97.4	2772	4	US-09-825-147-1
4	2625.2	97.4	3111	4	US-09-825-147-3
5	518.4	19.2	2196	4	US-09-949-016-1823
6	518.4	19.2	2335	4	US-09-492-361-1
7	516	19.2	2273	3	US-09-177-650-88
8	510	18.9	2169	3	US-09-105-058C-22
9	509.8	18.9	582	4	US-09-495-050A-303
10	465.4	17.3	896	3	US-09-105-058C-1
11	464	17.2	2814	3	US-09-177-650-90
12	460.8	17.1	2565	3	US-09-105-058C-26
13	460.8	17.1	2914	3	US-09-177-650-6
14	452	16.8	575	4	US-09-495-050A-305
15	425	15.8	3287	3	US-09-105-058C-19
16	423.4	15.7	3232	3	US-09-177-650-1
17	423.4	15.7	3237	3	US-09-177-650-95
18	421.4	15.6	900	3	US-09-105-058C-3
19	420.6	15.6	900	3	US-09-105-058C-5
20	363.8	13.5	930	3	US-09-105-058C-17
21	334.2	12.4	735	3	US-09-105-058C-7
22	276.4	10.3	284	4	US-09-495-050A-304
23	267.8	9.9	2028	3	US-09-634-920-1
24	267.8	9.9	2028	4	US-09-840-125-1
25	267.8	9.9	3181	3	US-09-135-021-1
26	267.8	9.9	3181	3	US-09-135-020-1
27	267.8	9.9	3181	3	US-09-135-010A-1

28	267.8	9.9	3181	3	US-09-444-871-1	9-1	Sequence 1, Appli
29	267.8	9.9	3181	3	US-09-597-735-1	1	Sequence 1, Appli
30	267.8	9.9	3181	3	US-09-444-295-1	1	Sequence 1, Appli
31	267.8	9.9	3181	3	US-09-597-732-1	1	Sequence 1, Appli
32	267.8	9.9	3181	3	US-09-597-731-1	1	Sequence 1, Appli
33	266.6	9.9	2734	3	US-09-135-021-79	79	Sequence 79, Appli
34	266.6	9.9	2821	3	US-09-135-010A-115	115	Sequence 115, App
35	266.6	9.9	2821	3	US-09-597-735-115	115	Sequence 115, App
36	266.6	9.9	2821	3	US-09-597-732-115	115	Sequence 115, App
37	266.6	9.9	2821	4	US-09-597-731-115	115	Sequence 115, App
38	266.6	9.9	2924	4	US-09-949-016-32	32	Sequence 32, Appli
39	258.4	9.6	3182	3	US-09-135-021-5	5	Sequence 5, Appli
40	251.8	9.3	2633	4	US-09-949-016-3215	3215	Sequence 3215, Ap
41	134.6	5.0	251	4	US-09-495-050A-296	296	Sequence 296, App
42	95.8	3.6	171	3	US-09-177-650-102	102	Sequence 102, App
43	95.8	3.6	58543	4	US-09-949-016-13565	13565	Sequence 13565, A
44	95.2	3.5	1481	4	US-09-949-016-4101	4101	Sequence 4101, App
45	84.8	3.1	649	3	US-09-177-650-118	118	Sequence 118, App

ALIGNMENTS

RESULT 1
US-09-590-304-1
; Sequence 1, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHAN
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-09-590-304-1

Query Match		99.8%	Score 2689.2;	DB 4;	Length 3137;
Best Local Similarity		99.9%	Pred No. 0;		
Matches 2691;		Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
Qy	1	ATGAAGGATGTGGAGTCGGGCGGGCGGCGAGGCTGCTGAACTCGGAGCCGCCAGGGGC	60		
Db	1	ATGAAGGATGTGGAGTCGGGCGGGCGGCGAGGCTGCTGAACTCGGAGCCGCCAGGGGC	60		
Qy	61	GACGGCTTCTACTGCTGGGACCCGCGCGCCAGCTTGGTGGCGGGCGGCTGCGCTG	120		
Db	61	GACGGCTTCTACTGCTGGGACCCGCGCGCCAGCTTGGTGGCGGGCGGCTGCGCTG	120		
Qy	121	AGGAGAGCCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGAGAGCGCTCTCT	180		
Db	121	AGGAGAGCCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGAGAGCGCTCTCT	180		
Qy	181	TACACGAGTACCGAGAGCTGCGGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG	240		
Db	181	TACACGAGTACCGAGAGCTGCGGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG	240		
Qy	241	TACACGAGTACCGAGAGCCCGGGCTGGGGTTCATCTACCAAGCTTCTGTTTTCTC	300		
Db	241	TACACGAGTACCGAGAGCCCGGGCTGGGGTTCATCTACCAAGCTTCTGTTTTCTC	300		
Qy	301	CTTGCTTTGGTGTCTGATTTTGTACGTTTCTTACCATCCCTGAGCACAAAATG	360		
Db	301	CTTGCTTTGGTGTCTGATTTTGTACGTTTCTTACCATCCCTGAGCACAAAATG	360		
Qy	361	GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGCTGTTTGGTTGAGTTTC	420		

Db		1441	CCACCACCTTAAAACTGTCTCATTTCCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG	1500
Qy	GCCTCAAGTTGCCTCTTTGATCCTCGTGGATGATTTGCTCTTTGGTTGGAGTTC	1501	AAGTTTAAAGGAAACGTTACGTTCCATATGATGATTAAGAGATGTCATTGAACAATATTTCTGCT	1560
Db		1501		1560
Qy		1561	GTCATCTGGACATGTTGTTAGAAATTAAGAGCTTCAAAACACGTTGTTGATCAAAATCTT	1620
Db		1561	GTCATCTGGACATGTTGTTAGAAATTAAGAGCTTCAAAACACGTTGTTGATCAAAATCTT	1620
Qy		1621	GGAAAAGGCGCAATCAATCAGATGAAGAGCGAGAGAAAATACAGCAGACATCAG	1680
Db		1621	GGAAAAGGCGCAATCAATCAGATGAAGAGCGAGAGAAAATACAGCAGACATCAG	1680
Qy		1681	ACCAAGAGCGATCTCAGTATGCTCGGTGCGGTGTTCAAGGTTGAAAGACAGGATCAGTCC	1740
Db		1681	ACCAAGAGCGATCTCAGTATGCTCGGTGCGGTGTTCAAGGTTGAAAGACAGGATCAGTCC	1740
Qy		1741	ATAGAGTCCAAAGCTGGACTGCTTACTAGACATCTATCAACAGGTCCTTTCGGAAAGGCTCT	1800
Db		1741	ATAGAGTCCAAAGCTGGACTGCTTACTAGACATCTATCAACAGGTCCTTTCGGAAAGGCTCT	1800
Qy		1801	GCCTCAGCCCTCGCTTTGGCTTCATTTCCAGATCCCACTTTTGAATGTGAACAGACATCT	1860
Db		1801	GCCTCAGCCCTCGCTTTGGCTTCATTTCCAGATCCCACTTTTGAATGTGAACAGACATCT	1860
Qy		1861	GACTATCAAGCGCTGTGGATAGCAAGATCTTTTCGGGTTCCGCAAAAACAGTGGCTGC	1920
Db		1861	GACTATCAAGCGCTGTGGATAGCAAGATCTTTTCGGGTTCCGCAAAAACAGTGGCTGC	1920
Qy		1921	TTATCAGATCAATAGTGGCCAAATCTCGAGAGCGCTGAGTTCAATCTGAGCGCCAAAT	1980
Db		1921	TTATCAGATCAATAGTGGCCAAATCTCGAGAGCGCTGAGTTCAATCTGAGCGCCAAAT	1980
Qy		1981	GAGTTCAGTGGCCAGACTTTCTAGCGCTTACTGACAGTCAAGCAACACAG	2040
Db		1981	GAGTTCAGTGGCCAGACTTTCTAGCGCTTACTGACAGTCAAGCAACACAG	2040
Qy		2041	GTCCCAATTAGTCAAGCGATGCTCAGAGTGGGAGCCCAACCAACCAATTCGAAACCAA	2100
Db		2041	GTCCCAATTAGTCAAGCGATGCTCAGAGTGGGAGCCCAACCAACCAATTCGAAACCAA	2100
Qy		2101	ATAAATACGGCACCAGCGAGCGCCCAACCACTTACAGATCCCACTCTCTCCCA	2160
Db		2101	ATAAATACGGCACCAGCGAGCGCCCAACCACTTACAGATCCCACTCTCTCCCA	2160
Qy		2161	GCCATCAAGCATCTGCCAGCGAGCAAACTCTGCACCCCTAACCCCTGACGGCTTACAGGA	2220
Db		2161	GCCATCAAGCATCTGCCAGCGAGCAAACTCTGCACCCCTAACCCCTGACGGCTTACAGGA	2220
Qy		2221	AGCATTTCTGACGTCACCTGCTGCTTGGCTTCCAGGAAAATGTTCAAGTTGCACAG	2280
Db		2221	AGCATTTCTGACGTCACCTGCTGCTTGGCTTCCAGGAAAATGTTCAAGTTGCACAG	2280
Qy		2281	TCAATCTCAGGAGGAGCGCTTATGAGGAAAAGCTTTTACATGGAGGAGAACTCTG	2340
Db		2281	TCAATCTCAGGAGGAGCGCTTATGAGGAAAAGCTTTTACATGGAGGAGAACTCTG	2340
Qy		2341	TTGTCCTGCTGCTCCATGCTGCGGAGGACTTGGGCAAAATCTTTGTTGTTGCAAAACCTG	2400
Db		2341	TTGTCCTGCTGCTCCATGCTGCGGAGGACTTGGGCAAAATCTTTGTTGTTGCAAAACCTG	2400
Qy		2401	ATCAGGTCGAGCGGAGGAACTGAATATACATTTTTCAGGAGTGTAGTCAAGTGGCTCCAGA	2460
Db		2401	ATCAGGTCGAGCGGAGGAACTGAATATACATTTTTCAGGAGTGTAGTCAAGTGGCTCCAGA	2460
Qy		2461	GGCAGCAGAAATTTTTTACCCCAATGAGGGAATCCAAATTTGTTTATATGATGAAGAG	2520
Db		2461	GGCAGCAGAAATTTTTTACCCCAATGAGGGAATCCAAATTTGTTTATATGATGAAGAG	2520
Qy		2521	GTGGGTCCGAGAGAGACAGAGACAGACTTTTGTATGCCGACCGCAGCTGCCAGGGAA	2580
Db		2521	GTGGGTCCGAGAGAGACAGAGACAGACTTTTGTATGCCGACCGCAGCTGCCAGGGAA	2580

Accession	Sequence	Position
Qy	GCTGCCCTTTGCATCAGAGCTCTTAAGACATGGAGGTCAGATCATCTCAGAGCATTTGT	2640
Db	GCTGCCCTTTGCATCAGAGCTCTTAAGACATGGAGGTCAGATCATCTCAGAGCATTTGT	2640
Qy	AAGSCAGAGGAAGGTACAGATGCCCTCAGCTTGGCTCATGTCAAACATGAATAAA	2694
Db	AAGSCAGAGGAAGGTACAGATGCCCTCAGCTTGGCTCATGTCAAACATGAATAAA	2694

RESULT 2

US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. 6617131
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEEBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CENTRAL NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-813-148-1

Query Match	99.5%	Score 2681.2	DB 4	Length 3074
Best Local Similarity	99.7%	Pred. No. 0		
Matches 2686	Conservative 0	Mismatches 8	Indels 0	Gaps 0

QY	1	ATGNAGATGTGGAGTCGGGCCGGGGCAGAGGTGCTGCTGAACCTGGCAGCGCGCCAGGGGC	60
Db	215	ATGAAGATGTGGAGTCGGGCCGGGGCAGAGGTGCTGCTGAACCTGGCAGCGCGCCAGGGGC	274
QY	61	GACGGCTGCTACTGCTGGGACACCGCGCGGCCACGCTTGTGTGCGCGCGGTGGGCTG	120
Db	275	GACGGCTGCTACTGCTGGGACACCGCGCGGCCACGCTTGTGTGCGCGCGGTGGGCTG	334
QY	121	AGGAGAGCGCCCGGGGCAAGCAGGGGGCCGGATGAGCCTGTCTGGGGAAAGCCGCTCTCT	180
Db	335	AGGAGAGCGCCCGGGGCAAGCAGGGGGCCGGATGAGCCTGTCTGGGGAAAGCCGCTCTCT	394
QY	181	TACACGATGACCAAGCTGCGGCGCAACGCTCAAGTACCGGGGGTGCAGAACTACCTG	240
Db	395	TACACGATGACCAAGCTGCGGCGCAACGCTCAAGTACCGGGGGTGCAGAACTACCTG	454
QY	241	TACAACTGCTGGAGACACCCCGCGCTGGCGGTTCATCTACCAACGCTTTGCTTTTCTC	300
Db	455	TACAACTGCTGGAGACACCCCGCGCTGGCGGTTCATCTACCAACGCTTTGCTTTTCTC	514
QY	301	CTTGCTTTGGTTGCTTGAATTTTGTCAAGTGTTTTCTACCATCCCTGAGCACACAAATTG	360
Db	515	CTTGCTTTGGTTGCTTGAATTTTGTCAAGTGTTTTCTACCATCCCTGAGCACACAAATTG	574
QY	361	GCCTCAAAGTTGCCTTTGATCCTGGAGTTGCGATGATGTTGCTCTTTTGGAGTTC	420
Db	575	GCCTCAAAGTTGCCTTTGATCCTGGAGTTGCGATGATGTTGCTCTTTTGGAGTTC	634
QY	421	ATCAATCGAATCTGGTCTCGGGGTGCTGTGTCGATATAGAGGATCGCAAGGAAGACTG	480
Db	635	ATCAATCGAATCTGGTCTCGGGGTGCTGTGTCGATATAGAGGATCGCAAGGAAGACTG	694

Qy	481	AGGTTTGCTCGAAAGCCCTTCTGTGTTATATAGATACAAATGTTCTTATTCGGTTCAAATAGCA	540
Db	695	AGGTTTGCTCGAAAGCCCTTCTGTGTTATATAGATACCAATGTTCTTATTCGGTTCAAATAGCA	754
Qy	541	GTTGTTTCTCGAAAACCTCAGGGTAAATATTTTTGGCCACGTCGACATCAGAAGTCTCCGT	600
Db	755	GTTGTTTCTCGAAAACCTCAGGGTAAATATTTTTGGCCACGTCGACATCAGAAGTCTCCGT	814
Qy	601	TTCTCATAGATCCTCCGCATGTCGCGCATGGACCGAAGGGGAGGCATTTGGAAATTAATCTG	660
Db	815	TTCTCATAGATCCTCCGCATGTCGCGCATGGACCGAAGGGGAGGCATTTGGAAATTAATCTG	874
Qy	661	GGTTTCAGTGGTTATGCTCTACAGCAAGGAATTAATTCACAGCTTGGTATACATAGAGATTTTG	720
Db	875	GGTTTCAGTGGTTATGCTCTACAGCAAGGAATTAATTCACAGCTTGGTATACATAGAGATTTTG	934
Qy	721	GTTCTTATTTTTTCGTCCTTTCTTTGTCATCTGCTGGAAAGGATGCCAATAAAGAGTTT	780
Db	935	GTTCTTATTTTTTCGTCCTTTCTTTGTCATCTGCTGGAAAGGATGCCAATAAAGAGTTT	994
Qy	781	TCTACATATGCAGATGCTCTCTGGTGGGGCACAAATTACATTGACAACTATGGCTATGGA	840
Db	995	TCTACATATGCAGATGCTCTCTGGTGGGGCACAAATTACATTGACAACTATGGCTATGGA	1054
Qy	841	GACAAACCTCCCCTAACTTGGCTGGGAAGATGCTTTTCTCAGGCTTTGCACTCTCTTGGC	900
Db	1055	GACAAACCTCCCCTAACTTGGCTGGGAAGATGCTTTTCTCAGGCTTTGCACTCTCTTGGC	1114
Qy	901	ATTCTTCTTTTCGACTTCTCTGCGGCATCTTTGGCTCAGGTTTTCGATTTAAAGATACAA	960
Db	1115	ATTCTTCTTTTCGACTTCTCTGCGGCATCTTTGGCTCAGGTTTTCGATTTAAAGATACAA	1174
Qy	961	GAACAAACACCGCCAGAAAACTTTTGAAAAAGGAAGAACCCAGCTGCCAACCTCATTCAG	1020
Db	1175	GAACAAACACCGCCAGAAAACTTTTGAAAAAGGAAGGAAGAACCCAGCTGCCAACCTCATTCAG	1234
Qy	1021	TGTGTTTGGGTAGTTACGCGATGATGAGAAATCTGTTTCCATTCGAACTGGAAGCCCA	1080
Db	1235	TGTGTTTGGGTAGTTACGCGATGATGAGAAATCTGTTTCCATTCGAACTGGAAGCCCA	1294
Qy	1081	CACTTGAAGCCCTTGACACCTTCAGCCCTTACCAAGAAAGAACCAAGGGGAAGCATCAAGC	1140
Db	1295	CACTTGAAGCCCTTGACACCTTCAGCCCTTACCAAGAAAGAACCAAGGGGAAGCATCAAGC	1354
Qy	1141	AGTCAGAAGCTAAGTTTAAAGAGCGAGTCGCGCATGGCTAGCCGCCAGGGGCCAGAGTATT	1200
Db	1355	AGTCAGAAGCTAAGTTTAAAGAGCGAGTCGCGCATGGCTAGCCGCCAGGGGCCAGAGTATT	1414
Qy	1201	AAGAGCCGACAAGCCTCAGTAGTGACAGGAGTCCCCAAGCACCGACATCAGACGCGAG	1260
Db	1415	AAGAGCCGACAAGCCTCAGTAGTGACAGGAGTCCCCAAGCACCGACATCAGACGCGAG	1474
Qy	1261	GGCAGTCCACCAAGTGCAGAGAGCTGGAGCTTCAAACGACCGAACCCCGCTTCCGGCCC	1320
Db	1475	GGCAGTCCACCAAGTGCAGAGAGCTGGAGCTTCAAACGACCGAACCCCGCTTCCGGCCC	1534
Qy	1321	TCGCTGGCCCTCAAAAGTTCTCAGCCAAAACCAACCAAGTATGATGCTGACACAGCCCTTGGC	1380
Db	1535	TCGCTGGCCCTCAAAAGTTCTCAGCCAAAACCAACCAAGTATGATGCTGACACAGCCCTTGGC	1594
Qy	1381	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATCAGTGGGAAGACCTCAAC	1440
Db	1595	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATCAGTGGGAAGACCTCAAC	1654
Qy	1441	CCACCACTTAAACTGTCAATTCAGGCTATCAGAAATTTATGAAATTTTCAATGTCAAAACCG	1500
Db	1655	CCACCACTTAAACTGTCAATTCAGGCTATCAGAAATTTATGAAATTTTCAATGTCAAAACCG	1714
Qy	1501	AAGTTTAAAGGAACGTTTACGTCCTATGATGATAAAGATGTCATTCGAACCAATATTCGTCT	1560
Db	1715	AAGTTTAAAGGAACGTTTACGTCCTATGATGATAAAGATGTCATTCGAACCAATATTCGTCT	1774
Qy	1561	GGTCATCTCGACATGTTGTGTAGAAATTTAAAGCCCTTCAAAACAGCGTGTGATCAAAATTCCT	1620

GENERAL INFORMATION:		Query Match		DB 4; Length 3111;	
APPLICANT: Hu, Yi		97.4%; Score 2625.2;		DB 4; Length 3111;	
APPLICANT: Kieke, James Alvin		Best Local Similarity 98.9%; Pred. No. 0;		DB 4; Length 3111;	
APPLICANT: Turner, C. Alexander Jr.		Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;		DB 4; Length 3111;	
APPLICANT: Nehls, Michael C.				DB 4; Length 3111;	
APPLICANT: Friedrich, Glenn				DB 4; Length 3111;	
APPLICANT: Zambrowicz, Brian				DB 4; Length 3111;	
APPLICANT: Sands, Arthur T.				DB 4; Length 3111;	
TITLE OF INVENTION: No. 6767736e1 Human Ion Channel Protein and				DB 4; Length 3111;	
TITLE OF INVENTION: Polynucleotides Encoding the Same				DB 4; Length 3111;	
FILE REFERENCE: LEX-0160-USA				DB 4; Length 3111;	
CURRENT APPLICATION NUMBER: US/09/825,147				DB 4; Length 3111;	
CURRENT FILING DATE: 2001-04-03				DB 4; Length 3111;	
PRIOR APPLICATION NUMBER: US 60/194,255				DB 4; Length 3111;	
PRIOR FILING DATE: 2000-04-03				DB 4; Length 3111;	
NUMBER OF SEQ ID NOS: 3				DB 4; Length 3111;	
SOFTWARE: FastSeq for Windows Version 4.0				DB 4; Length 3111;	
SEQ ID NO 3				DB 4; Length 3111;	
LENGTH: 3111				DB 4; Length 3111;	
TYPE: DNA				DB 4; Length 3111;	
ORGANISM: homo sapiens				DB 4; Length 3111;	
US-09-825-147-3				DB 4; Length 3111;	
Qy.	1	ATGAAGGATGTGGAGTCGGGCGGGGCGGAGGGTGTGCTGAACCTCGGAGCGCGCGAGGGG	60		
Db	165	ATGAAGGATGTGGAGTCGGGCGGGGCGGAGGGTGTGCTGAACCTCGGAGCGCGCGAGGGG	224		
Qy	61	GAGGCGCTGCTACTGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	120		
Db	225	GAGGCGCTGCTACTGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	284		
Qy	121	AGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	180		
Db	285	AGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	344		
Qy	181	TACAGGATGACAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240		
Db	345	TACAGGATGACAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	404		
Qy	241	TACAACTGCTGGAGAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	300		
Db	405	TACAACTGCTGGAGAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	464		
Qy	301	CTTGCTCTTGGTGTGATTTTGTGAGTGTGATTTTGTGAGTGTGATTTTGTGAGTGTG	360		
Db	465	CTTGCTCTTGGTGTGATTTTGTGAGTGTGATTTTGTGAGTGTGATTTTGTGAGTGTG	524		
Qy	361	GCCTCAAGTTGCCTTGTGATTTTGTGAGTGTGATTTTGTGAGTGTGATTTTGTGAGT	420		
Db	525	GCCTCAAGTTGCCTTGTGATTTTGTGAGTGTGATTTTGTGAGTGTGATTTTGTGAGT	584		
Qy	421	ATCAATTCGAATCTGGTCTGGGCGGTTGCTGTGATTTTGTGAGTGTGATTTTGTGAGT	480		
Db	585	ATCAATTCGAATCTGGTCTGGGCGGTTGCTGTGATTTTGTGAGTGTGATTTTGTGAGT	644		
Qy	481	AGGTTTGTGCGAAAGCCCTTCTGTTTATAGATACCAATTTTGTGAGTGTGATTTTGTG	540		
Db	645	AGGTTTGTGCGAAAGCCCTTCTGTTTATAGATACCAATTTTGTGAGTGTGATTTTGTG	704		
Qy	541	GTTGTTTCTGCGAAAGCCCTTGTGTTTGTGAGTGTGATTTTGTGAGTGTGATTTTGTG	600		
Db	705	GTTGTTTCTGCGAAAGCCCTTGTGTTTGTGAGTGTGATTTTGTGAGTGTGATTTTGTG	764		
Qy	601	TTCTTACAGATCCTCCGATGGTGGCGATGGAGCGGAGGGGAGGACCTTGGAAATTTCTG	660		
Db	765	TTCTTACAGATCCTCCGATGGTGGCGATGGAGCGGAGGGGAGGACCTTGGAAATTTCTG	824		
Qy	661	GGTTTCAGTGGTTTGTGCTCAGAGCAAGGAAATTAATACAGCTTTGGTACATAGGATTTTG	720		

1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
1938 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACTTTTGAATGTGAACAGACATCT 1997
1861 GACTATCAAGCCCTGTGTGATAGCAAGATCTTTGGGTTCCGCAAAACAGTGGCTGC 1920
1998 GACTATCAAGCCCTGTGTGATAGCAAGATCTTTGGGTTCCGCAAAACAGTGGCTGC 2057
1921 TTATCCAGATCAACTAGTGTCCCAACATCTCGAGAGCCCTGCAGTTCATTCTGAGCCCAAT 1980
2058 TTATCCAGATCAACTAGTGTCCCAACATCTCGAGAGCCCTGCAGTTCATTCTGAGCCCAAT 2117
1981 GAGTTCAAGTCCAGACTTTCTACGCGCTTTAGCCCTTACTATGCACAGTCAAGCAACACAG 2040
2118 GAGTTCAAGTCCAGACTTTCTACGCGCTTTAGCCCTTACTATGCACAGTCAAGCAACACAG 2177
2041 GTGCCAAATTAGTCAAGGATGGCTCAGCAGTGGGAGCCACCAACACATTCGCAACCAA 2100
2178 GTGCCAAATTAGTCAAGGATGGCTCAGCAGTGGGAGCCACCAACACATTCGCAACCAA 2237
2101 ATAAATACGGCCACCAAGCCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
2238 ATAAATACGGCCACCAAGCCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2297
2161 GCATCAAGCATCTGCCAGGCGAGAACTCTGCACCCCTTAACCTTCGAGGCTTACAGGAA 2220
2298 GCCATCAGCATCTGCCAGGCGAGAACTCTGCACCCCTTAACCTTCGAGGCTTACAGGAA 2357
2221 AGCATTTCTGAGCTCACCACTGCTTGTGCTTCAAGGAAATTTGTCAGTTCACAG 2280
2358 AGCATTTCTGAGCTCACCACTGCTTGTGCTTCAAGGAAATTTGTCAGTTCACAG 2417
2281 TCAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
2418 TCAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2477
2341 TTGCTGTCTGTGCCATGTGCGGAGGAGCTTTGGGCAAACTTTGCTGTGCAAAACCTG 2400
2478 TTGCTGTCTGTGCCATGTGCGGAGGAGCTTTGGGCAAACTTTGCTGTGCAAAACCTG 2537
2401 ATCAGGTGACCGAGGAACTGAATATCAACTTTTCAGGAGTGTAGTGGCTCCAGA 2460
2538 ATCAGGTGACCGAGGAACTGAATATCAACTTTTCAGGAGTGTAGTGGCTCCAGA 2597
2461 GGCAGCCCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTATTAATGATCAAGAG 2520
2598 GGCAGCCCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTATTAATGATCAAGAG 2657
2521 GTGGGTCCCGAAGACAGACAGACACTTTTGTATGCGCACCGCAGCTGCCAGGGAA 2580
2658 GTGGGTCCCGAAGACAGACAGACACTTTTGTATGCGCACCGCAGCTGCCAGGGAA 2717
2581 GTGGCTTTGATCAGACTCTTAAGGACTGAAGGTGACGATCATCTCAGAGCATTTGT 2640
2718 GTGGCTTTGATCAGACTCTTAAGGACTGAAGGTGACGATCATCTCAGAGCATTTGT 2777
2641 AAGCAGGAGAAAGTACAGATCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2694
2778 AAGCAGGAGAAAGTACAGATCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2831

RESULT 5
US-09-949-016-1823
; Sequence 1823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1823
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1823

Query Match 19.2%; Score 518.4; DB 4; Length 2196;
Best Local Similarity 60.1%; Pred. No. 1.2e-143;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;
QY 217 TACCGCGGGTGCAGAACTACCTGTACAAACGTGTGGAGAGACCCCGGGCTGGCGTTTC 276
Db 181 TACCGCGCGCTGCAGAACTGGGGGTACAAAGTGTGGAGCGGCCCGCGCTGGCGTTTC 240
QY 277 ATCTACACGCTTTCTGTTTCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 336
Db 241 GTCTACCAAGCTTTTCTATATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 300
QY 337 ACCATCCCTGAGCAGACAAATTTGCCCTCAAGTTGCCCTTGTATCTCGAGTTCGTGATG 396
Db 301 ACTATCCAGGAGCACAGGAACTTGCACCAAGAGTGTCTCTCATCTTGGAAATTCGTGATG 360
QY 397 ATTGTGCTTTTGGTGTTCATCATTCGAATCTGCTCTGCGGGTGTCTGTTGTTGTTGTTGTT 456
Db 361 ATCTGTTGTTTGGGCTTGGAGTACATCTGTCGGGTCTGTCGCGGAGTCTGCTGCTGCCG 420
QY 457 TATGAGAGTGGCAGGAGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 516
Db 421 TACCGAGATGGCAGGCTCGCTTCGGCTTTGCCAGAAAGCCCTTCTGTGTCTATCGACTTC 480
QY 517 ATTGTCTTATCGCTTCAATAGCAGTGTCTTCTGCAAAACCTCAGGGTAAATATTTTGGC 576
Db 481 ATCTGTTGTTGCTCGCTCGGTGCGCTCATCGCGCGGGTACCCAGGGCAACATCTTCGCC 540
QY 577 ACGTCTGCACTCAGAACTCTCGTTTCTCAGATCTCTCCGATCTCCGATGGTGGCAGACCGA 636
Db 541 ACGTCTCGGCTGCGCAGCATCGCTTCTGTCAGATCTCTGCGCATGCTGCGCATGACCGC 600
QY 637 AGGGAGGACCTTGGAAATTAAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 696
Db 601 CGCGCGGACCTGGAAGCTCTGGGCTCAGTGTGTACGCGCATAGCAAGGAGCTGATC 660
QY 697 ACAGCTTGGTACATAGGATTTTGGTCTTATTTTCTGTTCTTCTTCTGTTCTATCTGGTG 756
Db 661 ACCGCTGGTACATCGGGTCTCTGTTGTTCTATCTTCGGCTCTTCTGTTCTACCTGGCT 720
QY 757 GAAAGGATGCCAATAAAGATTTTCTACATATGAGATGTTCTCTGTTGTTGTTGTTGTTGTT 816
Db 721 GAGAAGGACGCCAATCTCGACTTCTCTCTCTAGCGCGACTCGCTCTGTTGTTGTTGTTGTTGTT 780
QY 817 ACATTGACACTATTTGGCTATGGAGCAAAACTCCCTTAACCTGCTGGGAGATGTTCTT 876
Db 781 ACATTGACACCATCGGCTATGGTGAAGACACCGCACACATGGCTGGGAGGTTCTCTG 840
QY 877 TCTGAGGCTTTGCACTCTCTTGGCATTTCTTTTCTGTTCTTCTGCTGCTGCTGCTGCTGCT 936
Db 841 GCTGCTGGCTTTCGCTTACTGGGCACTCTTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 937 TCAGGTTTTCGATTAAGAGTCAAGAACCAACACCGCCAGAAACACTTTTGGAGAAAGAGG 996
Db 901 TCCGCTTTTGGCTTGAAGTCCAGGAGCAGCACCGGAGAGAGCACTTCGAGAGAGCGGAGG 960
QY 997 AACCCAGTCCGCAACCTCATTCAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1056
Db 961 ATCGCGGAGGCAACCTCATCCAGGCTGCTTGGGCTGTTACTCCACCGATATGAGCCGG 1020

Patent No. 6794161
GENERAL INFORMATION:
APPLICANT: JENTSCH, Thomas J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
FILE OF INVENTION: POTASSIUM CHANNELS
FILE REFERENCE: 2815-127P
CURRENT APPLICATION NUMBER: US/09/492,361
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2335
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(2335)
NAME/KEY: CDS
LOCATION: (83)..(2170)
US-09-492-361-1
Query Match 19.2%; Score 518.4; DB 4; Length 2335;
Best Local Similarity 60.1%; Pred. No. 1.3e-143; Indels 165; Gaps 8;
Matches 1103; Conservative 0; Mismatches 566;
217 TACCGCGGCTGCAGAACTTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGCGCTTC 276
Db TACCGCGGCTGCAGAACTTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGCGCTTC 379
277 ATCTACCAAGCTTTCGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 336
Db ATCTACCAAGCTTTCGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 439
380 GTCTACCAAGCTTTCGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 499
337 ACCATCCCTGAGCACACAAATTTGGCTTCAAGTTTGCCTTTCCTTTCCTTTCCTTTCCTTTC 396
Db ACTATCCAGAGCACACAAATTTGGCTTCAAGTTTGCCTTTCCTTTCCTTTCCTTTCCTTTC 499
397 ATTGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 456
Db ATTGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 559
500 ATCGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 516
457 TATAGAGGATGGCAAGAAAGACTTGTCTTCAAAAGCCCTTCTTGTGTATAGATAC 619
Db TACGAGGATGGCAAGAAAGACTTGTCTTCAAAAGCCCTTCTTGTGTATAGATAC 619
517 ATTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 576
Db ATTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 679
620 ATCGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 636
577 ACCTTCTCAGTCTGAGAGTCTTCCGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 739
Db ACCTTCTCAGTCTGAGAGTCTTCCGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 739
637 AGGGAGGCACTTGGAAATTTACTTGGGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 696
740 CGCGCGGCACTTGGAAATTTACTTGGGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 756
697 ACAGCTTGTATACATAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 859
800 ACCGCTTGTATACATAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 816
757 GAAAGAGTGCATAAAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 919
860 GAGAGAGTGCATAAAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 876
817 ACATTGCAACTATTTGGCTATGGAGACAAACTCCCTTAACTTGGCTTGGGAGAGTCTTCTT 979
920 ACATTGCAACTATTTGGCTATGGAGACAAACTCCCTTAACTTGGCTTGGGAGAGTCTTCTT 936
877 TCTGAGGCTTGTGACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1039
980 GCTGCTGCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT

1057 GTTTCATTCGAACTTGGAGGACCACTTGAAGGCTTTCACACCTTCGAGC----- 1107
Db GTTTCATTCGAACTTGGAGGACCACTTGAAGGCTTTCACACCTTCGAGC----- 1080
1021 GCCTACCTGACAGCCACTTGTACTATGACAGTATCTCCATCTTCAGAGCTG 1080
1108 CCTACCAAGAAAGCAAGGGGAGCATCAAGCAGTCAGAAGCTA----- 1152
Db CCTACCAAGAAAGCAAGGGGAGCATCAAGCAGTCAGAAGCTA----- 1140
1081 GCCCTCTTGTGTAGCACGTGCAACGGGCCCGCAATGGGGCTCAGGCCCTCGAGGTG 1140
1153 ----- 1152
1141 CGGCGGCGCGGTACCCGAGGAGCACCTCCCGTTACCCGCGCTTGCACCTCCAC 1200
1153 -----AGTTTAAAGGAGCA 1167
1201 CGGCGGCGGACACCTCTTCTTGCCTTGGGAAAGCAGCGGATGGCATCAAGACCGC 1260
1168 GTGCGCATGGCTAGCCCGAGGGGCGAGA-----GTATTAAAGCCGACAAAGCTCAGTA 1221
Db GTGCGCATGGCTAGCCCGAGGGGCGAGA-----GTATTAAAGCCGACAAAGCTCAGTA 1220
1261 ATCCGCATGGCAGCTCCAGCGCGGAGCGGTCTTCCAAAGCAGCATCTGGCACCTCCA 1320
1222 GGTGACAGGAGGTCCCAAGCACGACATCACAGCCGAGG---GCAGTCCACCAAGTG 1278
Db GGTGACAGGAGGTCCCAAGCACGACATCACAGCCGAGG---GCAGTCCACCAAGTG 1278
1321 ACAATGCCACCTCCCAAGCAGCGAGGAGGTGGTGGGCGGATGCCCCCTTCCGAGACTC----- 1434
1279 CAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCCGCGCTTCCGCGCTTCAAAAGT 1338
Db CAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCCGCGCTTCCGCGCTTCAAAAGT 1338
1381 CAAAGAGCTGAGCTTCAATGACCGCACCCGCTTCCGCGCTTCCGAGACTC----- 1434
1339 TCTAGCCCAAAACCAAGTATGATGTGACACAGCCCTTGGCAGTATGATATGAT 1398
Db TCTAGCCCAAAACCAAGTATGATGTGACACAGCCCTTGGCAGTATGATATGAT 1398
1435 -----AAACCCCGCACCTTCTGCTGAGGATGCCC---CCTCAGAGGAGTATGACAG 1482
1399 GAAAGAGTGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1458
Db GAAAGAGTGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1458
1483 GAGAGAGCTACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1542
1459 ATTGAGCTATCAGAAATTTATGAAATTTATGAAATTTATGAAATTTATGAAATTTATGAAAT 1518
Db ATTGAGCTATCAGAAATTTATGAAATTTATGAAATTTATGAAATTTATGAAATTTATGAAAT 1518
1543 ATCCGCTCCATCAGGATCTCAAGTTCTCAAGTTCTCAAGTTCTCAAGTTCTCAAGTTCTCAAG 1602
1519 CGTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1578
Db CGTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1578
1603 CGACCGTACGCTGAGGAGCTCATGAGCAGTACTCAGCAGGCTCAGCAGGCTCAGCAGGCTCAG 1662
1579 TGTAGAAATTTAAAGCTTCAAAACAGCTGTTGATCAAAATTTTGGGAAAGGCT---AAATC 1635
Db TGTAGAAATTTAAAGCTTCAAAACAGCTGTTGATCAAAATTTTGGGAAAGGCT---AAATC 1635
1663 GGCCTGATCAAGAGCTGCAAACTCGGGTGGACCAAAATTTGGGTCGGGGCGCCGGGAC 1722
1636 ACATCAGATAGAGAGCGGAGGAAATAACAGCAGACATGAGACACAGACATCTC 1695
1723 AGGAAGCGCGGAGAGGCGGCAAGGGGCTTCCGCGCGGAGGTGGTGAATGAATC 1782
1696 AGTATGCTCGCTCGGCTGAGTCAAGGTTGAAAGAGGTAAGTCAAGTCAAGTCAAGTCAAGTCA 1755
Db AGTATGCTCGCTCGGCTGAGTCAAGGTTGAAAGAGGTAAGTCAAGTCAAGTCAAGTCAAGTCA 1755
1783 AGCATGATGAGAGCGGCTGAGTCAAGTGGAGAGCAGTGCAGTCCATCAGCAGCAAGCTG 1842
1756 GACTGCTTACTAGACATCTATCAAGAGTCTTTCGGAAGGCTTCTGCTCAGCCCTCGCT 1815
Db GACTGCTTACTAGACATCTATCAAGAGTCTTTCGGAAGGCTTCTGCTCAGCCCTCGCT 1815
1843 GACTGCTTGTGGCTTCTATTCGCGCTGCTGCTG-----GCTCTGGCAGCTTGGCCAGC 1896
1816 TTGCTTCTTCCAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT 1875
Db TTGCTTCTTCCAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT 1875
1897 CTGGGCGCGTGAAGTGGCGCTGTTGACCCCGACATCACTCCGACTACCAAGCCCT 1956
1876 GTGATAGCAAGATCTTTCGGGTTCCGCAAAA 1909
Db GTGATAGCAAGATCTTTCGGGTTCCGCAAAA 1909
1957 GTGGACCAAGGACATCTCGTCTCCGACAGA 1990

Db 607 TTGCAATCTTGGGATGATCCGTATGACCGGAGGGTGGCACTGGAAGCTTTGGGA 666
Qy 664 TCAGTGGTTTATGCTCAGACGAGGAATTAATACACAGCTTGTGTACATAGGATTTTGGTT 723
Db 667 TCGGTAGTCTACGCTCAGACGAGGAGCTGGTACCTGCTGTGTACATTTGGCTTCTCTGC 726
Qy 724 CTTATTTTTCCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
Db 727 CTATCTTGGCTTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
Qy 784 ACATATGAGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
Db 787 ACCTACGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
Qy 844 AAAATCTCCCTAACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
Db 847 AAGTACCTCAGACTGGAACGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
Qy 904 TCTTTCTTTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
Db 907 TCGTTCTTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
Qy 964 CAACACCGCCAGAAACATTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1023
Db 967 CAGATCGGCAAAACATTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1026
Qy 1024 GTTTGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047
Db 1027 GCTGAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
Qy 1048 ---GAGAAATCTGTTTCCATTCGAACCTGGAAGCAACATTTGAAGGCTTGCACACTGC 1104
Db 1087 TAGACGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
Qy 1105 AG-----CCTACCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1159
Db 1147 AGACTCATCCACTCTGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
Qy 1160 AGGAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1219
Db 1207 CTCACCTTAGGAAGGAGCCAGACAGGCAATCACCAGCCGCTGCTGCTGCTGCTGCTGCT 1266
Qy 1220 TAGGTACAGAGGCTCCAGACCGACGACATCACAGC----- 1256
Db 1267 AAGGAAAGGGTCTCCCGAGGCTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
Qy 1257 ---CGAGGAGTCCACAAAGTGCAGAGAGCTGGAGCTTCAAAGCCGAAACCGCTTC 1314
Db 1327 CTTGATACAGCCGAGCAGGAGTGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
Qy 1315 CGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1374
Db 1387 CGCAGGCTTTCCGCATCAAGGGTGTGCTATCCCGGAGGATTCAGAGAGCAAGCAAGCTTC 1446
Qy 1375 CTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1434
Db 1447 CTTGGGAGGAGCATGCTAGAGCAACAAGAGCTGTAACCTGCGAGTTTGTGACTGAAGAT 1506
Qy 1435 CTCACCCCAACCACTTAACTGTCTGAGCTATCAGAAATTAAGAAATTTATGTTGCA 1494
Db 1507 CTTACCCCTGGCTCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1566
Qy 1495 AAACGGAATTTAAGCAACGTTTACCTATGATGATGATGATGATGATGATGATGATGATGAT 1554
Db 1567 AAGCGAAAGTTCAAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1626
Qy 1555 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1614
Db 1627 TCGGCTGAGACACTTGGATATGTTGCTCCGCAATCAAGAGCTTGCAGACCAAGTGCAG 1686
Qy 1615 ATTCTTGAAGAGGCAATCATCATCAGATGAGAGAGCCGAGAGAGAAATTAACAGCAGAA 1674
Db 1687 ATTGTGG 1743

Qy 1675 CATGACACACAGACGATCTCAGTATGCTCGGTGCTCAAGTTTGAAGAAACAGGTA 1734
Db 1744 ACGGAGTCCCGGAGACAGCCAGCATGATGGAGCTTGGAGAGTGGAGAAACAGGTC 1803
Qy 1735 CAGTCCATAGAGTCCAGCTGGAGCTGCTTACTAGACATCTATCAACAG 1782
Db 1804 TTGTCCATGGAAGAGCTCGACTTCTTGGTGGAGCATCTATACACAG 1851

RESULT 8
US-09-105-058C-22
; Sequence 22, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanz, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; TITLE OF INVENTION: KNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
US-09-105-058C-22

Query Match 18.9%; Score 510; DB 3; Length 2169;
Best Local Similarity 58.1%; Pred. No. 3.9e-141;
Matches 1043; Conservative 0; Mismatches 670; Indels 81; Gaps 5;

Qy 64 GGCTGCTACTGTGGGCAACCGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 123
Db 67 GGCTTCTGGGGCTGAGACCCCGCGCGCGCGGCTCCACACGCGGCGGCGGCTACTCATC 126
Qy 124 GAGAGCGCGCGGGAAGAGGAGGCGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
Db 127 GCGGGCTCCAGGCGCGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186
Qy 184 ACGAGTAGCCAGAGCTGCGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
Db 187 GGAGCGGGAAGCGCGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246
Qy 244 AACGTGCTGAGAGACCGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
Db 247 AACGTGCTGAGAGCGCGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306
Qy 304 GTCTTTGGTTCCTTGAATTTTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
Db 307 GTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
Qy 364 TCAAGTTCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
Db 367 GAGGCGGCGCTCTACATCTTGGAAATCGTACTATCGTGTGCTGCTGCTGCTGCTGCTGCT 426
Qy 424 ATTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
Db 427 GTGAGATCTGGGCTGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
Qy 484 TTTGCTCGAAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
Db 487 TTTGCGAGGAAAGCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
Qy 544 GTTCTCTGCAAAACTCAGGGTAATATTTTGGCAGCTGTGCACTGCAAGTCTCCGTTTC 603

Db 547 CTGGTGTGTTCTCCAGGCGCAATGTCTTTGGCCATCTGCGCTTCGGAGCTTGGGGTTC 606
Qy 604 CTACAGATCTCCGCGATGTCGCGATGGACCGAAGGGGAGGCACCTTGGAAATTAATCTGGGT 663
Db 607 TTGCAATCTTCGGGATGATCGTATGGACCGGAGGGTGGCACCTTGGAAAGCTCTTGGGA 666
Qy 664 TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTACATAGGATTTTGGTT 723
Db 667 TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGCGCTGTACATTTGGCTTCTCTGC 726
Qy 724 CTTATTTTCTGTTCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTT 783
Db 727 CTCATCTCTGGCTCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTT 786
Qy 784 ACATATGAGATGCTCTGTTGGGGGCAAAATTAATGACAACTATTGGCTATGAGAC 843
Db 787 ACCTAGCAGATGCACTCTGGTGGGCTGTGATCACCTGACACCAATTTGGCTTACGGGAC 846
Qy 844 AAAAATCCCTAACCTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCTCTGGCAAT 903
Db 847 AAGTACCCTCAGACCTGGAACGGAGGCTGTGGCAGCGACCTTTACCTCATTTGTTGTC 906
Qy 904 TCTTTCTTGGATCTCTGCGGCAATCTTGGCTCAGGTTTGGCAATTAAGTAAAGTAAAGAA 963
Db 907 TCGTTCTTGGCTCTCTGCTGGCAATTTTGGGATCCGGCTTTGGCCCTGAAAGTCCAAGAG 966
Qy 964 CAACACCGCCAGAAACACTTTGAGAAAGAAAGCAAGCCAGCTGCGCACTCATTCAGTGT 1023
Db 967 CAGCATCGGCAAAACACTTTGAGAAACGGCGGAACCTTGGCGAGGCTGTGATCAGTCT 1026
Qy 1024 GTTTGGCGTAGTTACGCACTGATGAGAAAT----- 1054
Db 1027 GCCTGGAGATTCTATGCTACTAACTCTCAGCAGCGACCTGCACTCCAGCTGGCAGTAC 1086
Qy 1055 -----CTGTTTCCATTTGCAACCTGGAAGCCACACTTGAAGGCTTTGCAAC 1098
Db 1087 TACGAGCGGACAGTCACTGTCCCATGTACAGACTCATCCCACTCTGAAACCAAGCTGGAG 1146
Qy 1099 ACCTCAGCCCTACCAAGA----- 1131
Db 1147 CTGTGAGGAATCTCAAGAGCAAAATCTGGACTCCTCAGGAAGGAGCCAGCCAGAG 1206
Qy 1132 GCATCAAGCAGTCAGAAAGTAAAGTAAAGGAGCGAG---TGCGCATGGCTAGCCCGCAGG 1188
Db 1207 CCATCAAGAGTCAGAAAGTCAAGTCTGTTGAAAGATCGTGTCTCTCAGCCCCCGAGCATG 1266
Qy 1189 GGCAGAGATTAAGAGCCGCAAGCCCTCAGTGTGAGAGGTCGCCAAGCAAGCCAGC 1248
Db 1267 GGTGCAAGGAAAGGGGTCTCCCGAGGCCAGAGCGGTCCGCGGTCCCGCAGTCCGGAT 1326
Qy 1249 ATCAGAGCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACC 1308
Db 1327 CAGAGTCTTGTATGACAGCCGAGCAAGGTGCCAAGAGCTGAGCTTTGGTACCGCAGC 1386
Qy 1309 CGCTTCGGCCCTCGCTCGGCTCAAAAGTTCTCAGCCAAAACCAAGTGTATGATGCTGAC 1368
Db 1387 CGCACAGCCAGGCTTTCCGATCAAGGGTGTGATCCCGCAGAAATTCAGAACAGC 1446
Qy 1369 ACAGCCCTTGGCAGTGTATGATATGATGAAAGAGATGCCAGTGTGATGATGATGATG 1428
Db 1447 C---TCCCTGGGGAGGACATCGTAGAGGACAAAGAGCTGTAACTGGAGTTTGTGACT 1503
Qy 1429 GAAGACCTCACCCCACTTAAACTGCTATTCTGAGCTATCAGAAATTAATGAAATTTTCAAT 1488
Db 1504 GAAGATCTTACCCCTGGGCTCAAGTTAGCATCAGAGCTGTGTGTTTATGCGGTTCTTG 1563
Qy 1489 GTTGCAAAACGGAAGTTTAAAGAAACGTTTACGTCATATGATGTAAGAGATGTCATTGAA 1548
Db 1564 GTATCTAAGCGAAAGTTCAAAGAGAGTCTGCGCCCATATGATGATGATGATGATGATG 1623
Qy 1549 CAATATCTGCTGTCATCTGGACATGTTGTGTAGAAATTAAGGCTTCAACACAGCTGTT 1608

Db 1624 CAGTACTCGGCTGGACACTTGGATATGTTGTCCGCGCATCAAGAGCTTCAGTCCAGAGTG 1683
Qy 1609 GATCAAAATTTCTGGAAGGGCAATACATCAGATAGAGAGCGGAGAGAAATAACA 1668
Db 1684 GACCAGATTTGGGGCGGGGCCCAACAATAACGGATAAGGA---TCGCACCAAGGCCCA 1740
Qy 1669 GCAGAAATGAGACACACAGCATCTCAGTATGCTCGGTTCGGGTGGTCAAGGTTGAAAAA 1728
Db 1741 GCGGAAACGGAGCTGCCCGAAGACCCAGCATGATGGGACGGCTTTGGGAAGGTGGAGAA 1800
Qy 1729 CAGGTACAGTCCATAGATCCAAAGCTGAGCTGCCTACTAGACATCTATCAACAG 1782
Db 1801 CAGGTCTTGTCCATGAGAAAGAGCTCGACTTCTTGGTGAGCATCTATACACAG 1854

RESULT 9

US-09-495-050A-303
; Sequence 303, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Yang, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; PRIORITY FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIORITY FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1
US-09-495-050A-303

Query Match 18.9%; Score 509.8; DB 4; Length 582;
Best Local Similarity 99.4%; Pred. No. 1.8e-141;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 1621 GGAAAGGGCAATACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAACATGAG 1680
Db 1 GGAAGGGCAATACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAACATGAG 60
Qy 1681 ACCAGACGATCTCAGTATGCTCGGTGGGTGAGTTCAGAGTTGAAAAACAGGTACAGTCC 1740
Db 61 ACCAGACGATCTCAGTATGCTCGGTGGGTGAGTTCAGAGTTGAAAAACAGGTACAGTCC 120
Qy 1741 ATAGAGTCCAGCTGGAGTGCCTACTAGACATCTATCAACAGCTCCTTCGGAAAGGCTCT 1800
Db 121 ATAGAAATCCAGCTGGAGTGCCTACTAGACATCTATCAACAGCTCCTTCGGAAAGGCTCT 180
Qy 1801 GCCTCAGCCCTCGCTTTGGCTTCATCCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
Db 181 GCCTCAGCCCTCGCTTTGGCTTCATCCAGATCCACCTTTTGAATGTGAACAGACATCT 240
Qy 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCGCGCAAAAAACAGTGGCTGC 1920
Db 241 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCGCGCAAAAAACAGTGGCTGC 300
Qy 1921 TTATCCAGATCACTAGTGCCAAATCTCGAGAGGCTTCGAGTTCAATTCGACGCAAT 1980
Db 301 TTATCCAGATCACTAGTGCCAAATCTCGAGAGGCTTCGAGTTCAATTCGACGCAAT 360
Qy 1981 GAGTTCAAGTCCAGACTTTCTAGCGCTTACGCTTACTATGACAGTCAAGCAACAG 2040
Db 361 GAGTTCAAGTCCAGACTTTCTAGCGCTTACGCTTACTATGACAGTCAAGCAACAG 420
Qy 2041 GTGCCAATTAGTCAAGAGGATGGCTCAGAGTGGCAGCCCAACACCAATTTGCAAAACAA 2100

Db	429	AIYYTECGSATGWTSCGBATGGACCGGMRGGHGGCACCTGGAAAGCTBYTGGGWTCDGYV	488
Qy	670	GTATTGCTCACAGCAAGAAATTAATCAAGCTTGGTACATAGGATTTTGGTTCATT	729
Db	489	RUCTRYCYCACAGCAARGACTSRTSACKGSGTGTCATAYGTYTCTTBWSHCTCATC	548
Qy	730	TTTTGCTCTTTCCTTGCTCTATCTGGTGGAAAAGGATCCCAATAAGAGTTTTTCTACATAT	789
Db	549	CTKKCVTCRTTYTKGTSTACYTGGYWGAPAAASDGAWRBGAYSNMWYTGASACCTAY	608
Qy	790	GCAGATGCTCTCGTGGGSCACAAATFACATTGACAACTATTCGGCTATGGAGACAAACT	849
Db	609	GCRGATGCMCTTGGTGGGGYCTGATCACVCTGRCVACCATTGGCTAYGGRGACAAGMM	668
Qy	850	CCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTCGACCTCTTGGCATTTCTTTC	909
Db	669	CCYNARACSTGGRAMGSGMKCSHTDGGCGVCACSTTYWCCTMATYGGYGTCTCVTY	728
Qy	910	TTTGCACTTCTCGCGGCATTTCTGGCTCAGTTTTCGATTAAGAATACAGAACACAC	969
Db	729	TTYGCBCTKCGWCGDGCATVYTGGRCTCYGSGYTKGCCCTSAARGTBECARGACARAY	788
Qy	970	CGCCAGAAACACTTTTGAGAAAAGGAAGAACCCAGCTCCACACCTCATTCACTGTGTTTGG	1029
Db	789	MGKCARAARCACTTTGAAAFMGMGGAABCCDGDGCGHRETSATYCAKCKGCGCTGG	848
Qy	1030	CGTAGTTACGCAGCTGA	1046
Db	849	AGRTWYTYAGCYACVAA	865

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RESULT 11
US-09-177-650-90
; Sequence 90, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (202)..(2811)
US-09-177-650-90

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	Query Match	17.2%;	Score 454;	DB 3;	Length 2814;	
	Best Local Similarity	57.9%;	Prd. No. 2.5e-127;	Indels	66;	Gaps 5;
	Matches 952;	Conservative	3;	Mismatches 623;		
Qy	15	GTGGGCGGGCGAGGTGCTCTGAACTCGGCGACGCCAGGGCGCAGCGCTCTGTACT	74			
Db	294	GGCGGTGGCCGGCGACGAGGACCGAAGTGGGGTGGCGCCAGGAGACGTGGAGCAAGT	353			
Qy	75	GCTGGGCACCCGCGGGCCACCTTTGGTGGCGGCGCGGTGGCTGTGAGGAGAGCGCCG	134			
Db	354	CACCTTGGCGCTAGGGCCCGGACGCCACAAAGACGGGACCTGTGCTGGAGGGCGGTGG	413			
Qy	135	GGGCAGACAGGGGGCCCGGATGAGCTGCTGGGGGAAGCGGTCTCTTTACAGAGTAGCCA	194			
Db	414	CCGCGAAGAGGGCGACAGGAGGACCCCGCAGGGGCATCTGGGTCTCTGGCAAGACCCCCCT	473			

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Db      421 GTGCCAATTAGTCAAAAGCGATGGCTCAGAGTGCGAGCCACCAACACCATTTGCAAACCAA 480
QY      2101 ATAAATACGGCCACCCCAAGCCAGCCAGCCCCAACCAACTTTACAGATC 2145
Db      481 ATAAATACGGCCACCAAAAGCCAGAG-CCCAACAACCTTTACAGATC 524

RESULT 10
US-09-105-058C-1
; Sequence 1, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Bianar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIORITY FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificeal Sequence:Consensus
; OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
; OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
; OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
; US-09-105-058C-1

```

[illegible]

QY	195	GAGCTGCC-----GGCCCAAGTCAAGTACGGCGGGTCGAGAACTACCTGTACAA	245
DB	474		533
QY	246	CGTGTGGAGAGACCCCGCGCTGGCGGTTTCATCTACCACGCTTTCGTTTTCTCCTTGT	305
DB	534		593
QY	306	CTTTGGTTTGTGATTTTGTTCAGTGTTCATCCATCCCTGAGCACACAAATTTGGCCTC	365
DB	594		653
QY	366	AAGTTTGCTTTCATCTCGGAGTTTCGTGATGTTTCGTTTCGTTTGGAGTTTCATCAT	425
DB	654		713
QY	426	TCGAATCTGTGCTCGGGTTTCTGTTGCGATATAGAGGATGGCAAGAGACTGAGGTT	485
DB	714		773
QY	486	TGCTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATCGCTTCAATAGCAGTTGT	545
DB	774		833
QY	546	TTCTGCAAAACTCAGGTTAATTTTGGCACGTCCTGCACCTCAGAGTCTCCGTTTCCT	605
DB	834		890
QY	606	ACAGATCTCTCGCATGTGTGCGATCGACCGAAGGGGAGGCACCTTGGAAATTTACTGGGTTTC	665
DB	891		950
QY	666	AGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTACATAGGATTTTGTGTTCT	725
DB	951		1010
QY	726	TATTTTTTCGTTTCCTTGTCTATCTGTTGGAAGGATG-----	766
DB	1011		1070
QY	767	-----CCAATAAGAGTTTTCTCATATGCAGATGCTCTCTGGTGGGGCACAAT	815
DB	1071		1130
QY	816	TACATTGCAAACTATTGGCTATGAGACAAAACCTCCCTTAATCTGGCTGGGAAGATGCT	875
DB	1131		1190
QY	876	TTCTCGAGGCTTTGCACCTCTCTGCAATTTCTTTCTTTCGCACTTCCTCCCGGCAATCTTGG	935
DB	1191		1250
QY	936	CTCAGGTTTTGCATTAAGGTACAAAGAACACACCGCCAGAAAACTTTTCAGAAAAAGAAG	995
DB	1251		1310
QY	996	GAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTTACGCACTGATGAGAAATC	1055
DB	1311		1370
QY	1056	TGTTTTCCATTGCAACCTTGAAGGCACACTTGAAGGCCCTGCACACCTGCAGCCCTACCAA	1115
DB	1371		1430
QY	1116	GAAGAACAAGGGGAAGCATCAAGCAGTTCAGAGCTAAGTTTTTAAGGAGCGAGTGGCGCAT	1175
DB	1431		1490
QY	1176	GGCTAGCCCCCAGGGCCAGAGTATTAGAGCCGCAAGCCCTTCAGTAGGTGACAGGAGGTC	1235
DB	1491		1532
		-----AGGAAGCTATTTCAC	1532

Qy	1236	CCCAAGCAGCCGACATCATCAGCGGAGGCGAGTCCCAACAAAAGTCAGAAAGAGCTGGAGCTT	1299
Db	1533	CCCTCTGAATGTAGATGCCATAGAAAGAACCCCTTCCAAAGAGGCCAAAGGCTGTGTGGCTT	1592
Qy	1296	CAACGACCGAACCCGGCTTCGGCCCTCGCTGCGGCTCAAAAGTTCTCAGCCAAAACCCAGT	1355
Db	1593	AAACAATAAGAGGGTTTCCGCACCGCTTCCGCATGAAAGCCTACGCTTCTTGGCAGAG	1652
Qy	1356	GATAGATGCTGACACAGCCCTTGGCACTGATGATGATATGATGAAAGAGATGCCAGTG	1415
Db	1653	WTCTGAAGATGCTGGGACAGCGACCC-----CATGGCAGAAGACAGGGGCTATGGGAA	1706
Qy	1416	TGATGTATCAGTGAAGAACCTCACCCACACATTTAAACCTGCTATTGAGAGCTATCAGAAT	1475
Db	1707	TGACWTCTCTCATTTGAGACATGATCCCTCCCTTAAAGGCTGCCATCCGAGCTGTGAGAAT	1766
Qy	1476	TATGAAATTTTCATGCTTCAAAACGGAAGTTTAAAGGAAACGCTTACGTCATATGATGTAAA	1535
Db	1767	TCTACAGTTCGCTCTATATATAAAAAAGTTCAAGAGAGACGTTGAGGCTTTATGATGTAA	1826
Qy	1536	AGATGTCAITTGAAACAATTTCTGTGCTCATCTGGACATGTTGTGTAGAAATTTAAAGCCCT	1595
Db	1827	AGATGTGATTGAGCAGTATTCGCGCGACATCTTGACATGCTTTCCAGGATAAAGTACCT	1886
Qy	1596	TCAACACAGCTGTGATCAAAATTCT	1619
Db	1887	ACAGACAAGAATAGATGATTTT	1910
RESULT 12			
US-09-105-058C-26			
; Sequence 26, Application US/09105059C			
; Patent No. 6403360			
; GENERAL INFORMATION:			
; APPLICANT: Blonar, Michael A.			
; APPLICANT: Dworetzky, Steven			
; APPLICANT: Gribkoff, Valentin K.			
; APPLICANT: Levesque, Paul C.			
; APPLICANT: Little, Wayne A.			
; APPLICANT: Neubauer, Michael G.			
; APPLICANT: Yang, Wen-Pin			
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME			
; FILE REFERENCE: 3053-4052			
; CURRENT APPLICATION NUMBER: US/09/105,058C			
; CURRENT FILING DATE: 1998-06-26			
; PRIOR APPLICATION NUMBER: US 60/055,599			
; PRIOR FILING DATE: 1997-08-12			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: Patent In Ver. 2.1			
; SEQ ID NO 26			
; LENGTH: 2565			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-105-058C-26			
Query Match 17.1%; Score 460.8; DB 3; Length 2565;			
Best Local Similarity 57.9%; Pred. No. 2.2e-126;			
Matches 953; Conservative 0; Mismatches 627; Indels 66; Gaps 5;			
Qy	13	GAGTTCGGGCGGGGCGAGGGTGTGCTGAATCTCGGCAGCCGCCAGGGGCGACGCCCTGTCTA	72
Db	43	CGCGCGCGCGCGCGACGAGGAGCGMAAGTGGGGCTGGCGCCCGCGACGCTGGAGCAA	102
Qy	73	CTGCTGGGCACCCGCGGGCCACGCTTGTGGCGGGCGGGTGGCTTGAGGGAGAGCCGC	132
Db	103	GTCACTTTCGCTTCGGGGCGGAGCGCAAAAGACGGGACCCCTGCTGTGGAGGGCGGC	162
Qy	133	CGGGGCAAGCAGGGGGCCGGATGAGCCTCTCGGGAAGCCGCTCTTACACGAGTAGC	192
Db	163	GGCCGCGACAGGGGCGAGCGAGAGACCCCGCAGGGCATCGGGTCTCTGGCCAAAGACCCCG	222
Qy	193	CAGAGCTGCC-----GGCGCAACGTCGAAGTACCGCGGGGTGAGAACTACCTGTATC	243

Db 223 CTGAGCGCCAGTCAAGAGAACAAACGCAAGTACCGCGGCATCCAAACTTTGATCTAC 282
Qy 244 AAGTGTGTGAGAGACCCCGCGCTGGCGTTTCATCTACACGCTTTCGTTTTTCTCCTT 303
Db 283 GAGCGCTGTGAGAGACCGCGCGCTGGCGTTCATCTACACGCTTTCGTTTTTCTCCTT 342
Qy 304 GTCTTTGGTTGCTGATTTTGTTCAGTGTGTTTCTACCATCCCTGAGCACACAAATTTGGCC 363
Db 343 GTCTTGGGTGCTTGATTTCTGGCTGCTCTGACACACATTCAGAGATGAGACTGTCTCG 402
Qy 364 TCAAGTTGCTCTTTGATCTCTGAGTTCGTGATGATGCTGCTTTGGTTTGGATTCATC 423
Db 403 GGAGACTGGCTTCTGTTACTTGGAGACATTTGCTATTTTCTTTTGGAGCCGAGTTTGT 462
Qy 424 ATTCCGATCTGCTGGGTGCTGTTGTCGATATAGAGATGGCAAGAGACTGAGG 483
Db 463 TTGAGGATCTGGCTGCTGATGTTGCTGCGATACAAAGCTGCGGGCCGACTGAAG 522
Qy 484 TTTCGCTGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATGCTTCAATAGAGTT 543
Db 523 TTTCGAGGAAGCCCTGCTGATGTTGACATCTTTGCTGATTTGCTCTGTGCCAGTG 582
Qy 544 GTTCTGCAAAAATCTCAGGGTAATATTTTTCGACGCTGCACTCAGAGCTCTCCGTTTC 603
Db 583 GTTGTGTGGGAAACCAAGGCAATGTTCTGGCCACCT---CCCTGCGAAGCCTGCGCTTC 639
Qy 604 CTACAGATCTCCGATGCTGCGATGGACCGAAGGGGAGGCACTTGGAAATTAATCTGGGT 663
Db 640 CTGCGAGATCTTGGCATGCTCGGATGGACCGGAGAGTGGCACCTGGAAGCTTCTGGGC 699
Qy 664 TCAGTGGTTTATGCTCAGCAAGAAATTAATCAAGCTTGGTACATAGATTTTGGTT 723
Db 700 TCAGCACTGTGCGCCACAGCAAGAACTCATACGCGCTGGTACATCGGTTTCTTGACA 759
Qy 724 CTTATTTTTCGCTTCTTCTGCTATCTGCTGGAAGAGATGCT--- 768
Db 760 CTCATCTCTTCTTCAITTTCTGCTTCTGCTGGAAGAGATGCT--- 768
Qy 769 -----AATAAGAGTTTCTACATGAGATGCTCTCTGTTGGTGGGCA 813
Db 820 CAAGGAGAGAGATGAAGAGAGTTTGAGACCTATGAGATGCTCTGTTGGGCGCTG 879
Qy 814 ATTACATGACAACTATTGGCTATGGACACAACTCCCTTAACCTTGGCTGGGAAGATTG 873
Db 880 ATCACACTGGCCACCATTTGGCTATGAGACAGACACCAACAACTGGGAAGCGCTGTG 939
Qy 874 CTTTCTGAGGCTTTCACCTCTTGGCAATTTCTTTTGGCACTTCTTCTGCGGCAATTTT 933
Db 940 ATTGCGCCACCTTTTCTTAAATTTGGGCTCTCTTTTGGCCCTTCCAGCGGCACTCTG 999
Qy 934 GGCTCAGGTTTTCATTAAGATGACAGAAACACCGCCAGAACACTTTGAGAAAGA 993
Db 1000 GGCTCCGGGTGGCCCTCAAGGTGAGAGCAACACCGTCAAGAGCACTTTGAGAAAGG 1059
Qy 994 AGGAAACCAAGCTCCCACTTCACTGAGTGTGTTGGCGTGTGTTAGCGAGCTGATGAGAA 1053
Db 1060 AGGAAGCAGCTGCTGAGCTCATTTAGGCTGCTGAGGTATTATGCTACCAACCCCAAC 1119
Qy 1054 TCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCTTGGACCTGAGCGCTTACC 1113
Db 1120 AGGATTGACCTGTTGGCGACATGAGATTTTATGAATCAGTCTCTTTCTTTCTTCTTC 1179
Qy 1114 AAGAAAGAACAGGGGAGAGATCAAGCAGTCAGAGCTAAGTTTAAAGAGCGAGTGGCG 1173
Db 1180 AGGAAAGAACAGTGGAGGAGAGATCCAGCCAAAGCTGGTCTCTTGGATCGGTTCCG 1239
Qy 1174 ATGCTTAGCCCCAGGGCCAGAGATTATAGAGCCGCAAGCCTTCAGTGTGAGAGG 1233
Db 1240 CTTTCTTAATCTCGTGGTAGCAATACTAA-----AGGAAAGCTATT 1281
Qy 1234 TCCCAAGCAGCCAGATCACAGCGGAGGCTCCCAACCAAGTGCAGAGAGCTGGAG 1293
Db 1282 ACCCTCTGATGTAGATGCCATAGAAGAGTCTTCTTAAGAACCAAGAGCTGTGGC 1341

Qy 1294 TTCAACGACGAAACCGCTTCCGGCTTCGCTCGCTCAAAAGTTCTCAGCCAAAACCA 1353
Db 1342 TTAAACAATAAAGAGCGTTTTCGACGCGCTTCGATGAAAGCCT-----ACGCTTTC 1395
Qy 1354 GTGATAGATGCTGACACAGCGCTTGGCACTGATGATGATATATGATGAAAAGAGATGCCAG 1413
Db 1396 TGGCAGAGTTCTGAAGATGCGGGACAGGTGACCCCATGGCGAAGACAGGGCTATGGG 1455
Qy 1414 TGTGATGATCAGTGAAGACCTCACCCACCACTTAAACTGTCAATTCGAGCTATCAGA 1473
Db 1456 AATGACTTCCCATCGAAGACATGATCCCAACCCCTGAAGCGCGCATCCGAGCGCTCAGA 1515
Qy 1474 ATTATGAATTTTCATGTTGCAAAACGGAAGTTTAAAGAAACGTTTACGTCCATATGATGTA 1533
Db 1516 ATTTACAAATTCGCTCTCTATATAAAANATTCAGGAGACTTTGAGGCTTTACGATGTG 1575
Qy 1534 AAAGATGTCATTGAACAATATTTCTGCTGGTCACTGTCGACATGTTGTGTAGAAATTAAGC 1593
Db 1576 AAGATGTTGATGAGCAGTATTTCTGCGGCGATCTCGACATGCTTCCAGGATAAGTAC 1635
Qy 1594 CTTCAAAACAGGTGTTGATCAAAATTTCT 1619
Db 1636 CTTCAAGACGAGATAGATATGATTTT 1661

RESULT 13
US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; OTHER INFORMATION: has appeared in one individual.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.

FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

Query Match 17.1%; Score 460.8; DB 3; Length 2914;
Best Local Similarity 57.9%; Pred. No. 2.4e-126;
Matches 953; Conservative 0; Mismatches 627; Indels 66; Gaps 5;

QY 13 GAGTCGGGCGGGGAGGAGTGTCTGAACCTGGCAGCCGCGCAGGGGCGACGGCCCTGCTA 72
DB 115 GCGGGCGGCGCGCGACAGAGAGCGGAAAGTGGGCTGGCGCCCGCGACGTGGAGCAA 174

QY 73 CTGCTGGGCAACCGCGCGCCACGCTTGGTGGCGGCGGCTGGCTGAGGGAGAGCCGC 132
DB 175 GTCACTTGGCGCTGGGGCGGAGCGCGACAAGACGGACCTGTCTGTGAGGGCGGC 234

QY 133 CGGGGCAAGCAGGGGCGCGGATGAGCTGTCTGGGGAAGCCGCTCTCTTACAGAGTAGC 192
DB 235 GCGCGGACAGGGGCGCGGAGGACCCCGCAGGGCATCGGCTCTCTGGCCAAGACCCCG 294

QY 193 CAGAGCTGCC-----GGCGCAAGTCAAGTACCGCGGGTGCAGAACTACCTGTAC 243
DB 295 CTGAGCGGCCAGTCAAGAGAACAACACGCCAAGTACCGGGCGCATCCAACTTTGATCTAC 354

QY 244 AACGTCTGAGAGACCCCGCGCTGGGCTGTCATCTACACGCTTTGGTTTTCTCTCTT 303
DB 355 GACGCGCTGGAGAGCCCGGGCTGGGCGCTGCTTTACCGCTTGGTGTCTCTGATT 414

QY 304 GTCTTTGGTGTGATTTTGTCACTGTTTCTTACCATCCCTGAGCACACAAATTTGGCC 363
DB 415 GTCTGGGGTGTGATTCTGGCTGTCTGACCACTTCAAGAGTAGTGTCTCTG 474

QY 364 TCAAGTGTCTTGTGATCTGAGATTGATGATGTTGCTGTTTGGTTTGGAGTTTATC 423
DB 475 GGAGACTGGCTTCTGTACTGAGAGCATTTGTGATTTTTCATCTTTGGAGCCGAGTTTGT 534

QY 424 ATTGCAATCTGTCTGCGGGTGTCTGTCGATATAGAGGATGCAAGAGACTGAGG 483
DB 535 TTGAGATCTGGGCTGCGATGTTGCTGCCGATACAAAGGCTGGCGGGCGCGACTGAAG 594

QY 484 TTTGCTCGAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCTTCAATAGCAGTT 543
DB 595 TTTGCGCAGGAAGCCCTGTGTCATTTGGACATCTTTGTCTGATTTGCTCTGTGCCAGTG 654

QY 544 GTTCTGCAAAACTCAGGGTAATTTTGGCAGCTGTGCACTCAGAACTCCGTTTC 603
DB 655 GTTGTGTGGGAAACCAAGGCAATGTTCTGGCCACCT---CCCTGCGAAGCCTGGCGTTC 711

QY 604 CTACAGATCTCCGATGTGCGCATGGACCGAAGGGAGGACCTTGGAAATTTACTGGGT 663
DB 712 CTGCAATCTGGGATGCTGCGATGTCGACCGAGGATGGGACCTGGAAGCTTCTGGGC 771

QY 664 TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTATACATAGGATTTTGGTT 723
DB 772 TCAGCCATCTGTGCCACAGCAAGAACTCATCAGCCCTGTGTACATCGTTTCTGTACA 831

QY 724 CTTATTTTCTGCTTCTGCTCTATCTGGTGGAAAGGATGCC----- 768
DB 832 CTCATCTTTTCTTCTTCTGCTACCTGTTGAGAAAGAGCTCCAGAGGTGGATGCA 891

QY 769 -----AATAAGATTTTCTACATATGCAAGTCTCTCTGGTGGGCGACA 813
DB 892 CAAGAGAGGAGATGAAGAGAGTTTGAGACTATGCAAGTGCCTGTGGTGGGCGCTG 951

QY 814 ATTACATTGACAACTATTGGCTATGGAGCAAAACTCCCTTAACCTTGGCTGGGAAGATTG 873
DB 952 ATCACATGCGCCACCATTTGGCTATGGAGACAGACACCAAAACGTGGGAAGCGCTGTG 1011

QY 874 CTTTCTGAGGCTTTGCACTCTCTGGCATTTCTTTCTTTGCACTTCTCTGCGCGCATTTCT 933
DB 1012 ATTGGCGGCACCTTTTCTTAAATTGGCGTCTCTTTTGGCTTTCCAGCGGCGCATCTGT 1071

QY 934 GSCTCAGGTTTTTGCAATTAAGATCAAGAACCAACCGCCAGAACACCTTTTGAGAAAGA 993
DB 1072 GGTCCGGGCTGGCCCTCAGGTGCGAGGACCAACCGTCAAGACACTTTGAGAAAGG 1131

QY 994 AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGACAGCTGATGAGAAA 1053
DB 1132 AGGAAGCCAGCTGCTGAGCTCATTCAGGCTGCTGAGGATTTATGCTACCAACCCCAAC 1191

QY 1054 TCTGTTTCCATTGCAACCTGGNAGCCACATTTGAAGGCTTGCACACCTGACAGCCCTACC 1113
DB 1192 AGGATGTACCTGGTGGCCACATGAGAGATTTTATGAATCAGTCGTCTCTTTCTTTCTTC 1251

QY 1114 AAGAAAGAACCAAGGGGAAAGCATCAAGCAGTCAAGAGCTAAAGTTTAAAGGAGGAGTGGCC 1173
DB 1252 AGGAAGAACACGTGGAGCGACATCCAGCCAAAGCTGGGTCTCTTGGATCGGTTGCG 1311

QY 1174 ATGGCTAGCCCGAGGGCCAGAGTATTAAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGG 1233
DB 1312 CTTTCTAATCTCGTGGTAGCAATACTAA-----AGGAAAGCTATTT 1353

QY 1234 TCCCAAGCACCGACATCACAGCCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGGAGC 1293
DB 1354 ACCCTCTGAATGTAGATGCCATAGAGAAAGTCTCTTAAAGAACCAAGGCTCTGTGGC 1413

QY 1294 TTCAACGACCGAACCCGCTTCCGGCCCTCGCTGGCCCTCAAAAGTTCTCAGCCAAAACCA 1353
DB 1414 TTAAACAATAAGAGCGTTTCGACGCGCTTCGCAATGAAAGCCT-----ACGTTTC 1467

QY 1354 GTGATGATGTCACACAGCCCTTGGCACTGATGATGATATGATGATAAAGGATGCCAG 1413
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QY 1414 TGTGATGATCAGTGGAGAGCTCACCCACCACTTAAACTGTCTATTCGACGTATCAGA 1473
DB 1528 AATGACTTCCCATCGAAGACATGATCCCACTCCCTGAAAGGCGCCATCCGAGCCGTCAGA 1587

QY 1474 ATTATGAATTTTCAATGTTGCAAAACGGAAGTTTAAAGAAACGTTACGTCCATATGATGA 1533
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QY 1594 CTTCAACACAGTGTGATCAAAATTTCT 1619
DB 1708 CTTCAAGCAGAGATAGATATGATTTT 1733

RESULT 14

US-09-495-050A-305
; Sequence 305, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 305
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006F6

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; NAME/KEY: unsure
; LOCATION: 486, 510, 552, 573
; OTHER INFORMATION: a, t, c, g, or other
US-09-495-050A-305

Query Match 16.8%; Score 452; DB 4; Length 575;
Best Local Similarity 95.0%; Pred. No. 3.2e-124;
Matches 509; Conservative 0; Mismatches 22; Indels 5; Gaps 4;

QY 1621 GGAAGGGGCAATCACATCAGATAGAGAGCGGAGAGAAATAACAGCAGAACATGAG 1680
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QY 1681 ACCACAGACCATCTCAGTATGCTCGGTTCGGTTCAGAGTTGAAAAACAGGTACAGTCC 1740
Db 61 ACCACAGACCATCTCAGTATGCTCGGTTCGGTTCAGAGTTGAAAAACAGGTACAGTCC 120

QY 1741 ATAGAGTCCAAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCCTTCGAAAGGCTCT 1800
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Db 181 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 240

QY 1861 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCGACAAAAACAGTGGCTGC 1920
Db 241 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCGACAAAAACAGTGGCTGC 300

QY 1921 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGCGCTGCAAGTTTCATTTGACGCCAAAT 1980
Db 301 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGCGCTGCAAGTTTCATTTGACGCCAAAT 359

QY 1981 GAGTTCAGTGGCCAGACTTTTCTACGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG 2040
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QY 2041 GTGCCAAATAGTCAAAAGCGATGGCTCAGCAGTGGGAGCGACCAACACCATTTGCAACCAA 2100
Db 418 GTGCCAA--TAGTCAAAAGCGATGGCTCAGCAGTGGGAGCGACCAACACCATTTGC--AAACAA 475

QY 2101 ATAATAGCGNACCAAGCCAGCAGCCCCCAACTTTTACAGATCCCCACCTCCTCT 2156
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RESULT 15
US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grikoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-19

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15 88, score 425, DB 3: Length 3287;

Search completed: April 11, 2005, 21:46:20

Job time : 446.638 secs

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3	2689.2	99.8	99.8	3137	6	AX056817	Sequence
4	2689.2	99.8	99.8	3137	9	AF202977	Homo sapi
5	2681.2	99.5	99.5	3074	6	AR323778	Sequence
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Db	241	TACAACGCTGCTGGAGAGACCCCGCGCTGGCGTTCACTACCAACGCTTCGTTTTCTC	300
Qy	301	CTTGCTCTTTGGTTGCTTGATTTTGTCACTGTTTCTACCATCCTGAGCAACAATTTG	360
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Qy	421	ATCATTCGAATCTGCTCTCGGGTTCGCTTCGATATAGAGATGCAAGGAAGCTG	480
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Db	901	ATTTCCTTTCTTTGCACTTCCTGCCGGCATCTTCGGCTCAGGTTTTCGATTTAAAGTACAA	960
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Db	1021	TGTTGTTGGCTAGTTATGCGAGCTCATGAGAAATCTGTTTCCATTGCAACTCGAAAGCCA	1080
Qy	1081	CACCTTGAAGCCTTTGCACACCTGCAAGAAAGAACCAAGGGGAAGCATCAAGC	1140
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QY	1381	TCGCTCGCCCTCAAAAGTTCTCAGCCAAAAACAGTGTAGATGCTGACACAGCCCTTGCGC	1380
DB	1381		1380
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DB	1621	GGAAAAAGGCAAAATCACATCAGATAAGAGCCCGAGAGAAAAATAACAGCAGNACATGAG	1680
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DEFINITION Sequence 1 from patent US 6649371.
ACCESSION AR430568
VERSION AR430568.1 GI:40191384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3137)
AUTHORS Jentsch, T. J.
TITLE Potassium channel KCNQ5 and sequences encoding the same
JOURNAL Patent: US 6649371-A 1 18-NOV-2003;
FEATURES
Location/Qualifiers
source 1..3137
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 99.8%; Score 2689.2; DB 6; Length 3137;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Tue Apr 12 17:15:10 2005

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DEFINITION		member 5 (KCNQ5) mRNA, complete cds.	
ACCESSION		AF202977	
VERSION		1	
KEYWORDS			
SOURCE			
ORGANISM		Homo sapiens (human)	
REFERENCE			
AUTHORS		Jentsch, T.J., Hechenberger, M., Weinreich, F., Kubisch, C. and	
TITLE		KCNQ5, a novel potassium channel broadly expressed in brain,	
JOURNAL		mediates M-type currents	
MEDLINE		J. Biol. Chem. 275 (31), 24089-24095 (2000)	
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AUTHORS		Schroeder, B.C., Hechenberger, M., Weinreich, F., Kubisch, C. and	
TITLE		Jentsch, T.J.	
Direct Submission			
Submitted (09-NOV-1999)		ZMNH, Hamburg University, Martinistrasse	
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Location/Qualifiers			
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gene			
CDS			

ORIGIN			
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ACCESSION AR393778
VERSION AR393778.1 GI:40120748
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3074)
AUTHORS Steinmeyer,K., Lerche,C., Scherer,C., Seebohm,G. and Busch,A.E.
TITLE Nucleic acid molecule encoding the potassium channel protein, KCNQ5
JOURNAL Patent: US 6617131-A 1 09-SEP-2003;
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ORIGIN

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DEFINITION Sequence 1 from Patent WO0170811.
ACCESSION AX253254
VERSION AX253254.1 GI:16073802
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Lerche, C., Scherer, C., Seebohm, G., Busch, A. and Steinmeyer, K.
TITLE Potassium channel protein kcnq5, a target for diseases of central
nervous system and cardiovascular system
JOURNAL Patent: WO 0170811-A 1 27-SEP-2001;
Aventis Pharma Deutschland GmbH (DE)
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DEFINITION			Homo sapiens voltage-gated potassium channel (KCNQ5) mRNA, complete cds.
ACCESSION			AF249278
VERSION			AF249278.1
KEYWORDS			GI:9651966
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS			1 (bases 1 to 3074) Lerche,C., Scherer,C.R., Seeböhm,G., Derst,C., Wei,A.D., Busch,A.E. and Steinmeyer,K.
TITLE			Molecular cloning and functional expression of KCNQ5, a potassium channel subunit that may contribute to neuronal M-current diversity
JOURNAL			J. Biol. Chem. 275 (29), 22395-22400 (2000)
MEDLINE			20357367
PUBMED			10787416
REFERENCE			2 (bases 1 to 3074) Lerche,C., Scherer,C.R., Seeböhm,G., Derst,C., Wei,A.D., Busch,A.E. and Steinmeyer,K.
AUTHORS			Direct Submission
TITLE			Submitted (24-MAR-2000) Cardiovascular Diseases, Aventis Pharma
JOURNAL			Deutschland GmbH, Building H824, Frankfurt a. M. 65926, Germany
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ACCESSION AR565635
VERSION AR565635.1 GI:53981668
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2772)
AUTHORS Hu, Y., Kieke, J.A., Turner, C.A. Jr., Nehls, M.C., Friedrich, G.,
Zambrowicz, B. and Sands, A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 1 27-JUL-2004;
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AX268476
LOCUS AX268476 3111 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 3 from Patent WO0175108.
ACCESSION AX268476
VERSION AX268476.1 GI:16541653
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Hu, Y., Kieke, J.A., Turner, A.C., Nehls, M.C., Friedrich, G.B.,
Zambrowicz, B. and Sands, A.T.
Human ion channel protein and polynucleotides encoding the same
Patent: WO 0175108-A 3 11-OCT-2001;
JOURNAL Lexicon Genetics Incorporated (US)
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BD275572
LOCUS BD275572 3718 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Human Voltage-Gated Potassium Channel.
ACCESSION BD275572
VERSION BD275572.1 GI:33085340
KEYWORDS JP 2002543768-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3718)
AUTHORS Metzker, M. L., Li, W., Petrukhin, K. and Caskey, T. C.
TITLE Novel Human Voltage-Gated Potassium Channel
JOURNAL Patent: JP 2002543768-A 2 24-DEC-2002;
Merck and Co Inc
COMMENT OS Homo sapiens
PN JP 2002543768-A/2
PD 24-DEC-2002
PF 10-APR-2000 JP 2000611548
PR 14-APR-1999 US 60/129274
PI michael l metzker, wen li, konstantin petrukhin, thomas c caskey
CC
FH

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AUTHORS	Knizeva, M. and Han, M.	
	Direct Submission	
TITLE	Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,	
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Db	2041	CCTCCTCTCCAGGCATCAAGCATCTGCCAGGCCAGAACTCTGCAACCTTAACCTTGCA	2100
QY	2209	GGCTTAGAGGAAGATTTCTGAGCTCAGCAGCTGCTTGTGCTTCCCAAGGAATGTT	2268
Db	2101	GGCTTAGAGGAAGATTTCTGAGCTCAGCAGCTGCTTGTGCTTCCCAAGGAATGTT	2160
QY	2269	CAGGTTCGACAGTCAAACTCTCAACAGGACCGTCTATGAGGAAAGCTTTGACATGGGA	2328
Db	2161	CAGGTTCGACAGTCAAACTCTACCCAGGACCGTCTATGAGGAAAGCTTTGACATGGGA	2220
QY	2329	GGAGAAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2388
Db	2221	GGAGAAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2280
QY	2389	GTGCAAAACCTGATCAGGTTCGACGAGGAACTGAATATACAACTTCAGGAGTGAATCA	2448
Db	2281	GTGCAAAACCTGATCAGGTTCGACGAGGAACTGAATATACAACTTCAGGAGTGAATCA	2340
QY	2449	AGTGGCTCCAGAGGAGCAAGATTTTACCCCAATGAGGGAATCAAAATGTTTATA	2508
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QY	2509	ACTGATGAAGAGTGGTCCGAGACAGACAGACAGACACTTTTGTGTCGCGACCGCAG	2568
Db	2401	ACTGATGAAGAGTGGTCCGAGAGACAGACAGACACTTTTGTGTCGCGACCGCAG	2460
QY	2569	CCTGCCAGGAGGCTGCTTTCATCAGACTCTCTAAGGACTTGAAGGTCAAGTCACTCT	2628
Db	2461	CCTGCCAGGAGGCTGCTTTCATCAGACTCTCTAAGGACTTGAAGGTCAAGTCACTCT	2520
QY	2629	CAGAGCATTTGTAAGGACAGGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAAATG	2688
Db	2521	CAGAGCATTTGTAAGGACAGGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAAATG	2580
QY	2689	AAATAA 2694	
Db	2581	AAATAA 2586	

RESULT 15	AF263836	3108 bp	mRNA	linear	ROD 01-JUN-2000
LOCUS	AF263836				
DEFINITION	Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA, partial cds.				
ACCESSION	AF263836				
VERSION	AF263836.1	GI:8132998			
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1. (bases 1 to 3108)				
AUTHORS	Kniazeva, M. and Han, M.				
TITLE	A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5, is a candidate gene for retinal disorders				
JOURNAL	Unpublished				
REFERENCE	2. (bases 1 to 3108)				
AUTHORS	Kniazeva, M. and Han, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-MAY-2000) MDCB, University of Colorado at Boulder, Porter Biosciences Bldg., Boulder, CO 80309, USA				
FEATURES	Location/Qualifiers				
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	/sex="male"				
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	/dev_stage="9-11 weeks"				
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gene	/gene="Kcnq5"				
CDS	<1..2638				
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	/note="similar to the Homo sapiens voltage-gated potassium channel KCNQ5; member of the KCNQ family"				
	/codon_start=2				
	/product="voltage-gated potassium channel KCNQ5"				
	/protein_id="AA073447.1"				
	/db_xref="GI:8132998"				
	/translation="GDGDLGLGTRAAALCGGGGLRESRRKQGRMSLLGKPLSVTS SCSRRNVRRVQNYLVNLRPRGAWFVHAFVLLVFGCLILSVSTIPEHKLKLA SCLILFEMIVWFLEFIRIWSAGCCYRGWGRFARKPCVDTITVLIASI AVSAKTQGNIFATSLRSLRLQLRMVDRMRGRTWKLGSVVAHSEKELITAWI GFVLIFSSFLVVLVEKDANKFSTVADALWMGTITLTIGYDKTPTLWGLRLSAG FALGLSPFALVAGIXGSGFAGVQEHQKHEKRNPAANLIOCWRVSYAADEKSV STATWPHLKALHTCPTKKEGEASSQKLSFKRVRWASPRGOSIKRSOASVGRDR SPSTDTITAGSPTKVQKSWSFNDRTFRFRLKLSQSPKPDVADTALGIDVDYDEKQ CQDVSVEDLTPTKTVIRAIRIMKPHVAKRPFKTRFYDVKDVEIQESAGHLMCL RIKSLQTRVDQILGQMTSDKRSREKITAEHETDDPSMLARVVKVQVQVQIESKL DCLLDITYQVLRKGSALTASFOIPEPECQTSYQSPVDSKDLGSAQNSGCLTR SASANRSLGLOFILTENESAOFTYALSPTMHSOATQVPMSONDSVSVATNNANQI SAAPKPAATRTLOIPPLSAIKHLSPEPLSNPTGLQESISDVTTCLVASKESVOFA QSNLTIKDRSLFDMGGETILLSVRNWPKDLGKLSVQNLJESTELNLQFSGSESS GRSQSDQFPKWRSEKLFITDDEVGAETETDFTDTPPPPAGEAFSSSLRTGRSRS SQNICKTGDSDALSPLHVKLN"				
ORIGIN					
Query Match	82.3%	Score	2217.4;	DB 10;	Length 3108;
Best Local Similarity	90.0%;	Pred. No. 0;			
Matches 2374;	Conservative 0;	Mismatches 264;	Indels 0;	Gaps 0;	
QY	57	GGGCGACGGCTGCTACTGTCGGGCACCCCGCGGCGCACCGCTTGGTGGCGCGGTGG	116		
Db	1	GGGCGACGGCTGCTGTTGCTCGGCACCGCGCGGCGCTCGGCGAGCGCGCGCG	60		
QY	117	CCTGAGGAGAGCGCGCGCGGCGCAAGCAGGCGCGCGCGGCTGCTGGGAGCGCGCT	176		
Db	61	CTTGAGAGAGAGCGCGCGGCGCAAGCAGGCGCGCGCGGCTGCTGGGAGCGCGCT	120		
QY	177	CTCTTACACGAGTAGCCAGAGCTGCGCGCGCAACAGTCAAGTACCGCGGCGGTGCAACTA	236		

Tue Apr 12 17:15:10 2005

Qy	2397	CCTGATCAGGTCGACCGAGAACTGAATATACAACTTTCCAGGAGTGAAGTCAAGTGGCTC	2456
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Qy	2457	CAGAGGCAGCCAAAGATTTTACCCCAAATGGAGGAATCCAAATGTTTATTAACATGATGA	2516
Db	2401		
Qy	2517	AGAGTGGTCCCGAAGAGACAGAGACAGACACCTTTTGATGCCGCACCGCAGCCTGCCAG	2576
Db	2461		
Qy	2577	GGAAGCTGCCTTTTGCATCAGACTCTTAAGGACTTGAAGGTACAGATCATCTCAGAGCAT	2636
Db	2521		
Qy	2637	TTGTAAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCTAACTGAAATAA	2694
Db	2581		

Search completed: April 11, 2005, 16:49:33
Job time : 13351.3 secs

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 08:07:42 ; Search time 1379.41 Seconds
(without alignments)
11561.287 Million cell updates/sec

Title: US-09-810-796-2
Perfect score: 2694
Sequence: 1 atgaaggatgtggatcgagg.....ctcatgtcaactgaaataa 2694

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2694	100.0	2694	4	AAS14652 Human CDN
2	2694	100.0	2694	6	AAD27192 Human pot
3	2690.4	99.9	3071	4	AAS14651 Human CDN
4	2689.2	99.8	3137	4	AAC85414 Human KCN
5	2681.2	99.5	3074	4	AAB49499 Human KCN
6	2678.6	99.5	3074	10	ADB78684 Human pot
7	2630	97.6	2667	4	AAS14653 Human CDN
8	2625.2	97.4	3111	5	AAB43633 Human ion
9	2625.2	97.4	3111	5	AAB43634 Human ion
10	2585	96.0	3718	3	AAC64371 Human KCN
11	963.4	35.8	125910	3	AAC64370 Human KCN
12	518.4	19.2	2335	3	AAA47618 Pot
13	518.4	19.2	2335	10	ADE31698 Human 323
14	516	19.2	2273	2	AAAX57140 Mouse KCN
15	510	18.9	2169	2	AAAX57140 Mouse KCN
16	509.8	18.9	582	8	ACA04855 cDNA enco
17	500.6	18.6	7407	10	ADB78688 Human pot
18	500.6	18.6	7407	10	ADB78686 Human pot
19	500.6	18.6	7407	10	ADB78683 Human pot
20	500.6	18.6	7407	10	ADB78687 Human pot

21	500.6	18.6	7411	10	ADD29557 Human tum
22	500.6	18.6	7420	11	ADN38963 Cancer/an
23	500.6	18.6	7420	11	ADP65810 Human mRN
24	500.6	18.6	7420	11	ADP65731 Human pot
25	500.6	18.6	7420	12	ADL06495 Human tum
26	500.6	18.6	7863	10	ADJ56529 Human CDN
27	499	18.5	7407	10	ADB78685 Human pot
28	480.6	17.8	7413	5	AAS74832 DNA enco
29	478.4	17.8	7413	5	ADSI7851 Rattus no
30	477	17.7	2565	2	AAx81548 Human bra
31	477	17.7	3195	5	AAx81548 Human bra
32	466.6	17.3	3029	2	AAx81547 Human bra
33	465.8	17.3	2766	13	ADSI7849 Rattus no
34	465	17.3	548	6	ABA90234 Human ORF
35	464	17.2	2814	2	AAx57141 Mouse KCN
36	460.8	17.1	2565	2	AAx26596 Nucleotid
37	460.8	17.1	2914	2	AAx57059 Human KCN
38	460.8	17.1	2926	10	ADB78690 Human pot
39	460.8	17.1	2926	10	ADB78682 Human pot
40	459.2	17.0	2926	10	ADB78691 Human pot
41	459.2	17.0	2926	10	ADB78689 Human pot
42	457.4	17.0	2755	13	ADSI7847 Human KCN
43	455.8	16.9	1848	12	ADH51119 Potassium
44	455.8	16.9	1848	12	ADM77995 KCNQ2-15b
45	454.2	16.9	4512	10	ADJ56528 Rat cDNA

ALIGNMENTS

RESULT 1	
AAS14652	
ID	AAS14652 standard; cDNA; 2694 BP.
XX	
AC	AAS14652;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Human cDNA encoding a voltage gated potassium channel hKCNQ5-1.
XX	
KW	Human; ss; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW	cerebroprotective; neurotropic; analgesic; vision disorder;
KW	central nervous system disorder; epilepsy; migraine; hearing disorder;
KW	psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW	pain; gene therapy; splice variant.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	CDS
FT	1..2994
FT	/*tag= a
FT	/product= "hKCNQ5-1"
XX	
PN	WO200170759-A1.
XX	
PD	27-SEP-2001.
XX	
PF	20-MAR-2001; 2001WO-US009328.
XX	
PR	21-MAR-2000; 2000US-0190954P.
XX	
PA	(ICAG-) ICAGEN INC.
XX	
PI	Jegla TJ;
XX	
DR	WPI; 2001-611467/70.
DR	P-PSDB; AAU09020.
XX	
PT	Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT	identifying a compound modulating ion flux in eukaryotic cell or cell
PT	membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX	
PS	Claim 5; Page 62-63; 78pp; English.

XX The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy) is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-1
XX
SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;
Query Match 100.0%; Score 2694; DB 4; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB |||||
QY 61 GAGGCGCTGCTACTGCTGGCACCCGCGCGCACGCTGTGTGGCGGGCGGTGGCCTG 120
DB |||||
QY 61 GAGGCGCTGCTACTGCTGGCACCCGCGCGCACGCTGTGTGGCGGGCGGTGGCCTG 120
DB |||||
QY 121 AGGGAGAGCCGCGGGGCAAGCAGGGGCGCGGATGAGCTGTGGGGAACCGCTCTCT 180
DB |||||
QY 181 TACACGAGTAGCCAGAGTCGCGCGCACGCTCAAGTACCGCGGTGCAGAACTACCTG 240
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QY 181 TACACGAGTAGCCAGAGTCGCGCGCACGCTCAAGTACCGCGGTGCAGAACTACCTG 240
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DB |||||
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QY 361 GCCTCAAGTGTGCTTTGATCTTGGAGTTGCTGATGATGCTTTTGGTTTGGAGTTC 420
DB |||||
QY 361 GCCTCAAGTGTGCTTTGATCTTGGAGTTGCTGATGATGCTTTTGGTTTGGAGTTC 420
DB |||||
QY 421 ATCATTTGCAATCTGCTGCGGGTGTGCTGTTGATGATGATGATGATGATGATGATG 480
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DB |||||
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DB |||||
QY 1261 GGCAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACAGCCGCAACCCGCTTCCGGGCC 1320
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DB |||||
QY 1321 TCGCTGGGCTCAAAAAGTTCTCAGCCAAACCAAGTATAGATGCTGACACAGCCCTTGGC 1380
DB |||||
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DB |||||
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QY 1681 ACCACAGACGATCTCAGTATGCTCGGTGGTGTGAGTTGAAAGCAAGGTACAGTCC 1740
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DB |||||

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QY 2341 TTGCTGCTGTCCTCCATGCTGCGGAGGACTTTGGGCAATCTTTGCTGTGCAAAACCTG 2400
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QY 2641 AAGGAGGAGAAAGTACAGATGCTTCAAGTTCCTCATGTCAAACTGAAATAA 2694
Db |||||
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Db |||||

RESULT 3

AA514651
ID AA514651 standard; cDNA; 3071 BP.
AC AA514651;
XX
DT 18-DEC-2001 (first entry)
TX Human cDNA for voltage gated potassium channel hKCNQ5.
DE
DE Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200170759-A1.
XX
XX 27-SEP-2001.
XX
XX 20-MAR-2001; 2001WO-US009328.
XX
XX 21-MAR-2000; 2000US-0190954P.
XX
XX (ICAG-) ICAGEN INC.
XX Jegla TJ;
XX
XX WPI; 2001-611467/70.
XX
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximately alpha-subunits.
XX
XX Claim 5; Page 61-62; 78pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5

CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy) is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a representative cDNA for hKCNQ5
XX
SQ Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 0 U; 1 Other;
Query Match 99.9%; Score 2690.4; DB 4; Length 3071;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGGATGTGGAGTCGGGCGGCGGAGGCTGTGCTGAACCTCGGACGCCAGGGGC 60
Db |||||
QY 10 ATGAAGGATGTGGAGTCGGGCGGCGGAGGCTGTGCTGAACCTCGGACGCCAGGGGC 69
Db |||||
QY 61 GACGGCTCTACTGCTGGGACCCGCGGCGGAGGCTGTGCTGGGCGGCGGCTGGCTG 120
Db |||||
QY 70 GACGGCTCTACTGCTGGGACCCGCGGCGGAGGCTGTGCTGGGCGGCGGCTGGCTG 129
Db |||||
QY 121 AGGAGAGCCGCGGCGGAGGAGGCGGCGGAGGCTGTGCTGGGCGGCGGCTGTCT 180
Db |||||
QY 130 AGGAGAGCCGCGGCGGAGGAGGCGGCGGAGGCTGTGCTGGGCGGCGGCTGTCT 189
Db |||||
QY 181 TACAGAGTACCCAGAGCTGCGGCGGCGGAGGCTGTGCTGGGCGGCGGCTGTGCTG 240
Db |||||
QY 190 TACAGAGTACCCAGAGCTGCGGCGGCGGAGGCTGTGCTGGGCGGCGGCTGTGCTG 249
Db |||||
QY 241 TACAGAGTGTGGAGAGACCCGCGGCGGAGGCTGTGCTGGGCGGCGGCTGTGCTG 300
Db |||||
QY 250 TACAGAGTGTGGAGAGACCCGCGGCGGAGGCTGTGCTGGGCGGCGGCTGTGCTG 309
Db |||||
QY 301 CTGTGCTTGTGCTGCTGATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db |||||
QY 310 CTGTGCTTGTGCTGCTGATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 369
Db |||||
QY 361 GCCTCAAGTTCGCTTGTGATCCTGAGTTCGCTGATGATGCTGCTGCTGCTGCTGCTG 420
Db |||||
QY 370 GCCTCAAGTTCGCTTGTGATCCTGAGTTCGCTGATGATGCTGCTGCTGCTGCTGCTG 429
Db |||||
QY 421 ATCATTGCAATCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db |||||
QY 430 ATCATTGCAATCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 489
Db |||||
QY 481 AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCAATGTTTCTATCGCTTCAATAGCA 540
Db |||||
QY 490 AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCAATGTTTCTATCGCTTCAATAGCA 549
Db |||||
QY 541 GTTGTTCCTGCAAAACCTCAGGGTAATATTTTGGCCAGCTGTGCAAGTCTCCGT 600
Db |||||
QY 550 GTTGTTCCTGCAAAACCTCAGGGTAATATTTTGGCCAGCTGTGCAAGTCTCCGT 609
Db |||||
QY 601 TTCTTACAGATCCCTCCGATGCTGCGGATGCGGAGGCGGAGGCTGTGCAAAATCTG 660
Db |||||
QY 610 TTCTTACAGATCCCTCCGATGCTGCGGATGCGGAGGCGGAGGCTGTGCAAAATCTG 669
Db |||||
QY 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATACAGCTTGTGATCATAGGATTTTG 720
Db |||||
QY 670 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATACAGCTTGTGATCATAGGATTTTG 729
Db |||||
QY 721 GTTCTTATTTTTCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db |||||

1381	ACTGATGATGTATATGATGAAAGAGATGCCAGCTGTGATGTATCAGTGGGAAGACCTCACC	1440
Db		
1441	GCACCACTTAAACCTGTCAATTCGAGCTATCAGAAATTATGAAATTTCAATTTGCAAAACGG	1500
Qy		
1441	CCACCACTTAAACCTGTCAATTCGAGCTATCAGAAATTATGAAATTTCAATTTGCAAAACGG	1500
Db		
1501	AAGTTTAAAGGAAAGTTACGTCATATGATGTAAAGATGTCAATTTGAACAATATTCGTCT	1560
Qy		
1501	AAGTTTAAAGGAAACATTACGTCATATGATGTAAAGATGTCAATTTGAACAATATTCGTCT	1560
Db		
1561	GGTCATCTGGACATGTTGTGTAGAAATTAAGACCTTTCAACACGCTGTTGTGATCAAAATCTT	1620
Qy		
1561	GGTCATCTGGACATGTTGTGTAGAAATTAAGACCTTTCAACACGCTGTTGTGATCAAAATCTT	1620
Db		
1621	GGAAAAGGGCAAAATCACATCAGATAGAGAGCCGAGAGAAATAAACAGCAGAACATGAG	1680
Qy		
1621	GGAAAAGGGCAAAATCACATCAGATAGAGAGCCGAGAGAAATAAACAGCAGAACATGAG	1680
Db		
1681	ACACAGACGATCTCAGTATGCTCGGTCCGGTGGTCAGGTTTGAAGAACAGTACAGTCC	1740
Qy		
1681	ACCACAGACGATCTCAGTATGCTCGGTCCGGTGGTCAGGTTTGAAGAACAGTACAGTCC	1740
Db		
1741	ATAGAGTCCAAAGCTGGACATGCCCTACTAGACATCTATCAAACGGTCCCTTCGGAAGGGCTCT	1800
Qy		
1741	ATAGATCCAAAGCTGGACATGCCCTACTAGACATCTATCAAACGGTCCCTTCGGAAGGGCTCT	1800
Db		
1801	GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACACATCT	1860
Qy		
1801	GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACACATCT	1860
Db		
1861	GACTATCAAAGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCGCGCAAAAACAGTGGCTGC	1920
Qy		
1861	GACTATCAAAGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCGCGCAAAAACAGTGGCTGC	1920
Db		
1921	TTATCCAGATCAACTAGTGGCCAAACATCTCGAGAGGCTCGAGTTCAATCTGAGCGCCAAAT	1980
Qy		
1921	TTATCCAGATCAACTAGTGGCCAAACATCTCGAGAGGCTCGAGTTCAATCTGAGCGCCAAAT	1980
Db		
1981	GAGTTCAGTGCCAGACATTTCTACGGCTTAGCGCTTACTATGCACAGTCAAGCAACACAG	2040
Qy		
1981	GAGTTCAGTGCCAGACATTTCTACGGCTTAGCGCTTACTATGCACAGTCAAGCAACACAG	2040
Db		
2041	GTGCGAAATTAGTCAAAGCGATGGCTCAGCAGTGGCGACCCAAACCAATTCGAAACCAA	2100
Qy		
2041	GTGCGAATTAGTCAAAGCGATGGCTCAGCAGTGGCGACCCAAACCAATTCGAAACCAA	2100
Db		
2101	ATAAATACGGCACCCAGCCAGCAGCCCAACACTTTACAGATCCCACTCTCTCTCCCA	2160
Qy		
2101	ATAAATACGGCACCCAGCCAGCAGCCCAACACTTTACAGATCCCACTCTCTCTCCCA	2160
Db		
2161	GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCCCTAACCCCTTACAGGAA	2220
Qy		
2161	GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCCCTAACCCCTTACAGGAA	2220
Db		
2221	AGCATTTCTGACGTACACACTGCTGTTGGCTTCCAGGAAATGTTCAGTTGTCACAG	2280
Qy		
2221	AGCATTTCTGACGTACACACTGCTGTTGGCTTCCAGGAAATGTTCAGTTGTCACAG	2280
Db		
2281	TCAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGAGAGAACTCTG	2340
Qy		
2281	TCAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGAGAGAACTCTG	2340
Db		
2341	TTGTCGTCTGTGCCATGGTGCAGAGGACTTGGGCAAACTTTGTCGTGTGTCGAAACCTG	2400
Qy		
2341	TTGTCGTCTGTGCCATGGTGCAGAGGACTTGGGCAAACTTTGTCGTGTGTCGAAACCTG	2400
Db		
2401	ATCAGGTGCACCGAGGACTGAAATATACAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA	2460
Qy		
2401	ATCAGGTGCACCGAGGACTGAAATATACAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA	2460
Db		
2461	GGCAGCCAAAGATTTTATACCCCAAAATGGAGGAAATCCAAATTTGTTTATTAACATGATGAAGAG	2520
Qy		
2461	GGCAGCCAAAGATTTTATACCCCAAAATGGAGGAAATCCAAATTTGTTTATTAACATGATGAAGAG	2520
Db		

QY	2521	GTGGGTCCCGAAGACAGACAGACAGACACATTTTGTATGCCGACCGCAGCGCTGCCAGGAA	2580
Db	2521	GTGGGTCCCGAAGACAGACAGACAGACACATTTTGTATGCCGACCGCAGCGCTGCCAGGAA	2580
QY	2581	GCTGCCTTTTGCATCAGACATCTCTTAAGGACTGGAAGTCAAGATCATCTCAGACATTTGT	2640
Db	2581	GCTGCCTTTTGCATCAGACATCTCTTAAGGACTGGAAGTCAAGATCATCTCAGACATTTGT	2640
QY	2641	AAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATCTCAAACTGAAATAA	2694
Db	2641	AAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATCTCAAACTGAAATAA	2694
RESULT 5			
AAH49499	ID AAH49499 standard; DNA; 3074 BP.		
XX	XX	AAH49499;	
XX	XX	11-DEC-2001 (first entry)	
DT	XX	Human KCNQ5 DNA.	
DE	XX		
XX	XX	KCNQ5; potassium channel protein; human; neurological; cardiovascular;	
KW	KW	anticonvulsant; excitability modulator; membrane potential; neuron;	
KW	KW	voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;	
KW	KW	screening; central nervous system disease; cardiovascular disease; ds.	
XX	XX		
OS	XX	Homo sapiens.	
XX	XX		
Key	XX	Location/Qualifiers	
FT	FT	110..2908	
FT	FT	/*tag= a	
FT	FT	/product= "KCNQ5"	
XX	XX		
PN	XX	DE10013732-A1.	
XX	XX		
PD	XX	27-SEP-2001.	
XX	XX		
PF	XX	21-MAR-2000; 2000DE-01013732.	
XX	XX		
PR	XX	21-MAR-2000; 2000DE-01013732.	
XX	XX	(AVET) AVENTIS PHARMA DEUT GMBH.	
PA	XX		
XX	XX	Steinmeyer K, Lerche C, Scherer C, Seeborn G, Busch AE;	
PI	XX		
XX	XX		
DR	XX	WPI; 2001-571700/65.	
DR	XX	P-PSDB; AAB86979.	
XX	XX		
PT	XX	New DNA sequence encoding potassium channel KCNQ5, useful in screening	
PT	XX	for specific modulators, potential agents for treating central nervous	
PT	XX	system and cardiovascular diseases.	
XX	XX		
PS	XX	Claim 2a; Page 9-10; 20pp; German.	
XX	XX		
CC	XX	This invention describes a novel DNA sequence (I) encoding: (i) a	
CC	XX	polypeptide (II) with potassium channel KCNQ5 activity; (ii) a	
CC	XX	polypeptide with the amino acid (aa) sequence of KCNQ5. The products of	
CC	XX	the invention have neurological, cardiovascular and anticonvulsant	
CC	XX	activity and act as modulators of the voltage-dependent KCNQ5 potassium	
CC	XX	channel, a key regulator of membrane potential and modulator of	
CC	XX	excitability of electrically activated cells such as neurons and	
CC	XX	cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)	
CC	XX	are used to screen for compounds that modulate the activity of KCNQ5,	
CC	XX	potentially useful for treating central nervous system (e.g. epilepsy,	
CC	XX	and cardiovascular diseases. This sequence encodes the human potassium	
CC	XX	channel KCNQ5 protein described in the invention	
XX	XX		
SQ	XX	Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 U; 0 Other;	

Query Match 99.5%; Score 2681.2; DB 4; Length 3074;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 2686; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1 ATGAGGATGAGTTCGGCGCGGCGAGGCTGCTGAACTCGCGAGCGCCAGGGGC 60
Db 215 ATGAGGATGAGTTCGGCGCGGCGAGGCTGCTGAACTCGCGAGCGCCAGGGGC 274
QY 61 GACGGCTGCTACTGCTGGGACCCCGCGGCGAGGCTGCTGAGGCGGCGGCGGCTG 120
Db 275 GACGGCTGCTACTGCTGGGACCCCGCGGCGAGGCTGCTGAGGCGGCGGCGGCTG 334
QY 121 AGGAGAGCGCGCGGCGGCGAGGCGGCGGCGAGGCTGCTGAGGCGGCGGCGGCTG 180
Db 335 AGGAGAGCGCGCGGCGGCGAGGCGGCGGCGGCGAGGCTGCTGAGGCGGCGGCGGCTG 394
QY 181 TACAGAGTACGAGAGTTCGGCGGCGGCGAGGCTGCTGAGGCGGCGGCGGCGGCTG 240
Db 395 TACAGAGTACGAGAGTTCGGCGGCGGCGAGGCTGCTGAGGCGGCGGCGGCGGCTG 454
QY 241 TACAAAGTGTGAGAGAGCGCGGCGGCGGCGGCTGCTGAGGCGGCGGCGGCGGCTG 300
Db 455 TACAAAGTGTGAGAGAGCGCGGCGGCGGCGGCTGCTGAGGCGGCGGCGGCGGCTG 514
QY 301 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 515 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574
QY 361 GCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 575 GCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 634
QY 421 ATCAATTCGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 635 ATCAATTCGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 694
QY 481 AGGTTGCTCGAAAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 695 AGGTTGCTCGAAAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 754
QY 541 GTTGTCTTCTGAAAACCTCAGGTAATATTTTTCGACGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 755 GTTGTCTTCTGAAAACCTCAGGTAATATTTTTCGACGCTGCTGCTGCTGCTGCTGCTGCTG 814
QY 601 TTCTACAGATCCTCGCATGTGCGCATGGAACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 815 TTCTACAGATCCTCGCATGTGCGCATGGAACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 874
QY 661 GGTTCAGTGGTTTATGCTCAGAGCAAGGAATTAATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 875 GGTTCAGTGGTTTATGCTCAGAGCAAGGAATTAATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 934
QY 721 GTTCTTATTTTTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 935 GTTCTTATTTTTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 994
QY 781 TCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 995 TCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1054
QY 841 GACAAAACCTCCCTAACTTGGCTGGGAAGATTTCTGCTGAGGCTTTTTCCTGCTGCTGCTGCTGCTG 900
Db 1055 GACAAAACCTCCCTAACTTGGCTGGGAAGATTTCTGCTGAGGCTTTTTCCTGCTGCTGCTGCTGCTG 1114
QY 901 ATTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 1115 ATTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1174
QY 961 GAAACAACCGCGCAGAAACACTTTTCAGAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1020
Db 1175 GAAACAACCGCGCAGAAACACTTTTCAGAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1234
QY 1021 TGTGTTTGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
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Db 1235 TGTGTTTGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1294
QY 1081 CACTTGAAGGCTTTCACACCTGCGAGCCCTACCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1140
Db 1295 CACTTGAAGGCTTTCACACCTGCGAGCCCTACCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1354
QY 1141 AGTCAGAAAGCTAAAGTTTTTAAGGAGCGAGTGGCGCATGGCTAGCCCCAGGGGCGCAGAGTATT 1200
Db 1355 AGTCAGAAAGCTAAAGTTTTTAAGGAGCGAGTGGCGCATGGCTAGCCCCAGGGGCGCAGAGTATT 1414
QY 1201 AAGAGCCGACAAAGCCCTCAGTAGGTGACAGAGGCTCCCAAGACCGACGACATCAACAGCCGAG 1260
Db 1415 AAGAGCCGACAAAGCCCTCAGTAGGTGACAGAGGCTCCCAAGACCGACGACATCAACAGCCGAG 1474
QY 1261 GCGAGTCCCAACCAAGTGCAGAGCTGAGAGCTTCAACGACCGAAACCGCTTCCGGGCC 1320
Db 1475 GCGAGTCCCAACCAAGTGCAGAGCTGAGAGCTTCAACGACCGAAACCGCTTCCGGGCC 1534
QY 1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCCAGTGTAGATGCTGACACAGCCCTTGGC 1380
Db 1535 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCCAGTGTAGATGCTGACACAGCCCTTGGC 1594
QY 1381 ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
Db 1595 ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1654
QY 1441 CCACACCTTAAACCTGCTCATTCGAGCTATCAGATTTATGAAATTTTCATGTTGCAAAACGG 1500
Db 1655 CCACACCTTAAACCTGCTCATTCGAGCTATCAGATTTATGAAATTTTCATGTTGCAAAACGG 1714
QY 1501 AAGTTTAAAGGAAACGTTTACGTCCTATGATGTAAGAGATGTCATTTGAAACAAATTTCTGCT 1560
Db 1715 AAGTTTAAAGGAAACGTTTACGTCCTATGATGTAAGAGATGTCATTTGAAACAAATTTCTGCT 1774
QY 1561 GGTCACTGCGACATGTTGCTGATGATTTAAAGCCCTTCAAAACGCTGTTGATCAAAATTTCTT 1620
Db 1775 GGTCACTGCGACATGTTGCTGATGATTTAAAGCCCTTCAAAACGCTGTTGATCAAAATTTCTT 1834
QY 1621 GGAAAGGGGCAAAATCACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAACATGAG 1680
Db 1835 GGAAAGGGGCAAAATCACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAACATGAG 1894
QY 1681 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTTGAAGAAACAGGTACAGTCC 1740
Db 1895 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTTGAAGAAACAGGTACAGTCC 1954
QY 1741 ATAGAGTCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Db 1955 ATAGAAATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 2014
QY 1801 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
Db 2015 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 2074
QY 1861 GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGCAACAAACAGGTGGCTGC 1920
Db 2075 GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGCAACAAACAGGTGGCTGC 2134
QY 1921 TTATCCAGATCAACTAGTGCACAAATCTGAGAGGCTGCGAGTTCATTTCTGACGCGCAAT 1980
Db 2135 TTATCCAGATCAACTAGTGCACAAATCTGAGAGGCTGCGAGTTCATTTCTGACGCGCAAT 2194
QY 1981 GAGTTCAGTCCGACAGCTTTCTAGCGCTTAGCCCTACTATGCAAGTCAAGCAACAG 2040
Db 2195 GAGTTCAGTCCGACAGCTTTCTAGCGCTTAGCCCTACTATGCAAGTCAAGCAACAG 2254
QY 2041 GTGCCAATTTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCA 2100
Db 2255 GTGCCAATTTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCA 2314
QY 2101 ATAAATACGGCACCCAGCGAGCGCCCAACAACTTTTACAGATCCCACTCTCTCCGA 2160
Db 2315 ATAAATACGGCACCCAGCGAGCGCCCAACAACTTTTACAGATCCCACTCTCTCCGA 2374
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QY	2161	GCATCAAGCATCTGCCCGCCAGGCAGAAAACTCTGCACCCCTAACCCCTCAGCGCTTACAGGAA	2220
Db	2375	GCCATCAAGCATCTGCCCGCCAGGCAGAAACTCTGCACCCCTAACCCCTCAGCGCTTACAGGAA	2434
QY	2221	AGCATTTCTGACGTCACCACTCCCTCTGTGTGCTCCAAAGGAAAATGTTGAGTTGCACAG	2280
Db	2435	AGCATTTCTGACGTCACCACTCCCTCTGTGTGCTCCAAAGGAAAATGTTGAGTTGCACAG	2494
QY	2281	TCAAACTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGAGAAACTCTG	2340
Db	2495	TCAAACTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGAGAAACTCTG	2554
QY	2341	TTGTCTGCTGTCCCATGGTGCCGAAAGGACTTTGGGCAAACTTTTGTGCTGTGCAAAACCTG	2400
Db	2555	TTGTCTGCTGTCCCATGGTGCCGAAAGGACTTTGGGCAAACTTTTGTGCTGTGCAAAACCTG	2614
QY	2401	ATCAGGTGCGACCGAGGAATCGAATATACAACTTTTCAGGGAGTGAGTCAAGTGCGCTCCAGA	2460
Db	2615	ATCAGGTGCGACCGAGGAATCGAATATACAACTTTTCAGGGAGTGAGTCAAGTGCGCTCCAGA	2674
QY	2461	GGCAGCCGAAGATTTTATACCCCAAATGGAGGAAATCCAAAATGTTTATAACTGATGAAGAG	2520
Db	2675	GGCAGCCGAAGATTTTATACCCCAAATGGAGGAAATCCAAAATGTTTATAACTGATGAAGAG	2734
QY	2521	GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGTGATGCCGACCGCAGCCTGCCAGGGAA	2580
Db	2735	GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGTGATGCCGACCGCAGCCTGCCAGGGAA	2794
QY	2581	GCTGCCCTTGGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT	2640
Db	2795	GCTGCCCTTGGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT	2854
QY	2641	AAGCGAGGAGAAAGTACAGATGCCCTCAGTTGGCTCATGTCAAACTGAATAA	2694
Db	2855	AAGCGAGGAGAAAGTACAGATGCCCTCAGTTGGCTCATGTCAAACTGAATAA	2908

RESULT 6	
ADB78684	
ID	ADB78684 standard; cDNA; 3074 BP.
XX	
AC	ADB78684;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Human potassium channel subunit mutant cDNA SEQ ID NO:55.
XX	
XX	ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW	neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW	antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW	nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW	ion channel dysfunction; human.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO2003008574-A1.
XX	
PD	30-JAN-2003.
XX	
PF	08-JUL-2002; 2002WO-AU000910.
XX	
PR	18-JUL-2001; 2001AU-00006452.
PR	05-MAR-2002; 2002AU-0000910.
PR	13-MAY-2002; 2002AU-00002292.
XX	
PA	(BION-) BIONOMICS LTD.
PA	(WALL/) WALLACE R W.
XX	
PI	Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI	Berkovic SF, Scheffer IE;
XX	

WIPI; 2003-2393332/23.
 Identifying predisposition to an ion channel dysfunction, such as
 periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 schizophrenia, anxiety and depression, by detecting encoding-gene
 mutation events.
 Claim 6; SEQ ID NO 55; 106pp; English.
 The invention relates to a novel method for identifying a subject
 predisposed to a disorder associated with ion channel dysfunction. The
 method comprises ascertaining if at least one of the genes encoding ion
 channel subunits (ICS) has undergone a mutation event so that a cDNA
 derived from the subject has any of 134 nucleotide sequences. The method
 of the invention has neotrophic, neuroprotective, inotropic, antipyretic,
 antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
 neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
 ophthalmological activity. A polynucleotide of the invention acts as an
 ion channel agonist, or ion channel antagonist. The methods, isolated
 nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 modulator of an ion channel, cells and genetically modified non-human
 animal, are useful for the diagnosis and treatment of epilepsy and/or a
 disorder associated with ion channel dysfunction, such as hyper- or hypo-
 kalemic periodic paralysis, myotonias, malignant hyperthermia,
 myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
 depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 fibrosis, congenital stationary night blindness and total colour
 blindness. The present sequence represents a mutant cDNA of the
 invention. The sequence data for this patent is not represented in the
 printed specification, but was obtained in electronic format directly
 from wipo.int/pub/published_pat/sequences.
 sequence 3074 RP: 787 A; 784 C; 789 G; 714 T; 0 U; 0 Other;

Query Match	99.5%	Score	2679.6	DB	10	Length	3074
Best Local Similarity	99.7%	Pred. No.	0				
Matches	2685	Conservative	0	Mismatches	9	Indels	0
Gaps	0						
QY	1	ATGAAGGATGTGGAGTCCGGGCGGGGACAGGTGCTGTCTGAACTCGGACGCGCAGGGGC	60				
Db	215	ATGAAGGATGTGGAGTCCGGGCGGGGACAGGTGCTGAACTCGGACGCGCAGGGGC	274				
QY	61	GACGCGCTCTACTCTGGGCACCCGCGCGGCAGCTTGGTGGCGGCGGGTGGGCTG	120				
Db	275	GACGCGCTCTACTCTGGGCACCCGCGCGGCACGCTTGGTGGCGGCGGGTGGGCTG	334				
QY	121	AGGGAGAGCGCGGGGCAAGCAGGGGCGCCGGATGAGCCTGCTGGGGAACCGGCTCTCT	180				
Db	335	AGGGAGAGCGCGGGGCAAGCAGGGGCGCCGGATGAGCCTGCTGGGGAACCGGCTCTCT	394				
QY	181	TACACAGTACGAGCTGCCGGCGCAACGTCAAGTACCGCGCGGTGCAGAACTACCTG	240				
Db	395	TACACAGTACGAGCTGCCGGCGCAACGTCAAGTACCGCGCGGTGCAGAACTACCTG	454				
QY	241	TACACGTCCTGGAGAGACCCCGCGCTGGGCGTTCACTACACGCTTTTGTTTTCTC	300				
Db	455	TACACGTCCTGGAGAGACCCCGCGCTGGGCGTTCACTACACGCTTTTGTTTTCTC	514				
QY	301	CTTGTCTTTGGTTCCTGATTTTGTTCAGTGTTTTCTACCATCCCTGAGCACACAAATG	360				
Db	515	CTTGTCTTTGGTTCCTGATTTTGTTCAGTGTTTTCTACCATCCCTGAGCACACAAATG	574				
QY	361	GCCTCAAGTTGCCTCTTGATCTCTGGAGTTTCGTGATGATTTGCTCTTTGGTTTGAGTTC	420				
Db	575	GCCTCAAGTTGCCTCTTGATCTCTGGAGTTTCGTGATGATTTGCTCTTTGGTTTGAGTTC	634				
QY	421	ATCATTCGAATCTGGTCTCGGGTTCCTGCTGTCGATATAGAGGATGGCAAGGAAGACTG	480				
Db	635	ATCATTCGAATCTGGTCTCGGGTTCCTGCTGTCGATATAGAGGATGGCAAGGAAGACTG	694				

QY 481 AGGTTTGTCTGAAAGCCCTTCGTGTATAGATACCAITGTTCTTATCGCTTCAATAGCA 540
DB |||||
QY 695 AGGTTTGTCTGAAAGCCCTTCGTGTATAGATACCAITGTTCTTATCGCTTCAATAGCA 754
DB |||||
QY 541 GTTGTTCGCAAAAACCTCAGGGTAATATTTTGGCAAGTCTGCACTCAGAAAGTCTCCGT 600
DB |||||
QY 755 GTTGTTCGCAAAAACCTCAGGGTAATATTTTGGCAAGTCTGCACTCAGAAAGTCTCCGT 814
QY |||||
QY 601 TTCCTACAGATCCTCCGATGTCGCGATGAGCCGAAGGGGAGGACATTTGGAAAATTAATCTG 660
DB |||||
QY 815 TTCCTACAGATCCTCCGATGTCGCGATGAGCCGAAGGGGAGGACATTTGGAAAATTAATCTG 874
QY |||||
QY 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGTG 720
DB |||||
QY 875 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGTG 934
QY |||||
QY 721 GTTCTTATTTTTCGTTCTTCCTGCTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
DB |||||
QY 935 GTTCTTATTTTTCGTTCTTCCTGCTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 994
QY |||||
QY 781 TCTACATATGAGATGCTCTCTGGTGGGGCACAATTAATTCACAACATTAATGGCTATGGA 840
DB |||||
QY 995 TCTACATATGAGATGCTCTCTGGTGGGGCACAATTAATTCACAACATTAATGGCTATGGA 1054
QY |||||
QY 841 GACAAAACCTCCCTAACTTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCCCTTGGC 900
DB |||||
QY 1055 GACAAAACCTCCCTAACTTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCCCTTGGC 1114
QY |||||
QY 901 ATTTCTTTCTTTGCACTTCTCTCGCGGCAATTTCTGGCTCAGGTTTGGCAATTAAGATACAA 960
DB |||||
QY 1115 ATTTCTTTCTTTGCACTTCTCTCGCGGCAATTTCTGGCTCAGGTTTGGCAATTAAGATACAA 1174
QY |||||
QY 961 GAACAACACCGCCAGAAACACTTTTCAGAAAAGAAAGGAAACCCAGCTGCCAACCCTCAATTCAG 1020
DB |||||
QY 1175 GAACAACACCGCCAGAAACACTTTTCAGAAAAGAAAGGAAACCCAGCTGCCAACCCTCAATTCAG 1234
QY |||||
QY 1021 TGTGTTTGGCTGAGTACGCACTGATGAGAAATCTGTTTCCATTTGCAACCTTGGAAGCCA 1080
DB |||||
QY 1235 TGTGTTTGGCTGAGTACGCACTGATGAGAAATCTGTTTCCATTTGCAACCTTGGAAGCCA 1294
QY |||||
QY 1081 CACTTGAAGCCCTTGCAACCTTGCAAGCCCTTACCAAGAAAGAAACAAGGGGAGGACATCAAGC 1140
DB |||||
QY 1295 CACTTGAAGCCCTTGCAACCTTGCAAGCCCTTACCAAGAAAGAAACAAGGGGAGGACATCAAGC 1354
QY |||||
QY 1141 AGTCAGAAGCTAAGTTTAAAGAGCGAGTGCGCATGGCTAGCCGCCAGGGGCCAGAGTATT 1200
DB |||||
QY 1355 AGTCAGAAGCTAAGTTTAAAGAGCGAGTGCGCATGGCTAGCCGCCAGGGGCCAGAGTATT 1414
QY |||||
QY 1201 AAGAGCCGACAAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCCGACATCAACGCGAG 1260
DB |||||
QY 1415 AAGAGCCGACAAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCCGACATCAACGCGAG 1474
QY |||||
QY 1261 GGCAGTCCCAACAAAGTCAGAAAGCTGGAGCTTCAACGACCGAACCCTTCGGGCC 1320
DB |||||
QY 1475 GGCAGTCCCAACAAAGTCAGAAAGCTGGAGCTTCAACGACCGAACCCTTCGGGCC 1534
QY |||||
QY 1321 TCGCTGCGCCTCAAAGTTCTCAGCCAAAACAGTGATAGTGTGACACAGCCCTTGGC 1380
DB |||||
QY 1535 TCGCTGCGCCTCAAAGTTCTCAGCCAAAACAGTGATAGTGTGACACAGCCCTTGGC 1594
QY |||||
QY 1381 ACTGATGATGATATGATGAAAAGGATGCCAGTGTGATGATATCAGTGGAAAGACCTCAC 1440
DB |||||
QY 1595 ACTGATGATGATATGATGAAAAGGATGCCAGTGTGATGATATCAGTGGAAAGACCTCAC 1654
QY |||||
QY 1441 CCACACTTAAACTGTCAATTCGAGCTATCAGAAATTAATGAATTTTCAATGTTGCAAAACGG 1500
DB |||||
QY 1655 CCACACTTAAACTGTCAATTCGAGCTATCAGAAATTAATGAATTTTCAATGTTGCAAAACGG 1714
QY |||||
QY 1501 AAGTTTAAAGGAACCTTACGTCATATGATGTAAGATGTCATTTGAACAATTTCTGCT 1560
DB |||||
QY 1715 AAGTTTAAAGGAACCTTACGTCATATGATGTAAGATGTCATTTGAACAATTTCTGCT 1774
QY |||||
QY 1561 GGTCTATCGGACATGTTGTGTAGAAATTAAGCCCTTCAAAACAGCTGTTGATCAAAATTCCT 1620
DB |||||

DB |||||
QY 1775 GGTCAATCGGACATGTTGTGTAGAAATTAAGCCCTTCAAAACAGCTGTTGATCAAAATTCCT 1834
QY |||||
QY 1621 GGAAAAGGGCAAAATCACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAAATGAG 1680
DB |||||
QY 1835 GGAAAAGGGCAAAATCACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAAATGAG 1894
QY |||||
QY 1681 ACCCAGACGATCTCAGTATGCTCGTCCGGTGGTCAAGGTTGAAAACAGGTACAGTCC 1740
DB |||||
QY 1895 ACCCAGACGATCTCAGTATGCTCGTCCGGTGGTCAAGGTTGAAAACAGGTACAGTCC 1954
QY |||||
QY 1741 ATAGAGTCCAAAGCTGGACTGCTTACAGATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
DB |||||
QY 1955 ATAGAAATCCAAAGCTGGACTGCTTCTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 2014
QY |||||
QY 1801 GCCTCAGCCCTCGCTTTGGCTTCATCCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
DB |||||
QY 2015 GCCTCAGCCCTCGCTTTGGCTTCATCCAGATCCACCTTTTGAATGTGAACAGACATCT 2074
QY |||||
QY 1861 GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTCCGGGTTCCGCACAAAACAGTGGCTGC 1920
DB |||||
QY 2075 GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTCCGGGTTCCGCACAAAACAGTGGCTGC 2134
QY |||||
QY 1921 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCTGCGAGTTCATTTCTGACGCAAAAT 1980
DB |||||
QY 2135 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCTGCGAGTTCATTTCTGACGCAAAAT 2194
QY |||||
QY 1981 GAGTTCAAGTCCCGACACTTTCTACGCGTTAGCCCTTACTATGCAAGTCAAGCAACAG 2040
DB |||||
QY 2195 GAGTTCAAGTCCCGACACTTTCTACGCGTTAGCCCTTACTATGCAAGTCAAGCAACAG 2254
QY |||||
QY 2041 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCA 2100
DB |||||
QY 2255 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCA 2314
QY |||||
QY 2101 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2160
DB |||||
QY 2315 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2374
QY |||||
QY 2161 GCCATCAGCATCTGCCAGCCAGCAAACTCTGCACCTTAACCTCGCAGGCTTACAGGAA 2220
DB |||||
QY 2375 GCCATCAGCATCTGCCAGCCAGCAAACTCTGCACCTTAACCTCGCAGGCTTACAGGAA 2434
QY |||||
QY 2221 AGCATTTCTGACGTCACCACTGCTGCTTGTGCTCCAAAGGAAATGTTTCAGGTTGCACAG 2280
DB |||||
QY 2435 AGCATTTCTGACGTCACCACTGCTGCTTGTGCTCCAAAGGAAATGTTTCAGGTTGCACAG 2494
QY |||||
QY 2281 TCAAAATCTCAACAGGACCGTTCTATGAGGAAAAGCTTTTGACATGGGAGGAGAAATCTGT 2340
DB |||||
QY 2495 TCAAAATCTCAACAGGACCGTTCTATGAGGAAAAGCTTTTGACATGGGAGGAGAAATCTGT 2554
QY |||||
QY 2341 TTGTCTGTCTGCCATGGTCCGAAGACCTTGGGCAAACTTTTGTCTGTGCAAAACCTG 2400
DB |||||
QY 2555 TTGTCTGTCTGCCATGGTCCGAAGACCTTGGGCAAACTTTTGTCTGTGCAAAACCTG 2614
QY |||||
QY 2401 ATCAGGTCGACCGGAGGAATCAATATACAACTTTTCAGGAGTGTAGTCAAGTGGCTCCAGA 2460
DB |||||
QY 2615 ATCAGGTCGACCGGAGGAATCAATATACAACTTTTCAGGAGTGTAGTCAAGTGGCTCCAGA 2674
QY |||||
QY 2461 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATTAATGTGAAGAG 2520
DB |||||
QY 2675 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATTAATGTGAAGAG 2734
QY |||||
QY 2521 GTGGGTCGAGAGAGACAGACACTTTTGTGCGCCAGCCAGCCGCTGCCAGGGA 2580
DB |||||
QY 2735 GTGGGTCGAGAGAGACAGACACTTTTGTGCGCCAGCCAGCCGCTGCCAGGGA 2794
QY |||||
QY 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
DB |||||
QY 2795 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2854
QY |||||
QY 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCAAACTCAAAATAA 2694
DB |||||

Db	2855	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTTCATGTCACAACTGAATAA	2908
RESULT 7			
AAAS14653			
ID	AAAS14653	standard; cDNA; 2667 BP.	
XX	AAAS14653;		
AC			
XX	18-DEC-2001	(first entry)	
XX			
DE	Human	cDNA encoding a voltage gated potassium channel hKCNQ5-2.	
XX			
KW	Human; ss;	voltage-gated potassium channel; KCNQ5-2; nototropic;	
KW	cerebroprotective;	neurotropic; analgesic; vision disorder;	
KW	central nervous system disorder;	epilepsy; migraine; hearing disorder;	
KW	psychotic disorder;	seizure; learning disorder; memory disorder; stroke;	
KW	pain; gene therapy;	splice variant.	
XX			
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	CDS	1..2967	
FT		/*tag= a	
FT		/product= "hKCNQ5-2"	
XX			
PN	WO200170759-A1.		
XX			
PD	27-SEP-2001.		
XX			
PF	20-MAR-2001; 2001WO-US009328.		
XX			
PR	21-MAR-2000; 2000US-0190954P.		
XX			
PA	(ICAG-) ICAGEN INC.		
XX			
PI	Jegla TJ;		
XX			
DR	WPI; 2001-611467/70.		
DR	P-PSDB; AAU09021.		
XX			
PT	Polypeptides and polynucleotides of potassium channel KCNQ5 for		
PT	identifying a compound modulating ion flux in eukaryotic cell or cell		
PT	membrane expressing the protein, comprises KCNQ approximately alpha- subunits.		
XX			
PS	Claim 5; Page 63-64; 78pp; English.		
XX			
CC	The invention relates to an isolated polypeptide comprising an alpha-		
CC	subunit of a KCNQ potassium channel, with a subsequence having 65%		
CC	sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence		
CC	and forms a KCNQ potassium channel having the characteristic of voltage-		
CC	gating with at least an additional KCNQ alpha-subunit. Also included in		
CC	the scope of the invention are the nucleic acids encoding hKCNQ5		
CC	(including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression		
CC	vectors encoding them, antibodies against them, the use of 3-dimensional		
CC	computer modelling to identify molecules that bind to a KCNQ containing		
CC	potassium channel and modulate ion flux through the channel. The KCNQ		
CC	polypeptide is useful for identifying a compound that increases or		
CC	decreases ion flux through a potassium channel expressed in an eukaryotic		
CC	host cell or cell membrane. The compound (and the KCNQ nucleic acid when		
CC	used in gene therapy) is useful as a pharmaceutical agent for treating		
CC	diseases involving abnormal ion flux, such as disorders of the central		
CC	nervous system, such as epilepsy, migraines, hearing and vision problems,		
CC	psychotic disorders, seizures, learning and memory disorders, stroke and		
CC	pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a		
CC	human tissue and the use of a nucleotide sequence of KCNQ5 to search		
CC	computer databases to find variants of the sequence which are associated		
CC	with disease states, is useful for screening mutations of KCNQ5. The		
CC	present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-2		
XX			
SQ	Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 U; 0 Other;		
	Query Match	97.6%; Score 2630; DB 4; Length 2667;	

1021	TGTTGTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCGAACTCGGAAGCCA	1081
Qy	CAC TTGAAGGCCTTTGCACACCTGCAGGCCCTACCAAGAAGAAACAAGGGGGAAGCATCAAGC	1140
Db	CAC TTGAAGGCCTTGCAACCTGCAGCCCTACCAA-----	1115
Qy	AGTCAGAAAGCTAAGTTTTTAAGGAGCGAGTGGCGATGGCTAGCCCCAGGGGCGCAGAGTATT	1200
Db	--TCAGAAGCTAAGTTTTTAAGGAGCGAGTGGCGATGGCTAGCCCCAGGGGCGCAGAGTATT	1173
Qy	AAGAGCCGACAAGCCTCAGTAGGTGACAGAGAGTCCCAAGACACCGACATCACAGCCGAG	1260
Db	AAGAGCCGACAAGCCTCAGTAGGTGACAGAGAGTCCCAAGACACCGACATCACAGCCGAG	1233
Qy	GGCAGTCCCAACAAAGTGCAAGAGCTGGAGCTTCAACGACCGAAACCCGCTTCCGGGCC	1293
Db	GGCAGTCCCAACAAAGTGCAAGAGCTGGAGCTTCAACGACCGAAACCCGCTTCCGGGCC	1293
Qy	TCGCTGGCGCTCAAAAGTTCTCAGCCAAAACCAAGTATAGATGCTGACACAGAGCCTTGGC	1380
Db	TCGCTGGCGCTCAAAAGTTCTCAGCCAAAACCAAGTATAGATGCTGACACAGAGCCTTGGC	1353
Qy	ACTGATCATGTATATGATGAAAAAGGATGCCAGTGTGATGTCAGTGGGAAGACCTCACC	1440
Db	ACTGATCATGTATATGATGAAAAAGGATGCCAGTGTGATGTCAGTGGGAAGACCTCACC	1413
Qy	CCACCACCTTAAACCTGTCAATTCGAGCTATCAGAAATATGAAATTCATGTTGCAAAACGG	1500
Db	CCACCACCTTAAACCTGTCAATTCGAGCTATCAGAAATATGAAATTCATGTTGCAAAACGG	1473
Qy	AAGTTTAAAGAAACGTTACGTCCATATGATGTTAAAGATGTCATGTAACAATATTCGTCT	1560
Db	AAGTTTAAAGAAACGTTACGTCCATATGATGTTAAAGATGTCATGTAACAATATTCGTCT	1533
Qy	GGTCATCTGCACATGTTGTGTAGAAATTAAGACCTTCAACACGTTGTGATCAAAATTCCT	1620
Db	GGTCATCTGCACATGTTGTGTAGAAATTAAGACCTTCAACACGTTGTGATCAAAATTCCT	1593
Qy	GGAAAAAGGCAAAATCACATCAGATAAGAAAGCGCGAGAGAAAAATAACAGCAGAAACATGAG	1680
Db	GGAAAAAGGCAAAATCACATCAGATAAGAAAGCGCGAGAGAAAAATAACAGCAGAAACATGAG	1653
Qy	ACCAACAGACGATCTCAGTATGCTCGGTGGGTGATCAAGGTTGAAAAACAGGTACAGTCC	1740
Db	ACCAACAGACGATCTCAGTATGCTCGGTGGGTGATCAAGGTTGAAAAACAGGTACAGTCC	1713
Qy	ATAGAGTCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCTTCCGAAAGGCTCT	1800
Db	ATAGAGTCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCTTCCGAAAGGCTCT	1773
Qy	GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAAACAGACATCT	1860
Db	GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAAACAGACATCT	1833
Qy	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTCCGGGTTCCGACAAAAACAGTGGCTGC	1920
Db	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTCCGGGTTCCGACAAAAACAGTGGCTGC	1893
Qy	TTATCCAGATCAACTAGTGGCAACATCTCAGAGGCCCTGCAGTTTCATTCTGACGCCCAAT	1980
Db	TTATCCAGATCAACTAGTGGCAACATCTCAGAGGCCCTGCAGTTTCATTCTGACGCCCAAT	1953
Qy	GAGTTCAGTGCCACAGACTTTTCTACGCGCTTAGCGCTACTATGACACAGTCAAGCAACACAG	2040
Db	GAGTTCAGTGCCACAGACTTTTCTACGCGCTTAGCGCTACTATGACACAGTCAAGCAACACAG	2013
Qy	GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCAA	2100
Db	GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAACCATTTGCAAAACCAA	2073
Qy	ATAAATAAGCGGACCCAAAGCAGCAGGCCCAACAACTTTTACAGATCCCACTCTCTCTCCCA	2160
Db	ATAAATAAGCGGACCCAAAGCAGCAGGCCCAACAACTTTTACAGATCCCACTCTCTCTCCCA	2133

Qy	2161	GCATCAAGCATCTGCCAGCCGACGAACTCTCTGCAACCTTAACTTCCAGGCTTACAGGAA	2222
Db	2134	GCCATCAAGCATCTGCCAGCCGACGAACTCTGCAACCTTAACTTCCAGGCTTACAGGAA	2193
Qy	2221	AGCATTTCTGACGTCACCACTGCTTGTGGCCCTCCAAGGAAAATGTTCAAGTTTGACAG	2280
Db	2194	AGCATTTCTGACGTCACCACTGCTTGTGGCCCTCCAAGGAAAATGTTCAAGTTTGACAG	2253
Qy	2281	TCAAATCTCCAAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAACTCTG	2340
Db	2254	TCAAATCTCCAAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAACTCTG	2313
Qy	2341	TTGTCTGTCTGCCATGTCGCCGAGGACCTTGGGCAAAATCTTTGCTGTGCAAAACCTG	2400
Db	2314	TTGTCTGTCTGCCATGTCGCCGAGGACCTTGGGCAAAATCTTTGCTGTGCAAAACCTG	2373
Qy	2401	ATCAGGTCGACCCAGGAACTGAATATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2460
Db	2374	ATCAGGTCGACCCAGGAACTGAATATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2433
Qy	2461	GGCAGCCAAGATTTTACCCCAAATGAGGGAATCCAATTTGTTTAACTGATGAAGAG	2520
Db	2434	GGCAGCCAAGATTTTACCCCAAATGAGGGAATCCAATTTGTTTAACTGATGAAGAG	2493
Qy	2521	GTGGGTCCGAAAGACAGACAGACACATTTTGATGCCGACCGCAGCCTGCCAGGGAA	2580
Db	2494	GTGGGTCCGAAAGACAGACAGACACATTTTGATGCCGACCGCAGCCTGCCAGGGAA	2553
Qy	2581	GCTGCCCTTTGTCATCAGACTCTCTAAGGACTGGAGGTTCAGATCATCTCAGAGCATTTGT	2640
Db	2554	GCTGCCCTTTGTCATCAGACTCTCTAAGGACTGGAGGTTCAGATCATCTCAGAGCATTTGT	2613
Qy	2641	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAAACTGAATAA	2694
Db	2614	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAAACTGAATAA	2667
RESULT 8			
AAH43633			
ID	AAH43633 standard; cDNA; 2772 BP.		
XX			
AC	AAH43633;		
DT	21-JAN-2002 (first entry)		
XX			
DE	Human ion-channel forming protein ORF.		
XX			
Kw	Ion-channel forming protein; voltage-gated potassium channel; fetal;		
Kw	brain; thymus; prostate; heart; skeletal muscle; probe; ss.		
OS	Homo sapiens.		
XX			
PN	WO200175108-A1.		
PD	11-OCT-2001.		
XX			
PF	03-APR-2001; 2001WO-US010875.		
XX			
PR	03-APR-2000; 2000US-0194255P.		
XX			
PA	(LEXI-) LEXICON GENETICS INC.		
XX			
PI	Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;		
PI	Sands AT;		
XX			
DR	WPI; 2001-656987/75.		
XX			
PT	P-PSDB; AAB47678.		
XX			
PT	New human ion channel protein and polynucleotides encoding the protein,		
PT	useful in diagnosing or treating diseases, in drug screening, and in		
PT	clinical trial monitoring.		
XX			

Claim 1: page 34-35; 41pp; English.

The sequences in AAH43633-34 encode a novel ion-channel forming protein. The protein shares structural similarity with mammalian ion channel proteins, particularly voltage-gated potassium channel proteins. The protein is expressed in many human cell lines including fetal brain, brain, thymus, prostate, heart and skeletal muscle. The novel protein can be used in the diagnosis or treatment of diseases, in drug screening, and in clinical trial monitoring. The oligonucleotides may be used as hybridization probes for screening libraries, and assessing gene expression patterns (particularly using a micro array or high throughput chip format). The nucleic acids and novel protein can also be used in the identification, selection and validation of novel molecular targets for drug discovery, to screen collections of genetic material from patients who have a particular medical condition, to identify mutations associated with a particular disease, as a diagnostic or prognostic assay, and to screen for drugs which can be used to treat symptomatic or phenotypic manifestations of perturbing the normal function of novel human protein. The polypeptides are further used in generating antibodies

Sequence 2772 BP: 715 A; 700 C; 713 G; 644 T; 0 U; 0 Other;

Query Match 97.4% Score 2625.2; DB 5; Length 2772;

Query Match
Best Local Similarity 98.9%; Pred. No. 0;
57.1%; Pred. No. 0;

	Best local similarity	98.36%	Mismatches	3;	Indels	27;	Gaps	1;	
	Matches 2664:	Conservative	0;	Mismatches	3;	Indels	27;	Gaps	1;

Qy	1	ATGAAGAGATGTGGAGTCCGGCCGGGGCAGAGTGTGCTGAACTCGGACAGCCGCGAGGGGC	60
Db	106	ATGAAGAGATGTGGAGTCCGGCCGGGGCAGAGTGTGCTGAACTCGGACAGCCGCGAGGGGC	165
Qy	61	GACGGCTGTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGGTGGCGCTG	120
Db	166	GACGGCTGTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGGTGGCGCTG	225
Qy	121	AGGAGAGACCCCGGGGCAAGCAGGGGGCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT	180
Db	226	AGGAGAGACCCCGGGGCAAGCAGGGGGCCGGATGAGCCTCTGGGGAAGCCGCTCTCT	285
Qy	181	TACACGAGTAGCCAGAGCTCCGGCGCAGCTCAAGTACCCGGCGGCTGCAGAACTACCTG	240
Db	286	TACACGAGTAGCCAGAGCTCCGGCGCAGCTCAAGTACCCGGCGGCTGCAGAACTACCTG	345
Qy	241	TACAACTGCTGGAGAGACCCCGGGCTGGGCGTTCACTACACGCTTTCGTTTTCTC	300
Db	346	TACAACTGCTGGAGAGACCCCGGGCTGGGCGTTCACTACACGCTTTCGTTTTCTC	405
Qy	301	CTTGTCTTTGGTTGCTTGAATTTGTTCAGTGTTTCTACCATCCCTGAGCACACAAATTG	360
Db	406	CTTGTCTTTGGTTGCTTGAATTTGTTCAGTGTTTCTACCATCCCTGAGCACACAAATTG	465
Qy	361	GCCTCAAGTTGCCTCTTGATCTCGAGTTTCGTGATGTGCTCTTTGGTTTGAGTTTC	420
Db	466	GCCTCAAGTTGCCTCTTGATCTCGAGTTTCGTGATGTGCTCTTTGGTTTGAGTTTC	525
Qy	421	ATCATTCGAATCTGCTTCGGGGTTCGTTTGTGATATAGAGGATGGCAAGGAGACTG	480
Db	526	ATCATTCGAATCTGCTTCGGGGTTCGTTTGTGATATAGAGGATGGCAAGGAGACTG	585
Qy	481	AGGTTTGCTCGAAAGCCCTTCGTGTTATAGATACCAATGTCTTATCGCTTCAATAGCA	540
Db	586	AGGTTTGCTCGAAAGCCCTTCGTGTTATAGATACCAATGTCTTATCGCTTCAATAGCA	645
Qy	541	GTTGTTTCTGCAAAAACCTCAGGGTAATATTTTTGCCACGCTGTGCACTCAGAAGTCTCCGT	600
Db	646	GTTGTTTCTGCAAAAACCTCAGGGTAATATTTTTGCCACGCTGTGCACTCAGAAGTCTCCGT	705
Qy	601	TTTCCTACAGATCCTCCGATGTTGCCATGGACCGAAGGGGAGGCACTTTGGAAATTACTG	660
Db	706	TTTCCTACAGATCCTCCGATGTTGCCATGGACCGAAGGGGAGGCACTTTGGAAATTACTG	765
Qy	661	GGTTACAGTGGTTATGCTCACACAGGAATTAATCACAGCTTTGGTACATAGATTTTTG	720
Db	766	GGTTACAGTGGTTATGCTCACACAGGAATTAATCACAGCTTTGGTACATAGATTTTTG	825

QY	1801	GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCACCTTTGATGTGAACAGACATCT	1860
DB	1879	GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCACCTTTGATGTGAACAGACATCT	1938
QY	1861	GACTATCAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCGCGACAAAAACAGTGGCTGC	1920
DB	1939	GACTATCAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCGCGACAAAAACAGTGGCTGC	1998
QY	1921	TTATCCAGATCAACTAGTGGCCAAACATCTCGAGAGGCTGCAGTTCATCTTGACGCCAAAT	1980
DB	1999	TTATCCAGATCAACTAGTGGCCAAACATCTCGAGAGGCTGCAGTTCATCTTGACGCCAAAT	2058
QY	1981	GAGTTTCAGTGGCCACAGATTTCTACGCGCTTAGCCCTACTATGCACAGCTCAAGCAACACAG	2040
DB	2059	GAGTTTCAGTGGCCACAGATTTCTACGCGCTTAGCCCTACTATGCACAGCTCAAGCAACACAG	2118
QY	2041	GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCACTTGCAAAACCA	2100
DB	2119	GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCACTTGCAAAACCA	2178
QY	2101	ATAAATACGCCACCCNAGCCAGCAGCCCCAACACTTTACAGATCCACCTCTCTCCCA	2160
DB	2179	ATAAATACGCCACCCNAGCCAGCAGCCCCAACACTTTACAGATCCACCTCTCTCCCA	2238
QY	2161	GCCATCAAGCATCTGCCAGGCCAGAAAACCTCGCACCCCTAACCTCGAGGCTTACAGGAA	2220
DB	2239	GCCATCAAGCATCTGCCAGGCCAGAAAACCTCGCACCCCTAACCTCGAGGCTTACAGGAA	2298
QY	2221	AGCATTTTCAGCTCACCACTGCTTGTGGCTCCAAAGGAAAATGTTTACGTTGCACAG	2280
DB	2299	AGCATTTTCAGCTCACCACTGCTTGTGGCTCCAAAGGAAAATGTTTACGTTGCACAG	2358
QY	2281	TCAAATCTCACAAAGGACCGTTCTATCAGGAAAAGCTTTCACATGGGAGAGAGAACTCTG	2340
DB	2359	TCAAATCTCACAAAGGACCGTTCTATCAGGAAAAGCTTTCACATGGGAGAGAGAACTCTG	2418
QY	2341	TTGTCTGTCTGCCATGGTCCGAAAGACTTTGGGCAAACTTTTGTCTGTGCAAAACCTG	2400
DB	2419	TTGTCTGTCTGCCATGGTCCGAAAGACTTTGGGCAAACTTTTGTCTGTGCAAAACCTG	2478
QY	2401	ATCAGGTGCACCGAGGAACTGAATATACAACTTTCAGGGAGTCAAGTCAAGTGCTCCAGA	2460
DB	2479	ATCAGGTGCACCGAGGAACTGAATATACAACTTTCAGGGAGTCAAGTCAAGTGCTCCAGA	2538
QY	2461	GGCAGCCAAAGATTTTATCCCAATGGAGGGAATCCAAATTTGTTTATAACTGATGAAGAG	2520
DB	2539	GGCAGCCAAAGATTTTATCCCAATGGAGGGAATCCAAATTTGTTTATAACTGATGAAGAG	2598
QY	2521	GTGGGTCCGAAAGACAGACAGACACTTTTGTATGCCGACCGCAGCCCTGCCAGGGAA	2580
DB	2599	GTGGGTCCGAAAGACAGACAGACACTTTTGTATGCCGACCGCAGCCCTGCCAGGGAA	2658
QY	2581	GCTGCTTTTGCATCAGACTCTCTAAGGACTGGAGGTCACGATCATCTCAGAGCATTTGT	2640
DB	2659	GCTGCTTTTGCATCAGACTCTCTAAGGACTGGAGGTCACGATCATCTCAGAGCATTTGT	2718
QY	2641	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAATAA	2694
DB	2719	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAATAA	2772

RESULT 9

AAH43634

AAH43634
ID AAH43634 standard; cDNA; 3111 BP.

XX

AC AAH43634;

XX

DT 21-JAN-2002 (first entry)
vv

XX DE Human ion-channel forming protein coding sequence

DE Human ion-channel forming protein coding sequence.
XX

Ion-channel forming protein: voltage-gated potassium channel: fetal: xx

XX	OS	Homo sapiens.	
XX	XX		
XX	PH	Key	Location/Qualifiers
FT	FT	CDS	59..2831
FT	FT		/*tag= a
FT	FT		/product= "Human ion-channel forming protein"
XX	XX		
XX	PN	WO200175108-A1.	
XX	XX		
XX	PD	11-OCT-2001.	
XX	XX		
XX	PF	03-APR-2001; 2001WO-US010875.	
XX	XX		
XX	PR	03-APR-2000; 2000US-0194255P.	
XX	XX	(LEXI-) LEXICON GENETICS INC.	
XX	PA		
XX	XX	Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;	
XX	PI	Sands AT;	
XX	XX		
XX	DR	WPI: 2001-656987/75.	
XX	DR	P-PSDB; AAB47678.	
XX	XX		
XX	PT	New human ion channel protein and polynucleotides encoding the protein,	
XX	PT	useful in diagnosing or treating diseases, in drug screening, and in	
XX	PT	clinical trial monitoring.	
XX	XX		
XX	PS	Disclosure; Page 37-38; 41pp; English.	
XX	XX		
CC	CC	The sequences in AAH43633-34 encode a novel ion-channel forming protein.	
CC	CC	The protein shares structural similarity with mammalian ion channel	
CC	CC	proteins, particularly voltage-gated potassium channel proteins. The	
CC	CC	protein is expressed in many human cell lines including fetal brain,	
CC	CC	brain, thymus, prostate, heart and skeletal muscle. The novel protein can	
CC	CC	be used in the diagnosis or treatment of diseases, in drug screening, and	
CC	CC	in clinical trial monitoring. The oligonucleotides may be used as	
CC	CC	hybridization probes for screening libraries, and assessing gene	
CC	CC	expression patterns (particularly using a micro array or high throughput	
CC	CC	chip format). The nucleic acids and novel protein can also be used in the	
CC	CC	identification, selection and validation of novel molecular targets for	
CC	CC	drug discovery, to screen collections of genetic material from patients	
CC	CC	who have a particular medical condition, to identify mutations associated	
CC	CC	with a particular disease, as a diagnostic or prognostic assay, and to	
CC	CC	screen for drugs which can be used to treat symptomatic or phenotypic	
CC	CC	manifestations of perturbing the normal function of novel human protein.	
CC	CC	The polypeptides are further used in generating antibodies	
XX	XX		
XX	SS	Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;	

XX DE Human ion-channel forming protein coding sequence.

Db	2598	GGCAGCC	CAGATTTT	THACCAAT	GAGGGAT	CCAATTTG	TTTACTG	ATGAAG	2657
Qy	2521	GTGGTCCC	GAAAGAC	CAGACAG	ACACAT	TTTGTAT	CCGAC	CGCAGCT	GCACGGAA
Db	2658	GTGGTCCC	GAAAGAC	CAGACAG	ACATTTT	TGATCCG	CACCG	CAGCCT	GTCCAGGAA
Qy	2581	GCTGCC	TTTGCAT	CAGACTCT	CTAAG	GACTTGA	AGGTC	CAGATCAT	CTCAGAGCATTTGT
Db	2718	GCTGCC	TTTGCAT	CAGACTCT	CTAAG	GACTTGA	AGGTC	CAGATCAT	CTCAGAGCATTTGT
Qy	2641	AAGCAGGA	GAAGTAC	CAGATGC	CCCTC	AGCTT	GGCCTCAT	GTC	AAACTGAATAA
Db	2778	AAGCAGGA	GAAGTAC	CAGATGC	CCCTC	AGCTT	GGCCTCAT	GTC	AAACTGAATAA

RESULT 10	
AAC64371	
ID	AAC64371 standard; cDNA; 3718 BP.
XX	
XX	AAC64371;
XX	
XX	
XX	07-FEB-2001 (first entry)
XX	
DE	Human KCNQ5 (KCN6a) cDNA sequence SEQ ID NO:2.

XX	Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT	inhibitors and activators which can treat e.g. Stargardt-like macular
PT	dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX	
PS	Claim 3; Fig 2; 99pp; English.
XX	
CC	The present sequence encodes the human KCNQ5 (also called KCNQg) protein,
CC	which is a voltage-gated potassium channel protein. Human KCNQ5 has
CC	ophthalmological, auditory, central nervous system (CNS), cardioactive,
CC	anticonvulsant, gastrointestinal and muscular active activities.
CC	Sequences and methods from the present invention are useful for
CC	identifying activators or inhibitors of KCNQ5 protein. These activators
CC	and inhibitors are useful for treating Stargardt-like macular dystrophy,
CC	cone-rod dystrophy, Salla disease, age-related macular degeneration,
CC	other forms of macular degeneration, deafness, epilepsy, and different
CC	forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC	Stargardt-like macular dystrophy and cone-rod dystrophies are located at
CC	chromosome 6q
XX	
XX	
SQ	Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;
	Query Match 96.0%; Score 2585; DB 3; Length 3718;

Best Local Similarity 99.6%; Pred. No. 0; Matches 2591; Conservative 0; Mismatches 10; Indels 0; Gaps 0;			
QY	94	ACGCTTGGTGGCGCGCGGTGCCTTGAGGGAGAGCCGCGGGGCAAGCAGGGGGGCCCGG	153
DB	78	ACTGCTGAGACTGCGGCGGTGCCTTGAGGGAGAGCCGCGGGGCAAGCAGGGGGGCCCGG	137
QY	154	ATGAGCGCTGTGGGAAGCGCGTCTCTTACACAGTAGCAGAGCTCGCGGCGCAACGTC	213
DB	138	ATGAGCGCTGTGGGAAGCGCGTCTCTTACACAGTAGCAGAGCTCGCGGCGCAACGTC	197
QY	214	AAGTACCGGGGTGCAGAACTACCTGTCAACGTCCTGGAGAGACCCCGCGCTGGCG	273
DB	198	AAGTACCGGGGTGCAGAACTACCTGTCAACGTCCTGGAGAGACCCCGCGCTGGCG	257
QY	274	TTCACTTACCACGCTTTGTTTTTCTCTTGTCTTTGGTGTCTTGATTTTGTCAGTGTTT	333
DB	258	TTCACTTACCACGCTTTGTTTTTCTCTTGTCTTTGGTGTCTTGATTTTGTCAGTGTTT	317
QY	334	TCTACCATCCCTGAGCACACAAATTTGGGCTCAAGTTGCTCTTGATCTCTGGAGTTCTGT	393
DB	318	TCTACCATCCCTGAGCACACAAATTTGGGCTCAAGTTGCTCTTGATCTCTGGAGTTCTGT	377
QY	394	ATCAATTGTCGTCTTTGGTTTGGAGTTTCATCATTCGAATCTGGTCTCGGGTTGCTGTTGT	453
DB	378	ATCAATTGTCGTCTTTGGTTTGGAGTTTCATCATTCGAATCTGGTCTCGGGTTGCTGTTGT	437
QY	454	CGATATAGAGTAGGCAAGGAAGACCTGAGTTTGGCTCGAAAGGCCCTCTCTGTATTATAGAT	513
DB	438	CGATATAGAGTAGGCAAGGAAGACCTGAGTTTGGCTCGAAAGGCCCTCTCTGTATTATAGAT	497
QY	514	ACCAATTGTTCTTATCGCTTCAATPAGCAGTTGTTTCTGCAAAAACCTCAGGGTAATATTTTT	573
DB	498	ACCAATTGTTCTTATCGCTTCAATPAGCAGTTGTTTCTGCAAAAACCTCAGGGTAATATTTTT	557
QY	574	GCCAGTCTGCACTCAGAAAGTCTCCGTTTCTTACAGATCCTCCGCAATGTCGCCATGGAC	633
DB	558	GCCAGTCTGCACTCAGAAAGTCTCCGTTTCTTACAGATCCTCCGCAATGTCGCCATGGAC	617
QY	634	CGAAGGGGAGGCACTTTGGAAATTTACTGGGTTTCACTGCTTATGCTCACAAGCAAGGAATTA	693
DB	618	CGAAGGGGAGGCACTTTGGAAATTTACTGGGTTTCACTGCTTATGCTCACAAGCAAGGAATTA	677
QY	694	ATCACAGCTTGGTACATAGGAATTTTGGTTCTTTATTTTTTTCGCTTTCCTTGTCTATCTG	753
DB	678	ATCACAGCTTGGTACATAGGAATTTTGGTTCTTTATTTTTTTCGCTTTCCTTGTCTATCTG	737
QY	754	GTGGAAGAGTGCCTCAATAAGAGTTTCTACATATGCAGATGCTCTCTGGTGGGCGACA	813
DB	738	GTGGAAGAGTGCCTCAATAAGAGTTTCTACATATGCAGATGCTCTCTGGTGGGCGACA	797
QY	814	ATTACATTGCAACTATTGCTATGGCATGAGACAAACCTCCCTACTTGGCTGGCAAGATTG	873
DB	798	ATTACATTGCAACTATTGCTATGGCATGAGACAAACCTCCCTACTTGGCTGGCAAGATTG	857
QY	874	CTTTCTGCAGGCTTTGCACCTCCTTGGCAATTTCTTTCTTTGCACTTCTCGCGGCATTCTTT	933
DB	858	CTTTCTGCAGGCTTTGCACCTCCTTGGCAATTTCTTTCTTTGCACTTCTCGCGGCATTCTTT	917
QY	934	GGCTCAGGTTTTCATTTAAAGTACAAGAACAAACCGCCGAGAAAACACTTTGAGAAAAGA	993
DB	918	GGCTCAGGTTTTCATTTAAAGTACAAGAACAAACCGCCGAGAAAACACTTTGAGAAAAGA	977
QY	994	AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGGTAGTTTACCGACTGATGAGAAA	1053
DB	978	AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGGTAGTTTACCGACTGATGAGAAA	1037
QY	1054	TCTGTTTTCATTGCAACCTGGAAGCCACACTTTGAAGCCCTTGCACACCTGCAGCCCTACC	1113
DB	1038	TCTGTTTTCATTGCAACCTGGAAGCCACACTTTGAAGCCCTTGCACACCTGCAGCCCTACC	1097
QY	1114	AGAAAGAACAGGGGAAAGCATCAGCAGTCAAGAGCTAAGTTTAAAGGAGCGAGTGC	1173

Mutations in 3 known genes of the KCNQ branch of the potassium channel gene family underlie inherited cardiac arrhythmia's, neonatal epilepsy and in some cases associated with deafness. KCNQ4 has been mapped to the DFN2 locus for autosomal dominant hearing loss, and a dominant negative KCNQ4 mutation that causes deafness in a DFN2 pedigree has been identified. KCNQ4 is the first potassium channel gene underlying non-syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4

CC protein and the protein itself may be used in the prevention, treatment
CC and diagnosis of diseases associated with inappropriate KCNQ4 expression.
CC The nucleotides may also be used as DNA probes in diagnostic assays (e.g.
CC polymerase chain reactions (PCR)) to detect and quantify the presence
CC of similar nucleic acid sequences in samples and to identify mutations
CC within them, and hence which patients may be in need of restorative
CC therapy. They may also be used to study the expression and function of
CC KCNQ4 polypeptides and their role in metabolism, for example through the
CC production of transgenic animals. The KCNQ4 polypeptides may be used as
CC antigens in the production of antibodies and to identify modulators
CC (agonists and antagonists) of KCNQ4 expression and activity. The anti-
CC KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate
CC KCNQ4 expression and activity. They may be used in this way to treat
CC tinnitus, loss of hearing (especially progressive hearing loss, neonatal
CC deafness and presbycusis (deafness of the elderly)) and disease or
CC adverse conditions of the central nervous system (CNS) such as affective
CC disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by
CC trauma, stroke or neurodegenerative illness, cognitive deficits, mania,
CC compulsive behavior, dementia, depression, Huntington's disease, mania,
CC memory impairment, memory disorders and dysfunctions, motion disorders,
CC motor disorders, neurodegenerative diseases, Parkinson's disease,
CC Parkinson-like motor disorders, phobias, Pick's disease, psychosis,
CC schizophrenia, spinal cord damage, stroke and/or tremor. Conversely,
CC antisense nucleic acid molecules may be administered to down regulate
CC KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing
CC their expression
XX
SQ Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Query Match 19.2%; Score 518.4; DB 3; Length 2335;
Best Local Similarity 60.1%; Pred. No. 8.5e-142; Indels 165; Gaps 8;
Matches 1103; Conservative 0; Mismatches 566;
QY 217 TACCGCGCGGTGCAGAACTACTGTACAACTGCTGGAGAGACCCCGCGGCTGGCGGCTTC 276
DB 320 TACCGCGCGGTGCAGAACTGCGGTCTACAACTGCTGGAGAGCGCCCGCGGCTGGCGGCTTC 379
QY 277 AFTACACAGCTTCGTTTTCCTCTGCTCTTGGTTCCTGATTTGTCAGTCTTCT 336
DB 380 GTCTACACAGCTTCATATTTTGTGCTTTCAGCTCCCTCTCTCTCTGCTGCTGCTTC 439
QY 337 ACCATCCCTGACACACAAATTTGGCTTCAAGTTGCTCTTGTATCTCGAGTTCGTGATG 396
DB 440 ACTATCCAGGAGCACAGAACTTCCCAACGAGTCTCTCTCTCTCTGGAATTCGTGATG 499
QY 397 ATTGTGCTTTTGGTTTGGATTCAATTCGAACTCGCTTGGCGGTTGCTGTTGTCGA 456
DB 500 ATCGTGGTTTTCGGCTTGGAGTACATCGTCCGGGTCTGGTCCGCGGATGCTGTCGCGC 559
QY 457 TATAGGATGCAAGGAGACTGAGTTTGTCTGAAAGCCCTCTGTGTTATAGATACC 516
DB 560 TACCGAGGATGCGAGGTCGCTTCGCTTTCAGAAAGCCCTCTGTGTCATCGACTTC 619
QY 517 ATTGTTCTTATCGCTTCAATAGCAGTGTTCCTGCAAAATCTCAGGTAATATTTTGGC 576
DB 620 ATCGTGTTCGTGGCTCGGTGGCGTTCATCGCGCGGTACCCAGGGCAACATCTTCGC 679
QY 577 AGCTCTGCACTAGAGTCTCGTTTCTTACAGATCCCTCGCATCGTGGCGGATGACCGA 636
DB 680 ACCTCGCGCTGCGCAGCATGCGTTCTCTGCAATCTCGCATGCTGGCGGATGCGCATG 739
QY 637 AGCGGAGGCACTTGGAAATTTACTGGGTTTCAGTGGTTTATGCTCAGACGAAGGAATTAATC 696
DB 740 CGCGCGGACCTTGGAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGGAGCTGATC 799
QY 697 ACAGCTTGTGATAGATATTTTGGTTCTTATTTTTCGTTCTTCTCTCTCTCTCTCTG 756
DB 800 ACCGCTGTGATACATCGGTTCTGTTGCTCATCTTCGCTCTCTCTCTCTCTCTCTCTG 859
QY 757 GAAAGGATGCAATTAAGATTTTCTACATATGACAGATGCTCTCTGTTGGGCGCAATTT 816
DB 860 GAGAGGAGCGCCAACTCCGACTTCTCTCTCTACGCGCATCGCTCTGTTGGGCGGATTT 919

QY 817 ACATTGACAACTATTGGCTATGGAGACAAAACTCCCTTAACCTTGGCTGGGAAGATTGCTT 876
DB 920 ACATTGACAACTATCGGCTATGGTGAACAGAACCGCACATGGCTGGGAGGCTCTG 979
QY 877 TCTGAGGCTTTGGCACTCTCTTGGCATTTCTTTTTCATTGCACTTCTTCCGCGGATTTTGGC 936
DB 980 GCTGCTGGCTTGGCTTACTTGGCATCTCTTTCTTGGCTTGGCTTGGCGGATCTCTAGGC 1039
QY 937 TCAGTGTTCATTTAAAGTACAGAAACAAACCCGCGAGAACACTTTTGAGAAAAGAGG 996
DB 1040 TCCGGCTTTGGCTTGAAGTCCAGAGCAGCAGCCGCGAGAGCACTTCAGAGCGGAG 1099
QY 997 AACCCAGCTGCAACCTCATTCAGTGTGTGTTGGCGTAGTTAGCGAGCTGATGAGAAATCT 1056
DB 1100 ATGCGCGAGCCAACTCATCCAGGCTGCTTGGCGCTGTACTCCACCGATATGAGCGG 1159
QY 1057 GTTTCATTTGCACTGGAAGCCCACTTGAAGGCTTGCACACCTGACG----- 1107
DB 1160 GCTTACTTGACAGCCACCTGTTACTATGATGACATATCTCTCCCATCTTTCAGAGCTG 1219
QY 1108 CTTACCAAGAAAGAACAGGGAAGCATCAAGCAGTCAAGAGCTA----- 1152
DB 1220 GCGCTCTTGTGAGCACTGCAAGGCGCCCAATGGGGCTACGGGCCCTCGGAGGTG 1279
QY 1153 ----- 1152
DB 1280 CGCGCGCGCGGTACCCGACGAGCACCTCCCTTACCCGCGCGGTTGCCACCTGCCAC 1339
QY 1153 -----AGTTTAAAGAGCGA 1167
DB 1340 CGCGCGCGGAGCACCTTCTTTCCTGGGAAAGCAGCGGATGGGATCAAGACCGC 1399
QY 1168 GTCCGATAGTCCCGCAGGGGCCAGAG-----GTATTTAAGAGCGCAGACGCTCAGTA 1221
DB 1400 ATCCGATGGGAGCTCCAGCGCGGCGAGCGGTCTTCCAGCAGCAGCTGGCACCTCCA 1459
QY 1222 GGTGACAGGAGGTCCCAAGCACCGACATCAGCCGAGG---GCAGTCCCAACCAAGTG 1278
DB 1460 ACAATGCCACCTCCCAAGCAGCAGGAGTGGGTGAGGCCACAGCCCGCCCAAGAGTG 1519
QY 1279 CAGAGAGCTGGAGCTTCAAGCAGCGAACCCGCTTCCGCGCTCGCTGGCGCTCAAAAGT 1338
DB 1520 CAAAAGAGCTGGAGCTTCAATGACCCGACCGCTTCCGCGCATCTCTGAGACTC----- 1573
QY 1339 TCTCAGCAAAACAGTGTATGATGTGACACAGCCCTTGGCACTGATGATGATATGAT 1398
DB 1574 -----AAACCCCGCACCTCTGCTGAGGATGCCCC---CCTCAGAGGAGTAGCAGAG 1621
QY 1399 GAAAAGGATGCCAGTGTGATGTATCAGTGGAAAGACTCACCCCGCACCTTAAAGACTGTC 1458
DB 1622 GAGAAGAGCTACAGTGTGAGCTCACGTGGACGACATCATGCTGCTGTGAGACAGTC 1681
QY 1459 ATTGAGCTATCAGAAATTTGAAATTTTCAATTTGTCAAAACGGAAGTTTAAAGAAAAGCTTA 1518
DB 1682 ATCGCTCCATCAGGATTTCTCAAGTTCTCTGTTGCCAAAAGGAAATTTCAAGAGAGACTG 1741
QY 1519 CGTCCATATGATGTAAGATGTTCATTTGAACATATTTCTGCTGCTCATCTGGACATCTG 1578
DB 1742 CGACCGTACGACGTGGAAGGAGCTCATTTGACGAGTACTCAGCAGGCGCACCTTGGACATCTG 1801
QY 1579 TGTAGAAATTAAGAGCTTCAAAACACGTTGTGATCAAAATTTCTTGGAAAAGGCG---AAATC 1635
DB 1802 GCGCGGATCAAGAGCTTCAAACTCGGTTGACCAATTTGGGTGCGGGGCGCGGGAGC 1861
QY 1636 ACATCAGATAGAGAGCCGAGAGAAAATTAACAGAGAAACATGAGACACAGAGATCTC 1695
DB 1862 AGGAAGGCGCGGAGAGGCGCAAGGGGCGCTCCGACGCGGAGGTGGTGGATGAAATC 1921
QY 1696 AGTATGCTCGGTGGGTGCTCAAGGTTGAAAACAGAGTACAGTCCATAGAGTCCAAAGCTG 1755
DB 1922 AGCATGATGGGACCGGTGCTCAAGGTGAGAGGAGGTGAGTCCATTCGAGCACAAGCTG 1981
QY 1756 GACTGCTCTAGACATCTATCAACAGGTCTCTCGGAAAGGCTCTGCTCAGCCCTCGCT 1815

Db 1982 GACCTGCTGTTGGGCTTCTATTTCGGCTGCGCTG-----GCTCGGACCTCGGCCAGC 2035
Qy 1816 TTGGCTTATCCAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT 1875
Db 2036 TTGGGCGCGTGAAGTGGCTGTTCGACCCCGACATCACCCTCGACTACACAGCCCT 2095
Qy 1876 GTGGATAGCAAGAATCTTTTCGGGTTCCGACAAA 1909
Db 2096 GTGGACACGAGGACATCTCCGTCTCCGACAGA 2129

RESULT 13

ADE31698

ID ADE31698 standard; DNA; 2335 BP.

XX ADE31698;

XX 29-JAN-2004 (first entry)

XX Human 32394 gene #SEQ ID 55.

XX Antiarteriosclerotic; cardiant; vasotropic; antiinflammatory;

KW thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;

KW cardiovascular; disorder; ischaemia; aortic bending;

KW vascular heart disease; endocarditis; atrial fibrillation; heart failure;

KW angina; cardiomyopathy; cardiac death; gene; ds.

XX Homo sapiens.

XX WO2003065984-A2.

XX 14-AUG-2003.

XX 29-JAN-2003; 2003WO-US002571.

XX 01-FEB-2002; 2002US-0353224P.

XX 15-MAR-2002; 2002US-0364529P.

XX 19-APR-2002; 2002US-0373861P.

XX 29-APR-2002; 2002US-0376287P.

XX 12-JUN-2002; 2002US-0388080P.

XX 24-JUN-2002; 2002US-0390971P.

XX 03-JUL-2002; 2002US-0394130P.

XX 10-JUL-2002; 2002US-0394797P.

XX 21-AUG-2002; 2002US-0404904P.

XX 23-AUG-2002; 2002US-0405450P.

XX 04-SEP-2002; 2002US-0408070P.

XX 06-NOV-2002; 2002US-0424300P.

XX 05-DEC-2002; 2002US-0431042P.

XX 05-DEC-2002; 2002US-0431079P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;

XX Stagliano N, Perodin J, Rodriguez-Way A;

XX WPI; 2003-731468/69.

XX P-PSDB; ADE31699.

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CC 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
CC 6585 genes in cardiovascular disease states. The methods are useful in
CC diagnosing, preventing and treating cardiovascular disorders, such as
CC atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
CC stenosis, arterial inflammation, vascular wall remodeling, coronary
CC microembolism, tachycardia, bradycardia, pressure overload, aortic
CC bending, coronary artery ligation, vascular heart disease, valvular
CC disease, including but not limited to, valvular degeneration caused by
CC calcification, rheumatic heart disease, endocarditis, or complications of
CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
CC heart failure, sinus node dysfunction, angina, heart failure.
CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
CC including but not limited to, pericardial effusion and pericarditis;
CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
CC artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
CC cardiovascular developmental disorders. The methods may also be used for
CC identifying compounds that modulate cardiovascular disorders. Sequences
CC given in ADE31644-ADE31769 represent the genes and proteins that may be
CC regulated by a compound of the invention.
XX
XX Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Query Match 19.2%; Score 518.4; DB 10; Length 2335;

Best Local Similarity 60.1%; Pred. No. 8.5e-142;

Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

Qy 217 TACCGCGGCTGCAGAACTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGCGTTC 276
Db 320 TACCGCGGCTGCAGAACTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGCGTTC 379
Qy 277 ATCTACCAACGCTTTCGTTTCTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 336
Db 380 GTCTACCAACGCTTTCGTTTCTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 439
Qy 337 ACCATCCCTGAGCACAAATTCGCTTCAAGTTCCCTTTGATCTCTCGAGTTCGTGATG 396
Db 440 ACTATCCAGGAGCACCAGGAACCTTGCACAGTGTCTCTCTCATCTTGAATTCGTGATG 499
Qy 397 ATTCTGCTTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 456
Db 500 ATCGTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 559
Qy 457 TATAGAGATGGCAAGAAAGACTCAGGTTTCTCGAAAGCCCTTCTGTGTTATAGATACC 516
Db 560 TACCGAGATGGCAGGCTCGCTTCGCTTTCGCAAGAGCCCTTCTGTCTCATCGACTTC 619
Qy 517 ATTCTTCTTATCGCTTCAATAGCAGTGTCTTCTGCAAAAACCTCAGGGTAAATTTTTCGC 576
Db 620 ATCGTGTCTGTCGCTCGTGGCGCTCATCGCGCGGTACCCAGGGCAACATCTTCGCC 679
Qy 577 ACCTCTGCACTCAGAAGTCTCGTTTCTCAGATCTCTCGCATGTCGCGCATGGACCGA 636
Db 680 ACCTCTGCGCTCGCATGTCGCTTCTGTCAGATCTCTGTCAGATCTCTGTCAGATCTCTGTCAG 739
Qy 637 AGGGAGGCACTTGGAAATTAATCTGGTTCAGTGGTTCAGTGGTTCAGTGGTTCAGTGGTTCAG 696
Db 740 CGCGCGGCACTTGGAGCTCTGGGCTCAGTGGTTCAGTGGTTCAGTGGTTCAGTGGTTCAGTGG 799
Qy 697 ACAGCTTGGTACATAGGATTTTGGTCTTATTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTT 756
Db 800 ACCGCTTGGTACATCGGCTTCTGTCGCTCATCTTCGCTCTCTCTCTCTCTCTCTCTCTCTCT 859
Qy 757 GAAAGGATGCCAATAAAGATTTTCTACATATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 816
Db 860 GAGAAGGACGCCAACTCCGACTTCT 919
Qy 817 ACATTGCAACTATTGGCTATGGAGACAAACTCCCTTAACCTTGGCTGGGAAGATTGCTT 876
Db 920 ACATTGCAACTATCGGCTATGGTGAAGACCGCACACATGGCTGGGAGGGTCTCTG 979
Qy 877 TCTCAGGCTTTCGACTCCCTTGGCAATTTCTTTTTCGACTTCTCTCTCTCTCTCTCTCTCTCT 936

Db 980 GCTGCTGGCTTGGCTTACTGGGCACTCTTTCTTTGCCCTGCTGCCGCACTCCTAGGC 1039
Qy 937 TCAGGTTTTCATTAAGATCAAGAAACAACACCGCAGAAAAACATTTGAGAAAAAGG 996
Db 1040 TCGGCTTTGCTTGAAGTCCAGGAGCAGCAACCGGAGAACACATTCGAGAACGCGAG 1099
Qy 997 AACCCAGCTGCCAACCCTCACTTCACTGTGTTGGGTAGTTACGCACTGATGAAATCT 1056
Db 1100 ATGCCGACAGCAACCTCACTCCAGGCTGCTGGCGCTGTACTCCACCGATATGAGCGG 1159
Qy 1057 GTTTCATTCGAAGCTGGAAGCAGCACTTGAAGGCTTGCACACCTGCGAGC----- 1107
Db 1160 GCCTACTGACAGCACTGCTACTACTATGACAGTATCTCCATCTTCAGAGAGCTG 1219
Qy 1108 CCTACCAAGAAAGAACCAAGGGAGAGCATCAAGCACTGAGAACTA----- 1152
Db 1220 GCCCTCTGTTGAGCAGCTGCAACGGGCGCGCAATGGGGCCCTTACGGCCCTGGAGGTG 1279
Qy 1153 ----- 1152
Db 1280 CGCGGGCGCGGTACCCGAGCGAGACCCCTCCGTTTACCGGCCGTTGCCACCTGCCAC 1339
Qy 1153 -----AGTTTAAAGAGCGA 1167
Db 1340 CGCGCGGCGCAGCACTCTTCTGCTGCGGGAAGAGCAGCGGATGGGCATCAAGAGCCG 1399
Qy 1168 GTGCGCATGGGTAGCCCGAGGGCGAGA-----GTATTAGAGCCGACAAAGCTCAGTA 1221
Db 1400 ATCCGCATGGCAGCTCCAGCGGCGAGCGGTCTTCCAAAGCAGCAGCTGGCACCTCCA 1459
Qy 1222 GGTACAGGAGGTCCCAAGCAGCAGCATCACAGCGAGG--GCAGTCCACCAAAAGTG 1278
Db 1460 ACAATGCCACCTCCCAAGCAGCAGCAGGTGGTGAGGCCACACCCACCAAGGTG 1519
Qy 1279 CAGAAGAGCTGGAGCTTCAACAGCAGCAGCCGCTTCCGGGCCCTCGCTCGCCCTCAAAAGT 1338
Db 1520 CAAGAGCTGGAGCTTCAATGACCGCAGCCGCTTCCGGGCATCTCTGAGACTC----- 1573
Qy 1339 TCTCAGCCAAACAGATGATAGATGTGACACAGCCCTTGGCACTGATGATATATGAT 1398
Db 1574 -----AAACCCCGCACCTCTGCTGAGATGCC-----CCTCAGAGGAAGTAGCAGAG 1621
Qy 1399 GAAAGAGATCCAGTGTGATGTATCAGTGAAGACCTCACCCACCACTTAAACCTGTC 1458
Db 1622 GAGAAGACTACCAAGTGTGAGCTCAGGTGAGCAGCATCATGCTGCTGTGAACACAGTC 1681
Qy 1459 ATTGAGCTATCAGAAATTAATGAAATTTTCATGTTCCAAACGGAAGTAAAGAAACGTTA 1518
Db 1682 ATCCGCTCCATCAGATTCTCAAGTTCTGCTGGTGGCCAAAGGAAATTCAGAGGACACTG 1741
Qy 1519 CGTCCATATGATGAAAGATGTCAATTGAACAATATCTGTGCTCATCTGGACATGTTG 1578
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Qy 1579 TGTAGATTAAAGCTTCAACACAGTGTGATCAAAATCTTGGAAAGGGC-----AAATC 1635
Db 1802 GCGCGATCAGAGCCTCAAACTCGGTGACCAAAATTTGGTGGGGGCGCGGGAC 1861
Qy 1636 ACATCAGATAAGAGAGCGGAGAGAAATAACAGAGAAATATAGACACAGACAGATCTC 1695
Db 1862 AGGAAGCGCGGAGAGAGGCGACAAAGGGGCGCTCCGACGCGGAGGTGGTGGATGAAATC 1921
Qy 1696 AGTATGCTCGGTGGGTGCTCAAGGTTCAAAACAGGTACAGTCCATAGAGTCAAGCTG 1755
Db 1922 AGCATGATGGAGCGGTGGTCAAGGTGAGAGAGAGGTGCACTCATCGACCAAGAGCTG 1981
Qy 1756 GACTCGCTACTAGACATCTATCAACAGGTCTCTTCGAAAGGCTGTGCTCAGCCCTCGCT 1815
Db 1982 GACCTGCTGTGGGCTTCTATTTCGGCTGCTGCTG-----GCTGCGCACCTCGGCCAGC 2035
Qy 1816 TTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCTGATATCAAGCCCT 1875
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RESULT 14

AA557140
ID AAX57140 standard; DNA; 2273 BP.

XX AAX57140;

XX 22-JUL-1999 (first entry)

XX Mouse KCNQ2 cDNA.

XX KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; JME;
KW rolandic epilepsy; mutant; treatment; screening; epilepsy; detection;
KW gene therapy; drug screening; ss.

XX Mus musculus.

XX Location/Qualifiers

1. .2273

FT CDS

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Nucleic acid encoding potassium channels KCNQ2 and 3.

Claim 1; Page 153-156; 195pp; English.

This invention describes novel human and mouse potassium channel proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for diagnosis and prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves in cell-free form) are used to screen for agents that can be used to treat or prevent these forms of epilepsy. Fragments of the encoding nucleic acids are used as probes or primers, either for detecting mutations or for isolation of related sequences, while the complete sequences may be used in gene therapy to provide wild-type protein. Antibodies specific for mutant or wild-type proteins are used as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are useful in rational design of drugs and therapeutically (in replacement therapies). The forms of epilepsy associated with mutations in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are manifest), and better treatment options will be available.

Sequence 2273 BP; 486 A; 670 C; 653 G; 448 T; 0 U; 16 Other;

Query Match 19.2%; Score 516; DB 2; Length 2273;

Best Local Similarity 57.6%; Pred. No. 4.3e-141;

Matches 1030; Conservative 2; Mismatches 684; Indels 72; Gaps 4;

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Dβ 1801 CAGGTCCTTGTCATCGAAAGAAGTTCGACTTCTTGGTGAGCATCTATACACAG 1854

Search completed: April 11, 2005, 09:27:22
Job time : 1405.41 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 10:31:37 ; Search time 1499.51 Seconds
(without alignments)
10887.292 Million cell updates/sec

Title: US-09-810-796-2
Perfect score: 2694
Sequence: 1 atgaaggatgtggatgcggg.....ctcatgtcaactgaaataa 2694

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

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- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2694	100.0	2694	9 US-09-866-020-1	Sequence 1, Appli
2	2694	100.0	2694	9 US-09-810-796-2	Sequence 2, Appli
3	2694	100.0	2694	19 US-10-948-493-1	Sequence 1, Appli
4	2690.4	99.9	3071	9 US-09-810-796-1	Sequence 1, Appli
5	2689.2	99.8	3137	18 US-10-661-629-1	Sequence 1, Appli
6	2681.2	99.5	3074	9 US-09-813-148-1	Sequence 1, Appli
7	2630	97.6	2667	9 US-09-810-796-3	Sequence 3, Appli
8	2625.2	97.4	2772	9 US-09-825-147-1	Sequence 1, Appli
9	2625.2	97.4	2772	18 US-10-803-268-1	Sequence 1, Appli
10	2625.2	97.4	3111	9 US-09-825-147-3	Sequence 3, Appli
11	2625.2	97.4	3111	18 US-10-803-268-3	Sequence 3, Appli

12	518.4	19.2	2335	17	US-10-353-690-55	Sequence 55, Appli
13	518.4	19.2	2335	19	US-10-850-928-1	Sequence 1, Appli
14	516	19.2	2273	16	US-10-096-578-88	Sequence 88, Appli
15	510	18.9	2169	13	US-10-128-870-22	Sequence 22, Appli
16	510	18.9	2169	14	US-10-131-685-22	Sequence 22, Appli
17	509.8	18.9	582	15	US-10-313-542-303	Sequence 303, App
18	500.6	18.6	7411	18	US-10-335-053-6	Sequence 6, Appli
19	500.6	18.6	7420	17	US-10-295-027-281	Sequence 281, App
20	500.6	18.6	7420	18	US-10-643-795A-75	Sequence 75, Appli
21	500.6	18.6	7420	19	US-10-948-518-75	Sequence 75, Appli
22	500.6	18.6	7863	15	US-10-084-817-335	Sequence 335, App
23	478.4	17.8	5595	18	US-10-820-307-8	Sequence 8, Appli
24	465.8	17.3	2766	18	US-10-820-307-6	Sequence 6, Appli
25	465.4	17.3	896	13	US-10-128-870-1	Sequence 1, Appli
26	465.4	17.3	896	14	US-10-131-685-1	Sequence 1, Appli
27	465	17.3	548	10	US-09-826-734-269	Sequence 269, App
28	464	17.2	2814	16	US-10-096-578-90	Sequence 90, Appli
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32	457.4	17.0	2755	18	US-10-820-307-4	Sequence 4, Appli
33	455.8	16.9	1848	18	US-10-744-796-5	Sequence 5, Appli
34	454.2	16.9	4512	15	US-10-084-817-334	Sequence 334, App
35	452	16.8	575	15	US-10-313-542-305	Sequence 305, App
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38	425.4	15.8	455	17	US-10-242-535A-25396	Sequence 25396, A
39	425.4	15.8	455	17	US-10-085-783A-25396	Sequence 25396, A
40	425	15.8	3287	13	US-10-128-870-19	Sequence 19, Appli
41	425	15.8	3287	14	US-10-131-685-19	Sequence 19, Appli
42	423.4	15.7	1425	10	US-09-960-706-511	Sequence 511, App
43	423.4	15.7	1425	10	US-09-873-319-313	Sequence 313, App
44	423.4	15.7	1425	16	US-10-116-712-662	Sequence 662, App
45	423.4	15.7	1932	18	US-10-744-796-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US2002040000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: GROISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-020-1

Query Match 100.0%; Score 2694; DB 9; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGAAGGATGTGGAGTCGGGCGGCGGAGGTGCTGCTGAACCTGGCAGCGCCAGGGGC 60
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Qy 241 TACAACTGCTGAGAGACCCCGCGCTGGCGCTGATCTACCAAGCTTTCGTTTCTC 300
Db 241 TACAACTGCTGAGAGACCCCGCGCTGGCGCTGATCTACCAAGCTTTCGTTTCTC 300
Qy 301 CTTCGTTTGGTTCGTTGATTTTCTGAGTGTTCATACCATCCCTGAGCACACAAAATTG 360
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Qy 361 GCCTCAAGTTCGCTTGTATCCTGGAGTTCGTGATGATGTGCTTTTGGTGGATTC 420
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Qy 841 GACAAACTCCCTTAACTGGCTGGGAAGATGCTTTCTGAGGCTTTGCACTCCTTGGC 900
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Qy	1801	GCTCAGGCTCGCTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACACACATCT	1860
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Db	1861	GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGACAAAACAGTGGCTGC	1920
Qy	1921	TTATCCAGATCAACTAGTGCACATCTCGAGAGCCCTGAGTTCATCTCAGCGCAAAAT	1980
Db	1921	TTATCCAGATCAACTAGTGCACATCTCGAGAGCCCTGAGTTCATCTCAGCGCAAAAT	1980
Qy	1981	GAGTTTCAGTCCCAAGCTTTCTACGGCTTTAGCCCTTACTATGCACAGTCAAGCAACAG	2040
Db	1981	GAGTTTCAGTCCCAAGCTTTCTACGGCTTTAGCCCTTACTATGCACAGTCAAGCAACAG	2040
Qy	2041	GTGCCAATTAAGTCAAAAGCGATGGCTCAGCAGTGGGAGCCACCAACACCATTTGCAACCAA	2100
Db	2041	GTGCCAATTAAGTCAAAAGCGATGGCTCAGCAGTGGGAGCCACCAACACCATTTGCAACCAA	2100
Qy	2101	ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA	2160
Db	2101	ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA	2160
Qy	2161	GCCATCAAGCATCTGCCAGGCGAGAAATCTGTGCACCTTAACCTGTGAGGCTTACAGAA	2220
Db	2161	GCCATCAAGCATCTGCCAGGCGAGAAATCTGTGCACCTTAACCTGTGAGGCTTACAGAA	2220
Qy	2221	AGCATTTCTGACGTCAACCTGCTTGTGCTTCAAGGAAATGTTTCAAGTGTGCACAG	2280
Db	2221	AGCATTTCTGACGTCAACCTGCTTGTGCTTCAAGGAAATGTTTCAAGTGTGCACAG	2280
Qy	2281	TCAAATCTCAACAGGACCTTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2340
Db	2281	TCAAATCTCAACAGGACCTTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2340
Qy	2341	TTGTCTGTCTGCTCCATGTTGGGAGGACTTGGGCAATCTTTGTCTGTGCAAAACCTG	2400
Db	2341	TTGTCTGTCTGCTCCATGTTGGGAGGACTTGGGCAATCTTTGTCTGTGCAAAACCTG	2400
Qy	2401	ATCAGGTGACCGAGGAACTGAATATACAACTTTTCAGGGAGTGAAGTCAAGTGGCTCCAGA	2460
Db	2401	ATCAGGTGACCGAGGAACTGAATATACAACTTTTCAGGGAGTGAAGTCAAGTGGCTCCAGA	2460
Qy	2461	GGCAGCCAAAGATTTTATCCCAATGGAGGAATCCAAATTTGTTTATACTGATGAAGAG	2520
Db	2461	GGCAGCCAAAGATTTTATCCCAATGGAGGAATCCAAATTTGTTTATACTGATGAAGAG	2520
Qy	2521	GTGGTCCCGAAGACAGACAGACACATTTTGAATGCCGACCGCAGCTGCCAGGAA	2580
Db	2521	GTGGTCCCGAAGACAGACAGACACATTTTGAATGCCGACCGCAGCTGCCAGGAA	2580
Qy	2581	GCTGCTTTTGCATCAGACTCTTAAGGACTGGAAGTCAAGTCAATCTCAGAGCATTTGT	2640
Db	2581	GCTGCTTTTGCATCAGACTCTTAAGGACTGGAAGTCAAGTCAATCTCAGAGCATTTGT	2640
Qy	2641	AAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACCTGAAATAA	2694
Db	2641	AAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACCTGAAATAA	2694

RESULT 3

US-10-948-493-1

Sequence 1, Application US/10948493

Publication No. US20050064491A1

GENERAL INFORMATION:

APPLICANT: DWORETZKY, STEVEN I

APPLICANT: RAMANATHAN, CHANDRA S

APPLICANT: TROJNACKI, JOANNE T

APPLICANT: BOISARD, CHRISTOPHER G

APPLICANT: GRIKOFF, VALENTIN K

TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS

TITLE OF INVENTION: THEREOF

FILE REFERENCE: D0023 DIV

CURRENT APPLICATION NUMBER: US/10/948,493

CURRENT FILING DATE: 2004-09-23

PRIOR APPLICATION NUMBER: 60/207,389

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 2694

TYPE: DNA

ORGANISM: Homo sapiens

US-10-948-493-1

Query Match

Best Local Similarity 100.0%; Score 2694; DB 19; Length 2694;

Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAAGGATGTGGAGTCGGGCGGGGCGAGGTGCTGCTGAATCGGCGAGCGCGAGGGC	60
Db	1	ATGAAGGATGTGGAGTCGGGCGGGGCGAGGTGCTGCTGAATCGGCGAGCGCGAGGGC	60
Qy	61	GACGGCTGTCTACTGCTGGGCAACCGGCGGCCACCTTGTGTGCGCGCGGTGGCGCTG	120
Db	61	GACGGCTGTCTACTGCTGGGCAACCGGCGGCCACCTTGTGTGCGCGCGGTGGCGCTG	120
Qy	121	AGGAGAGCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGTGGGGAAGCGCTCTCT	180
Db	121	AGGAGAGCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGTGGGGAAGCGCTCTCT	180
Qy	181	TACACGAGTAGCCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGTGCGAAGTACCTG	240
Db	181	TACACGAGTAGCCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGTGCGAAGTACCTG	240
Qy	241	TACAACTGTCTGGAGAGACCCCGGCTGGGCGTTCATCTACACGCTTTCGTTTTCTC	300
Db	241	TACAACTGTCTGGAGAGACCCCGGCTGGGCGTTCATCTACACGCTTTCGTTTTCTC	300
Qy	301	CTTGTCTTTGTTGCTTGTGATTTTGTAGTGTTCATCCATCCCTGAGCACAAAATGT	360

Db	301	CTTGTCTTTGGTGTCTTGATTTTGTTCAGTGTTTTCTACCATCCTTGAGCACACAAAAATTG	360
Qy	361	GCCTCAAGTTGCCTCTTGATCCTGGAGTTCTGTGATGATTTGTCTGCTCTTTGGTTTGGAGTTC	420
Db	361	GCCTCAAGTTGCCCTTTGATCCTGGAGTTCTGTGATGATTTGTCTGCTCTTTGGTTTGGAGTTC	420
Qy	421	ATCATTCGAATCTGTCTGTGCGGGTTGCTGTTGTGCGATATAGAGATGGCAAGGAAGACTG	480
Db	421	ATCATTCGAATCTGTCTGTGCGGGTTGCTGTTGTGCGATATAGAGATGGCAAGGAAGACTG	480
Qy	481	AGTTTGTCTCGAAAGCCCTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	540
Db	481	AGTTTGTCTCGAAAGCCCTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	540
Qy	541	GTTTGTCTTCGAAAAAATCAGGGTAATAATTTTGGCCACGCTCTGCACCTCAGAAGTCTCCGT	600
Db	541	GTTTGTCTTCGAAAAAATCAGGGTAATAATTTTGGCCACGCTCTGCACCTCAGAAGTCTCCGT	600
Qy	601	TTCTTACAGATCTCTCCGATGGTGGCGATGACCGAAGGGGAGGCACTTGGAAATTAAGT	660
Db	601	TTCTTACAGATCTCTCCGATGGTGGCGATGACCGAAGGGGAGGCACTTGGAAATTAAGT	660
Qy	661	GGTTCAGTGGTTATGCTCAGCAAGGAATAATATCAGACCTTGGTACATAGGATTTTTTG	720
Db	661	GGTTCAGTGGTTATGCTCAGCAAGGAATAATATCAGACCTTGGTACATAGGATTTTTTG	720
Qy	721	GTTCTTATTTTTTTCGTCTTCTTCTGTCTATCTGTGGAAAAAGGATGCCAATAAAGAGTTT	780
Db	721	GTTCTTATTTTTTTCGTCTTCTTCTGTCTATCTGTGGAAAAAGGATGCCAATAAAGAGTTT	780
Qy	781	TCTACATATGAGATGCTCTCTGGTGGGGCAAAATTACATTGACAACTATTGGCTATGGA	840
Db	781	TCTACATATGAGATGCTCTCTGGTGGGGCAAAATTACATTGACAACTATTGGCTATGGA	840
Qy	841	GACAAACTCCCTTAACTTGGCTGGGAAGATGCTTCTCGAGGCTTTGCATCTCCTTGGC	900
Db	841	GACAAACTCCCTTAACTTGGCTGGGAAGATGCTTCTCGAGGCTTTGCATCTCCTTGGC	900
Qy	901	ATTTCTTTCTTTTGCACTTCTCTCGCGGCAATCTTGGCTCAGGTTTTCATTAAAGATCAAA	960
Db	901	ATTTCTTTCTTTTGCACTTCTCTCGCGGCAATCTTGGCTCAGGTTTTCATTAAAGATCAAA	960
Qy	961	GAAACAACCCGCCAGAAACACTTTTGAGAAAAAGAGAACCCAGTGCACACCTCATTCAG	1020
Db	961	GAAACAACCCGCCAGAAACACTTTTGAGAAAAAGAGAACCCAGTGCACACCTCATTCAG	1020
Qy	1021	TGTGTTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTTCCATTGGCAACTGGAAGCCA	1080
Db	1021	TGTGTTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTTCCATTGGCAACTGGAAGCCA	1080
Qy	1081	CACTTTGAGGGCTTGTGCACACCTGCAGCCCTACCAAGAAAGAAACCAAGGGGAAGCATCAAGC	1140
Db	1081	CACTTTGAGGGCTTGTGCACACCTGCAGCCCTACCAAGAAAGAAACCAAGGGGAAGCATCAAGC	1140
Qy	1141	AGTCAGAGCTAAGTTTTTAAGGAGCGAGTGCATGCTAGCCGCCAGGGGCCAGAGTATT	1200
Db	1141	AGTCAGAGCTAAGTTTTTAAGGAGCGAGTGCATGCTAGCCGCCAGGGGCCAGAGTATT	1200
Qy	1201	AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGTCTCCCAAGCAACCGACATCACAGCCGAG	1260
Db	1201	AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGTCTCCCAAGCAACCGACATCACAGCCGAG	1260
Qy	1261	GGCAGTCCCAACCAAGTGCAGAGCTGGAGCTTCAACGACCAACCCGCTTCCGGCCC	1320
Db	1261	GGCAGTCCCAACCAAGTGCAGAGCTGGAGCTTCAACGACCAACCCGCTTCCGGCCC	1320
Qy	1321	TCGCTGCGCCTCAAAAGTTCTCAGCAAAAACCAAGTATAGATGCTGACACAGCCCTTGGC	1380
Db	1321	TCGCTGCGCCTCAAAAGTTCTCAGCAAAAACCAAGTATAGATGCTGACACAGCCCTTGGC	1380
Qy	1381	ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGCTATCAGTGGGAAGACCTCAC	1440

QY	2521	GTGGTCCCGAAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA	2580
Db	2521	GTGGTCCCGAAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA	2580
QY	2581	GCTGCCCTTTCATCAGACTCTCTAAGGACTGGAAGGTTCAGATCATCTCAGAGCATTTGT	2640
Db	2581	GCTGCCCTTTCATCAGACTCTCTAAGGACTGGAAGGTTCAGATCATCTCAGAGCATTTGT	2640
QY	2641	AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA	2694
Db	2641	AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA	2694
RESULT 4			
US-09-810-796-1			
; Sequence 1, Application US/09810796			
; Patent No. US20020102677A1			
; GENERAL INFORMATION:			
; APPLICANT: Jeglia, Timothy James			
; APPLICANT: ICAGEN, Inc.			
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel			
; FILE REFERENCE: 018512-0050100S			
; CURRENT APPLICATION NUMBER: US/09/810,796			
; CURRENT FILING DATE: 2001-10-12			
; PRIOR APPLICATION NUMBER: US 60/190,954			
; PRIOR FILING DATE: 2000-03-21			
; NUMBER OF SEQ ID NOS: 17			
; SOFTWARE: Patent In Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 3071			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; OTHER INFORMATION: human outwardly rectifying, voltage-gated			
; OTHER INFORMATION: potassium channel KCNQ5-1			
; NAME/KEY: CDS			
; LOCATION: (10)..(2703)			
; OTHER INFORMATION: KCNQ5-1			
US-09-810-796-1			
Query Match 99.9%; Score 2690.4; DB 9; Length 3071;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
QY	1	ATGAAGGATGTGGAGTCGGGCGGGGCGAGGTGCTGTAACCTCGGACGCCGCGAGGGGC	60
Db	10	ATGAAGGATGTGGAGTCGGGCGGGGCGAGGTGCTGTAACCTCGGACGCCGCGAGGGGC	69
QY	61	GACGGCTGTACTGTCTGGGACCCGCGGCGGCGAGCTTGTGGCGGCGGCTGGCCTG	120
Db	70	GACGGCTGTACTGTCTGGGACCCGCGGCGGCGAGCTTGTGGCGGCGGCTGGCCTG	129
QY	121	AGGGAGAGCGCGCGGCGAAGAGAGGGGCGCGGATGAGCTGCTGGGGAAGCCGCTCTCT	180
Db	130	AGGGAGAGCGCGCGGCGAAGAGAGGGGCGCGGATGAGCTGCTGGGGAAGCCGCTCTCT	189
QY	181	TACACGAGTAGCCAGAGCTGCGGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG	240
Db	190	TACACGAGTAGCCAGAGCTGCGGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG	249
QY	241	TACACGAGTAGCCAGAGCGCGGCGGCGGCTTCATCTACACGCTTTTCGTTTTTCTC	300
Db	250	TACACGAGTAGCCAGAGCGCGGCGGCGGCTTCATCTACACGCTTTTCGTTTTTCTC	309
QY	301	CTTGCTCTTGGTGTGCTTGAATTTTGTCAAGTGTTCATCCATCCCTGAGCACAATAATG	360
Db	310	CTTGCTCTTGGTGTGCTTGAATTTTGTCAAGTGTTCATCCATCCCTGAGCACAATAATG	369
QY	361	GCCTCAAGTTGCCTCTTGCCTGGAGTTCGTGATGATGCTCTTGGTGTGGAGTTTC	420
Db	370	GCCTCAAGTTGCCTCTTGCCTGGAGTTCGTGATGATGCTCTTGGTGTGGAGTTTC	429

QY	421	ATCATTCGAATCTGGTCTCGGGTTCCTGTTGTCGATATAGAGATGGCAAGAACTG	480
Db	430	ATCATTCGAATCTGGTCTCGGGTTCCTGTTGTCGATATAGAGATGGCAAGAACTG	489
QY	481	AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATAACCAATTTCTTATCGCTTCAATAGCA	540
Db	490	AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATAACCAATTTCTTATCGCTTCAATAGCA	549
QY	541	GTTGTTCTGCAAAACCTCAGGGTAAATATTTTGCACGCTCTGCACATCAGAAGTCTCCGT	600
Db	550	GTTGTTCTGCAAAACCTCAGGGTAAATATTTTGCACGCTCTGCACATCAGAAGTCTCCGT	609
QY	601	TTCTTACAGATCTCCGATGCGCATGGACCGAAGGGGAGGACCTTGGAAATTAATCT	660
Db	610	TTCTTACAGATCTCCGATGCGCATGGACCGAAGGGGAGGACCTTGGAAATTAATCT	669
QY	661	GGTTTCAGTGGTTTATGCTCAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTGT	720
Db	670	GGTTTCAGTGGTTTATGCTCAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTGT	729
QY	721	GTCTTATTTTTCGTTCTTCTCTCTGTTGGAAGAGGATGCCAATAAAGAGTTT	780
Db	730	GTCTTATTTTTCGTTCTTCTCTCTGTTGGAAGAGGATGCCAATAAAGAGTTT	789
QY	781	TCTACATATGAGATGCTCTCTGTTGGGCGCAATTAATCAATGACAACTATTTGGCTATGGA	840
Db	790	TCTACATATGAGATGCTCTCTGTTGGGCGCAATTAATCAATGACAACTATTTGGCTATGGA	849
QY	841	GACAAACTCCCTTAACTTGGCTGGGAAGATGCTTTCTGAGGCTTTGCACTCTCTGGC	900
Db	850	GACAAACTCCCTTAACTTGGCTGGGAAGATGCTTTCTGAGGCTTTGCACTCTCTGGC	909
QY	901	ATTTCTTTCTTGGCACTTCTCTCGCGCATTTCTTGCTCAGGTTTTCATTAAGAGTACAA	960
Db	910	ATTTCTTTCTTGGCACTTCTCTCGCGCATTTCTTGCTCAGGTTTTCATTAAGAGTACAA	969
QY	961	GAAACACACCGCCAGAAACACTTTGAGAAAGAGAACCCAGCTGCCAATCTATTTCAG	1020
Db	970	GAAACACACCGCCAGAAACACTTTGAGAAAGAGAACCCAGCTGCCAATCTATTTCAG	1029
QY	1021	TGTGTTTGGCTAGTTTACGCGCTGATGAGAAATCTGTTTCCATTCGAACCTGGAGCCA	1080
Db	1030	TGTGTTTGGCTAGTTTACGCGCTGATGAGAAATCTGTTTCCATTCGAACCTGGAGCCA	1089
QY	1081	CACCTTGAAGSCCTTGACACCTGACCTTCAAGAAAGAACCAAGGGGAGGATCAACG	1140
Db	1090	CACCTTGAAGSCCTTGACACCTGACCTTCAAGAAAGAACCAAGGGGAGGATCAACG	1149
QY	1141	AGTCAGAGTAAAGTTTAAAGGAGCGAGTGCATGGCTAGCCCGAGGGGCGCAGAGTATT	1200
Db	1150	AGTCAGAGTAAAGTTTAAAGGAGCGAGTGCATGGCTAGCCCGAGGGGCGCAGAGTATT	1209
QY	1201	AAGAGCGCAACAGCTCAGTAGGTGACAGAGGTCCCAAGACCCAGATCACAGCCGAG	1260
Db	1210	AAGAGCGCAACAGCTCAGTAGGTGACAGAGGTCCCAAGACCCAGATCACAGCCGAG	1269
QY	1261	GGCAGTCCCAACAAAGTGCAGAGAGCTTCAAGACCCGAGAACCCGCTTCCGCGCC	1320
Db	1270	GGCAGTCCCAACAAAGTGCAGAGAGCTTCAAGACCCGAGAACCCGCTTCCGCGCC	1329
QY	1321	TGCTGCGCTCAAAAGCTTCTCAGCCAAACACAGTAGTAGATGCTGACACAGCCCTTGGC	1380
Db	1330	TGCTGCGCTCAAAAGCTTCTCAGCCAAACACAGTAGTAGATGCTGACACAGCCCTTGGC	1389
QY	1381	ACTGATGATGATATGATGAAAGAGTGCAGTGTGATGATGATGATGATGATGATGATGAT	1440
Db	1390	ACTGATGATGATATGATGAAAGAGTGCAGTGTGATGATGATGATGATGATGATGATGAT	1449
QY	1441	CCACCACTTAAACCTGCTTCAAGAGCTATCAGAAATTAATGAAATTTTCAATTTGCAAAACGG	1500
Db	1450	CCACCACTTAAACCTGCTTCAAGAGCTATCAGAAATTAATGAAATTTTCAATTTGCAAAACGG	1509
QY	1501	AAGTTTAAAGGAAACGTTTACGTCATATGATGATGATGATGATGATGATGATGATGATGAT	1560

841 GACAAACTCCCTAACTTGGCTGGAGAGATTGCTTTCTGAGGCTTTTGCACTCTCTGGC 900
841 GACAAACTCCCTAACTTGGCTGGAGAGATTGCTTTCTGAGGCTTTTGCACTCTCTGGC 900
901 ATTCTCTTTTGGCACTTCTGCTCCGGCACTCTTGGCTCAGGTTTGGCAATTAAGTACAA 960
901 ATTCTCTTTTGGCACTTCTGCTCCGGCACTTCTTGGCTCAGGTTTGGCAATTAAGTACAA 960
961 GAACAAACCCGACAGAAACACTTTTCAGAAAGAGAGAACCCAGCTGCCAACCCTCAATTCAG 1020
961 GAACAAACCCGACAGAAACACTTTTCAGAAAGAGAGAACCCAGCTGCCAACCCTCAATTCAG 1020
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1021 TGTGTTTGGCGTAGTTACCGACCTGATGAGAAATCTGTTTCATTTGCAACCTTGAAGCCA 1080
1081 CACTTGAAGGCTTGCACACCTGCAGCCCTACCAAGAAAGAACAGGGGAGCATCAAGC 1140
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1141 AGTCAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGCCAGAGTATT 1200
1116 --TCAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGCCAGAGTATT 1173
1201 AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1260
1174 AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1233
1261 GGCAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGGCC 1320
1234 GGCAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGGCC 1293
1321 TCGCTGCGCTCAAAAGTTCTCAGCCCAAAAGAGTGCAGTGTGATGTATCAGTGGAGAGCTCACC 1380
1294 TCGCTGCGCTCAAAAGTTCTCAGCCCAAAAGAGTGCAGTGTGATGTATCAGTGGAGAGCTCACC 1353
1381 ACTGATGATGTATGATGAAAGAGTGCAGTGTGATGTATCAGTGGAGAGCTCACC 1440
1354 ACTGATGATGTATGATGAAAGAGTGCAGTGTGATGTATCAGTGGAGAGCTCACC 1413
1441 CCACACCTTAAACTGTGCTGAGTATCAGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTG 1500
1414 CCACACCTTAAACTGTGCTGAGTATCAGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTG 1473
1501 AAGTTTAAAGAAACCTGAGTCCATATGATGTAAGAGTGTCAATTTGAACAATTTCTGCT 1560
1474 AAGTTTAAAGAAACCTGAGTCCATATGATGTAAGAGTGTCAATTTGAACAATTTCTGCT 1533
1561 GGTCACTCGGACATGTTGTGTAAGAAATTAAGAGCTTCAAAACACGCTGTTGATCAAAATTTCT 1620
1534 GGTCACTCGGACATGTTGTGTAAGAAATTAAGAGCTTCAAAACACGCTGTTGATCAAAATTTCT 1593
1621 GGAAAGGGCAATCACATCAGATGAAGAGCCGAGAGAAATTAACAGCGAGAAATGAG 1680
1594 GGAAAGGGCAATCACATCAGATGAAGAGCCGAGAGAAATTAACAGCGAGAAATGAG 1653
1681 ACCAGAGCGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAGACAGGTACAGTCC 1740
1654 ACCAGAGCGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAGACAGGTACAGTCC 1713
1741 ATAGAGTCCAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTTCGGAAGGCTCT 1800
1714 ATAGAGTCCAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTTCGGAAGGCTCT 1773
1801 GCTCAGGCTCGCTTTGGCTTCAATTCAGATGCCACCTTTTGAATTTGAACAGACATCT 1860
1774 GCTCAGGCTCGCTTTGGCTTCAATTCAGATGCCACCTTTTGAATTTGAACAGACATCT 1833
1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGGCAAAACAGTGGCTGC 1920
1834 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGGCAAAACAGTGGCTGC 1893

1921 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCCTGCAGTTTCATTTGACGCAAAAT 1980
1894 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCCTGCAGTTTCATTTGACGCAAAAT 1953
1981 GAGTTGAGTCCGAGACATTTCTAGCGGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2040
1954 GAGTTGAGTCCGAGACATTTCTAGCGGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2013
2041 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAACCAAA 2100
2014 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAACCAAA 2073
2101 ATAAATACGGCAACCCAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2160
2074 ATAAATACGGCAACCCAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2133
2161 GCCATCAAGCATCTGCGCCAGGCGAGAACTCTGCAACCTTAAACCTTGAGGCTTACAGAA 2220
2134 GCCATCAAGCATCTGCGCCAGGCGAGAACTCTGCAACCTTAAACCTTGAGGCTTACAGAA 2193
2221 AGCATTTCTGACGTCACCACTGCTTGTGCTTCCCAAGGAAATGTTTTCAGTTGACAG 2280
2194 AGCATTTCTGACGTCACCACTGCTTGTGCTTCCCAAGGAAATGTTTTCAGTTGACAG 2253
2281 TCAATCTCACAAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTG 2340
2254 TCAATCTCACAAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTG 2313
2341 TTGCTGTCTGTCCATGCTGCGGAGGACCTTGGGCAAAATCTTTGCTGTGTCGCAAAACCTG 2400
2314 TTGCTGTCTGTCCATGCTGCGGAGGACCTTGGGCAAAATCTTTGCTGTGTCGCAAAACCTG 2373
2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2460
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2461 GSCAGCCAAAGATTTTTACCCCAATGGAGGAAATCCAAATTTGTTTATTAACCTGATGAAG 2520
2434 GSCAGCCAAAGATTTTTACCCCAATGGAGGAAATCCAAATTTGTTTATTAACCTGATGAAG 2493
2521 GTGGTCCGAGAGACAGACACACTTTTGTGTCGCGCACCGCAGCTTCCAGGGAA 2580
2494 GTGGTCCGAGAGACAGACACACTTTTGTGTCGCGCACCGCAGCTTCCAGGGAA 2553
2581 GCTGCTTTGATCAGACTCTTAAGGACTCGAAGGTCAAGATCATCTCAGAGCAATTTGT 2640
2554 GCTGCTTTGATCAGACTCTTAAGGACTCGAAGGTCAAGATCATCTCAGAGCAATTTGT 2613
2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
2614 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667

RESULT 8

US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. US20020042505A1el Human Ion Channel Protein and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 1									
; LENGTH: 2772									
; TYPE: DNA									
; ORGANISM: homo sapiens									
US-09-825-147-1									
Query Match 97.4%; Score 2625.2; DB 9; Length 2772;									
Best Local Similarity 98.9%; Pred. No. 0;									
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;									
QY	1	ATGAAGATGTCGAGTTCGGGCGGCGGCGAGGCTGCTGCTGAACCTCGGAGCGCGCAGGGC	60	DB	1006	ATTTCCTTTCTTTGACCTTCTCTGCGCGGCACTTCTTGCGTCAAGTTTGTCAATTAAGAATACAA	1065		
DB	106	ATGAAGATGTCGAGTTCGGGCGGCGGCGAGGCTGCTGCTGAACCTCGGAGCGCGCAGGGC	165	QY	961	GAACAACACCCCGAGAAACACTTTTGAGAAAGAGAAACCCAGCTGCCAACCTCAATTCAG	1020		
QY	61	GACGGCTGCTACTGCTGGGACACCGCGCGGCACGCTTGGTGGCGGCGGCGGTGGCGCTG	120	DB	1066	GAACAACACACCCCGAGAAACACTTTTGAGAAAGAGAAACCCAGCTGCCAACCTCAATTCAG	1125		
DB	166	GACGGCTGCTACTGCTGGGACACCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCGCTG	225	QY	1021	TGTGTTTGGCGTAGTTACGCGAGCTGATGAGAAATCTGTGTTTCCATTTGCAACTCGGAAGCCA	1080		
QY	121	AGGGAGAGCGCGGCGGCAAGCAGCGGGCCGCGATGAGCTGCTGGGGAAGCGCGCTCTCT	180	DB	1126	TGTGTTTGGCGTAGTTACGCGAGCTGATGAGAAATCTGTGTTTCCATTTGCAACTCGGAAGCCA	1185		
DB	226	AGGGAGAGCGCGGCGGCAAGCAGCGGGCCGCGATGAGCTGCTGGGGAAGCGCGCTCTCT	285	QY	1081	CACTTGAAGGCTTGGCAACCTCGAGCCCTTACCAAGAAAGAAACAAGGGGAAGCATCAAGC	1140		
QY	181	TACACGAGTAGCAGAGCTGCGCGCGCAACGTCACAGTACCGGCGGCTGCAGAACTACTG	240	DB	1186	CACTTGAAGGCTTGGCAACCTCGAGCCCTTACCAA-----	1220		
DB	286	TACACGAGTAGCAGAGCTGCGCGCGCAACGTCACAGTACCGGCGGCTGCAGAACTACTG	345	QY	1141	AGTCAGAAAGCTTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGGCGCAGAGTATT	1200		
QY	241	TACAACGCTGGAGAGACCGCGGCTGGGCGTTTCATCTACACGCTTTCGTTTTTCTC	300	DB	1221	--TCAGAAAGCTTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGGCGGCGCAGAGTATT	1278		
DB	346	TACAACGCTGGAGAGACCGCGGCTGGGCGTTTCATCTACACGCTTTCGTTTTTCTC	405	QY	1201	AAAGCCGACAGGCTTCAAGTGGTGAAGAGGCTTCCCAAGCAGCCGACATCACAGCCGAG	1260		
QY	301	CTTGCTCTTTGTTGCTGATTTTGTTCAGTGTGTTTCTACCATCTCGAGCAGCAAAAATTG	360	DB	1279	AAAGCCGACAGGCTTCAAGTGGTGAAGAGGCTTCCCAAGCAGCCGACATCACAGCCGAG	1338		
DB	406	CTTGCTCTTTGTTGCTGATTTTGTTCAGTGTGTTTCTACCATCTCGAGCAGCAAAAATTG	465	QY	1261	GGCAGTCCCAACAAAGTGCAGAAAGCTGGAGCTTCAAAGCAGCCGCTTCGGGCCC	1320		
QY	361	GCTCAAGTGTGCTTGCATCTGAGTTCGTGATGATGATGATGATGATGATGATGATGATG	420	DB	1339	GGCAGTCCCAACAAAGTGCAGAAAGCTGGAGCTTCAAAGCAGCCGCTTCGGGCCC	1398		
DB	466	GCTCAAGTGTGCTTGCATCTGAGTTCGTGATGATGATGATGATGATGATGATGATGATG	525	QY	1321	TGCTGGCGCTCAAAGTTCCTCAGCAAAACCCAGTGTAGATGCTGACACAGCCCTTGCG	1380		
QY	421	ATCATTCGAATCTGCTGCGGGTGTGCTGTTGTCGATATAGAGGATGCAAGGAACTG	480	DB	1399	TGCTGGCGCTCAAAGTTCCTCAGCAAAACCCAGTGTAGATGCTGACACAGCCCTTGCG	1458		
DB	526	ATCATTCGAATCTGCTGCGGGTGTGCTGTTGTCGATATAGAGGATGCAAGGAACTG	585	QY	1381	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATGATGATGATGATGATGATG	1440		
QY	481	AGGTTTGTGCAAGCCCTTCTGTTATAGATACCAATTTCTTATCGCTTCAATAGCA	540	DB	1459	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATGATGATGATGATGATGATG	1518		
DB	586	AGGTTTGTGCAAGCCCTTCTGTTATAGATACCAATTTCTTATCGCTTCAATAGCA	645	QY	1441	CCACCACTTAAACCTGTCTCAGCTATCAAGTATGAAATTTTCAATGTTTCAAAACCG	1500		
QY	541	GTTCCTTCTGCAAAACCTCAGGTAATATTTTGGCAGCTGTGCACTCAGAACTCTCGT	600	DB	1519	CCACCACTTAAACCTGTCTCAGCTATCAAGTATGAAATTTTCAATGTTTCAAAACCG	1578		
DB	646	GTTCCTTCTGCAAAACCTCAGGTAATATTTTGGCAGCTGTGCACTCAGAACTCTCGT	705	QY	1501	AAAGTTTAAAGGAAACCTGTACGTCCATATGATGTTAAAGATGTCATTTGAAACAATATCTGCT	1560		
QY	601	TTCTACAGATCTCCGCAATGTCGCAATGTCGCAATGTCGCAATGTCGCAATGTCGCAATG	660	DB	1579	AAAGTTTAAAGGAAACCTGTACGTCCATATGATGTTAAAGATGTCATTTGAAACAATATCTGCT	1638		
DB	706	TTCTACAGATCTCCGCAATGTCGCAATGTCGCAATGTCGCAATGTCGCAATGTCGCAATG	765	QY	1561	GGTCATCTGGACATGTTGTTGTTAGAAATTAAGAGCCTTCAACACAGCTGTTGATCAAAATCTT	1620		
QY	661	GGTTCAGTGTGTTATGCTCACAGCAAGAAATTAATCACAGCTTGTGACATAGATTTTGT	720	DB	1639	GGTCATCTGGACATGTTGTTGTTAGAAATTAAGAGCCTTCAACACAGCTGTTGATCAAAATCTT	1698		
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QY	721	GTTCCTTATTTTTCGCTCTTCTTCTGCTATCTGCTGGAAAGGATGCCAATAAGAGTTT	780	DB	1699	GGAAAGGCAAAATCAATCAGATCAAGAGAGCCGAGAGAAATTAACAGCAGAACTAGAG	1758		
DB	826	GTTCCTTATTTTTCGCTCTTCTTCTGCTATCTGCTGGAAAGGATGCCAATAAGAGTTT	885	QY	1681	ACCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGTTGAAAGAAACAGGTACAGTCC	1740		
QY	781	TCTACATATGAGATGCTCTCTGGTGGGCAAAATTAATTAATTAATTAATTAATTAATTAAT	840	DB	1759	ACCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGTTGAAAGAAACAGGTACAGTCC	1818		
DB	886	TCTACATATGAGATGCTCTCTGGTGGGCAAAATTAATTAATTAATTAATTAATTAATTAAT	945	QY	1741	ATAGAGTCCAAAGCTGGAGCTGCCCTACTAGACATCTATCAACAGGTCTCTCGGAAAGGCTCT	1800		
QY	841	GACAAACTCCCTAATCTGCTGGGCAAGATTCCTTCTGCAAGCTTTCACCTCTCTGCGC	900	DB	1819	ATAGAAATCCAAGCTGGAGCTGCCCTACTAGACATCTATCAACAGGTCTCTCGGAAAGGCTCT	1878		
DB	946	GACAAACTCCCTAATCTGCTGGGCAAGATTCCTTCTGCAAGCTTTCACCTCTCTGCGC	1005	QY	1801	GCCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCCACTCTTTCGAAATGTGAACAGACATCT	1860		
QY	901	ATTTCCTTTCTTGCACCTCTCTGCGGCAATTCCTTGGCTCAGGTTTTCATTAAGTACAA	960	DB	1879	GCCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCCACTCTTTCGAAATGTGAACAGACATCT	1938		


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QY 2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGGAGCCACCAACACCAATTCACAAACCA 2100
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Db 2119 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGGAGCCACCAACACCAATTCACAAACCA 2178
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QY 2101 ATAAATACGGCAACCCAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
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|
|
Db 2179 ATAAATACGGCAACCCAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2238
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|
QY 2161 GCATCAAGCATCTGCCAGGCCAGAACTCTGCACCTTAACCTTGCAGGCTTACAGGAA 2220
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|
|
Db 2239 GCATCAAGCATCTGCCAGGCCAGAACTCTGCACCTTAACTTGCAGGCTTACAGGAA 2298
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|
QY 2221 AGCATTTCTGAGCTCACCACTGCCTTGTGTGCTCCAGGAAATGTTTCAGGTTCACAG 2280
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Db 2299 AGCATTTCTGAGCTCACCACTGCCTTGTGTGCTCCAGGAAATGTTTCAGGTTCACAG 2358
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|
QY 2281 TCAATCTCACAAGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
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|
|
Db 2359 TCAATCTCACAAGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2418
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|
QY 2341 TTGCTCTGTCTGCCATGTGCGGAGGACTTTGGGCAATCTTTCTGTGCAAAACCTG 2400
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Db 2419 TTGCTCTGTCTGCCATGTGCGGAGGACTTTGGGCAATCTTTCTGTGCAAAACCTG 2478
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QY 2401 ATCAGGTGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2460
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Db 2479 ATCAGGTGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2538
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QY 2461 GCGACCCAAAGATTTTACCCCAATGGAGGGAATCCAAATGTTTATTAATGATGAAGAG 2520
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Db 2539 GCGACCCAAAGATTTTACCCCAATGGAGGGAATCCAAATGTTTATTAATGATGAAGAG 2598
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QY 2521 GTGGTCCGAGAGACAGACACACTTTTGTATGCGGACCGACCGCTGCCAGGAA 2580
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Db 2599 GTGGTCCGAGAGACAGACACACTTTTGTATGCGGACCGACCGCTGCCAGGAA 2658
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QY 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
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Db 2659 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2718
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QY 2641 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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Db 2719 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2772
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RESULT 9

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US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
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US-10-803-268-1

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Query Match 97.4%; Score 2625.2; DB 18; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

QY 1 ATGAAGGATGTGGAGTCCGGGCGGAGGAGGTGCTGCTGAACTCGGCACGCCCCAGGGGC 60
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Db 106 ATGAAGGATGTGGAGTCCGGGCGGAGGAGGTGCTGCTGAACTCGGCACGCCCCAGGGGC 165
|
|
|
QY 61 GACGGCTGTCTACTGCTCGGCACCCCGCGGGCAGCGTTGGTGGCGGGCGGGTGGCCTG 120
|
|
|
Db 166 GACGGCTGTCTACTGCTCGGCACCCCGCGGGCAGCGTTGGTGGCGGGCGGGTGGCCTG 225
|
|
|
QY 121 AGGAGAGCCCGCGGGCAAGCAGGGGCGCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
|
|
|
Db 226 AGGAGAGCCCGCGGGCAAGCAGGGGCGCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 285
|
|
|
QY 181 TACACGAGTAGCCAGAGCTGCGCGGCAACGTCAGGTACCGGCGGGTGCAGAACTACCTG 240
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|
|
Db 286 TACACGAGTAGCCAGAGCTGCGCGGCAACGTCAGGTACCGGCGGGTGCAGAACTACCTG 345
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QY 241 TACAACTGTGGAGAGACCCCGCGGGCTGGGGGTTTCATCTACACGCTTTGTTTTCTC 300
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|
|
Db 346 TACAACTGTGGAGAGACCCCGCGGGCTGGGGGTTTCATCTACACGCTTTGTTTTCTC 405
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|
QY 301 CTGCTTTGGTTCGTTGATTTGTCAGTGTTCATCTACCATCCCTGAGACACACAAATTTG 360
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Db 406 CTGCTTTGGTTCGTTGATTTGTCAGTGTTCATCTACCATCCCTGAGACACACAAATTTG 465
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QY 361 GCCTCAAGTTCCCTCTTGATCCTCGAGTTCGTGATGATTGTCGTTTGGTGGAGTTTC 420
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Db 466 GCCTCAAGTTCCCTCTTGATCCTCGAGTTCGTGATGATTGTCGTTTGGTGGAGTTTC 525
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QY 421 ATCATTCGAATCTCGGTCTGCGGGTTCGTTGTCGATATAGAGGATGCAAGAGACCTG 480
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Db 526 ATCATTCGAATCTCGGTCTGCGGGTTCGTTGTCGATATAGAGGATGCAAGAGACCTG 585
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QY 481 AGGTTGCTCGAAAGCCCTCTGTTTATAGATACCATTTGTTTATCGCTTCAATAGCA 540
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Db 586 AGGTTGCTCGAAAGCCCTCTGTTTATAGATACCATTTGTTTATCGCTTCAATAGCA 645
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Db 646 GTTGTTCCTGCAAAACTCAGGGTAATATTTTGGCACGCTCTGCACCTCAGAACTCCGT 705
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Db 706 TTCTACAGATCTCCGATGCGGATGCGGATGCAAGGAGGAGGACCTTGGAAATACCTG 765
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QY 661 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCAGCTTGGTACATAGGATTTTGG 720
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Db 766 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCAGCTTGGTACATAGGATTTTGG 825
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QY 721 GTTCTTATTTTTCGTCCTTTCTGTCATCTGTTGGGAAAGAGATGCAATAAGAGTTT 780
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Db 826 GTTCTTATTTTTCGTCCTTTCTGTCATCTGTTGGGAAAGAGATGCAATAAGAGTTT 885
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QY 781 TCTACATATGAGATGCTCTCTGTTGGGCAATTAATATGATGACAACTATTTGGCTATGGA 840
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Db 886 TCTACATATGAGATGCTCTCTGTTGGGCAATTAATATGATGACAACTATTTGGCTATGGA 945
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QY 841 GACAAAATCCCTTAACCTTGGCTCGGAGATGCTTCTGTCAGGCTTTGCACTCTCTGGC 900
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Db 946 GACAAAATCCCTTAACCTTGGCTCGGAGATGCTTCTGTCAGGCTTTGCACTCTCTGGC 1005
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QY 901 ATTTCTTTTTCGTCATCTTCTGCGGCAATCTTGGCTCAGGTTTTCGATTTAAAGTACAA 960
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Db 1006 ATTTCTTTTTCGTCATCTTCTGCGGCAATCTTGGCTCAGGTTTTCGATTTAAAGTACAA 1065
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QY 961 GAACAAACCCGCGAGAAACACTTTTGAGAAAGAGAAAGCCAGCTGCCAACCTCATTTGAG 1020
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Db 1066 GAACAAACCCGCGAGAAACACTTTTGAGAAAGAGAAAGCCAGCTGCCAACCTCATTTGAG 1125
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[illegible]

QY	2221	AGCAATTTCTGAGTCAACCACTGCTTGTGTTGCTCTCAAGGAAATGTTTCTGAGTTGCACAG	2280	Db	225	GACGGCTCTACTGCTGGGCAACCCGCGCGCCACGCTCGGTGGCGGCGGTGGCGCTG	284
Db	2358	AGCAATTTCTGAGTCAACCACTGCTTGTGTTGCTCTCAAGGAAATGTTTCTGAGTTGCACAG	2417	QY	121	AGGGAGAGCCGCGGGGCAAGCAGGGGGCCGGGATGAGCCTGCTGGGGAAGCCGCTCTCT	180
QY	2281	TCAAATCTCAACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTTG	2340	Db	285	AGGGAGAGCCGCGGGGCAAGCAGGGGGCCGGGATGAGCCTGCTGGGGAAGCCGCTCTCT	344
Db	2418	TCAAATCTCAACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTTG	2477	QY	181	TACACAGTGTAGCCAGAGCTGCGGGGCAACCGTCAAGTACCGGGCGGGTGAGAACTTACCTG	240
QY	2341	TTGTCTGTCTGCTCCATGTTGCGGAGGACTTGGGCAAAATCTTTGCTGTGCAAAACCTTG	2400	Db	345	TACACAGTGTAGCCAGAGCTGCGGGGCAACCGTCAAGTACCGGGCGGGTGAGAACTTACCTG	404
Db	2478	TTGTCTGTCTGCTCCATGTTGCGGAGGACTTGGGCAAAATCTTTGCTGTGCAAAACCTTG	2537	QY	241	TACAAAGTGTAGCCAGAGCTGCGGGGCAACCGTCAAGTACCGGGCGGGTGAGAACTTACCTG	300
QY	2401	ATCAGGTGCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA	2460	Db	405	TACAAAGTGTAGCCAGAGCTGCGGGGCAACCGTCAAGTACCGGGCGGGTGAGAACTTACCTG	464
Db	2538	ATCAGGTGCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA	2597	QY	301	CTTGTCTTTTGTGTTGCTTCAATTTTGTCACTGTTTCTACCATCCCTGAGCACACAAAATTG	360
QY	2461	GGCAGCCCAAGATTTTATCCCAATGGAGGAAATCCAAATGTTTATTAAGTGAAGAG	2520	Db	465	CTTGTCTTTTGTGTTGCTTCAATTTTGTCACTGTTTCTACCATCCCTGAGCACACAAAATTG	524
Db	2598	GGCAGCCCAAGATTTTATCCCAATGGAGGAAATCCAAATGTTTATTAAGTGAAGAG	2657	QY	361	GCTCAAGTTGGCTCTTGTATCCTGGAGTTCTGTGATTCGTGATTCGTCTTTGGTTTGGAGTTC	420
QY	2521	GTGGTCCGGAAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA	2580	Db	525	GCTCAAGTTGGCTCTTGTATCCTGGAGTTCTGTGATTCGTGATTCGTCTTTGGTTTGGAGTTC	584
Db	2658	GTGGTCCGGAAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA	2717	QY	421	ATCATTCGAATCTGCTTGCAGGCTTCTGTATAGATACCAATGTTCTTATCGCTTCAATAGCA	480
QY	2581	GCTGCTTTGATCAGACTCTTAAGGACTGGAAAGTCAAGTCAATCTCAGAGCAATTTGT	2640	Db	585	ATCATTCGAATCTGCTTGCAGGCTTCTGTATAGATACCAATGTTCTTATCGCTTCAATAGCA	644
Db	2718	GCTGCTTTGATCAGACTCTTAAGGACTGGAAAGTCAAGTCAATCTCAGAGCAATTTGT	2777	QY	481	AGGTTTGTCTGAAAGCCCTTCTGTATAGATACCAATGTTCTTATCGCTTCAATAGCA	540
QY	2641	AAGGAGGAGAACTGACAGATGCCCTCAGCTTGCCTATGTCAAACTGAAATAA	2694	Db	645	AGGTTTGTCTGAAAGCCCTTCTGTATAGATACCAATGTTCTTATCGCTTCAATAGCA	704
Db	2778	AAGGAGGAGAACTGACAGATGCCCTCAGCTTGCCTATGTCAAACTGAAATAA	2831	QY	541	GTTGTTTCTGCAAAAACCTCAGGGTAATATTTTGGTCCACGCTGCACTCAGAGTCTCCGT	600
RESULT 11							
US-10-803-268-3							
; Sequence 3, Application US/10803268							
; Publication NO. US20040157259A1							
; GENERAL INFORMATION:							
; APPLICANT: Hu, Yi							
; APPLICANT: Kieke, James Alvin							
; APPLICANT: Turner, C. Alexander Jr.							
; APPLICANT: Nehls, Michael C.							
; APPLICANT: Friedrich, Glenn							
; APPLICANT: Zambrowicz, Brian							
; APPLICANT: Sands, Arthur T.							
; TITLE OF INVENTION: Novel Human Ion Channel Protein and							
; TITLE OF INVENTION: Polynucleotides Encoding the Same							
; FILE REFERENCE: LEX-0160-USA							
; CURRENT APPLICATION NUMBER: US/10/803,268							
; CURRENT FILING DATE: 2004-03-18							
; PRIOR APPLICATION NUMBER: US/09/825,147							
; PRIOR FILING DATE: 2001-04-03							
; PRIOR APPLICATION NUMBER: US 60/194,255							
; PRIOR FILING DATE: 2000-04-03							
; NUMBER OF SEQ ID NOS: 3							
; SOFTWARE: FastSeq for Windows Version 4.0							
; SEQ ID NO 3							
; LENGTH: 3111							
; TYPE: DNA							
; ORGANISM: homo sapiens							
US-10-803-268-3							
Query Match 97.4%; Score 2625.2; DB 18; Length 3111;							
Best Local Similarity 98.9%; Pred. No. 0;							
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;							
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Db	165	ATGAAGATGTGAGTCCGGGCGGGGAGGAGTCTGCTGAACTCGGACGCCCGAGGGGC	224				
QY	61	GACGGCTGTACTGTGGGCAACCGCGGGCACCGCTTGTGGCGGCGGCTGGCTG	120				


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; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-55

Query Match      19.2%; Score 518.4; DB 17; Length 2335;
Best Local Similarity 60.1%; Pred. No. 1.8e-148;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

QY 217 TACCGCGGGTGCAGAACTACCTGTACAAAGTGTGAGAGAGACCCCGCGGCTGGGGCTTC 276
DB 320 TACCGCGGCTGCAGAACTGGGTCTCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 379
QY 277 ATCTACCAACGCTTTCGTTTCTCTTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTT 336
DB 380 GTCTACCAACGCTTTCATATTTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 439
QY 337 ACCATCCCTGAGCACACAAATTCGCTCAAGTTGCTCTTGTATCTCTGAGGTTTCGTGATG 396
DB 440 ACTATCCAGGAGACCCAGGAACTTGCACAGAGTCTCTCTCATCTTGGAAATTCGTGATG 499
QY 397 ATTGTCGTTTGTGTTGGAGTTTCATCATTCGAAATCTGGTCTGCGGTTGCTGTTGTCGA 456
DB 500 ATCGTGTGTTTCGGCTTGGAGTACATCGTTCGGGTCTGTTCCGCGGATGCTGTCGCGC 559
QY 457 TATAGAGATGGCAAGGAACTGAGTTGCTCGAAGCCCTTCTGTTGTTATAGATACC 516
DB 560 TACCAGGATGGCAGGTTCGCTTCGCTTTCGCAAGAGCCCTTCTGTTGTCATCGACTTC 619
QY 517 ATTGTTCTTTCGCTTCAATAGCAGTTGTTTCTGCAAAATCTCAGGGTAAATTTTTGCC 576
DB 620 ATCGTGTGTTTCGGCTTCGGTTCGCTCATCGCGGGGTACCCAGGCAACATCTTCGCC 679
QY 577 AGCTCTGCACCTCAGAAGTCTCGTTTCTCAAGATCTTCGCGATGTTGCGGATGAGCGGA 636
DB 680 AGCTTCGGCTGCGCAGCATGCGTTCCTCGCAGATCTCTGCGCATGTTGCGCATGAGCCG 739
QY 637 AGGGAGGACCTTGAATTAAGTGGTTCAGTGGTTTATGTCTCAGCAAGAAATTAATC 696
DB 740 CCGCGCGGACCTGGAAGCTGCTGGGCTCAGTGGTCTACGGCTACGAGGAGCTGATC 799
QY 697 ACAGCTTGTGTACATAGGAATTTTGGTCTTATTTTTCGTTCTTCTTGTCTATCTGTTG 756
DB 800 ACCGCTGTGTACATCGGGTTCCTGTTGCTCATCTTCGCTCTCTTCTGTTCTACCTGGCC 859
QY 757 GAAAAGGATGCCAATAAGATTTTCTACATATGAGATGCTCTCTGTTGGGGGACAAAT 816
DB 860 GAGAGAGCGCAACTCCGACTTCTCTCTACGCGGACTCGCTCTGTTGGGGGACGAT 919
QY 817 ACATTGACACTATTGGCTATGAGACAAATCCCTTAACCTTGGCTGGGAAGATTGCTT 876
DB 920 ACATTGACAAACATCGGCTATGTTGACAGACACCGCACACATGCTGGCAGGGTCTG 979
QY 877 TCTGAGGCTTTGCACTCTCTTGGCAATTTCTTTTGTGCACTTCTCTGCGGCAATTTCTGGC 936
DB 980 GCTGCTGGCTTGGCTTACTGGGCACTCTTCTTCTTGTGCTCTCTGCGGCAATCTTAGGC 1039
QY 937 TCAGGTTTTCATTAAAGTACAGAACACCGCCAGAAACACTTTTGAGAAAAGAGG 996
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RESULT 13
 US-10-850-928-1
 ; Sequence 1, Application US/10850928
 ; Publication No. US20050037460A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JENTSCH, Thomas J.

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QY 1108 CCTACCAAGAAAGAAACAGGGAGAGCATCAAGCAGTCAAGAGCTA----- 1152
DB 1220 GCCCTCTTTGTTTGGACACGTCGCAACGGGCGGCAATGGGGCTTACGGCCCTGGAGGTG 1279
QY 1153 ----- 1152
DB 1280 CGGCGGGCGGTTACCGAGCGGAGCACCTCCCGTTACCGCGCGTTGCCACCTGCCAC 1339
QY 1153 -----AGTTTAAAGAGGA 1167
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; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE

; FILE OF INVENTION: POTASSIUM CHANNELS

; FILE REFERENCE: 2815-127PUS2

; CURRENT APPLICATION NUMBER: US/10/850,928

; CURRENT FILING DATE: 2004-05-20

; PRIOR APPLICATION NUMBER: 09/492,361

; PRIOR FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

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; ORGANISM: Homo sapiens

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US-10-850-928-1

Query Match 19.2%; Score 518.4; DB 19; Length 2335;

Best Local Similarity 60.1%; Pred. No. 1.8e-148;

Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:10:16 ; Search time 8514.67 Seconds
(without alignments)
12043.352 Million cell updates/sec

Title: US-09-810-796-2
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_hc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2105.2	78.1	2729	9 AY407015	AY407015 Mus muscu
3	1822.2	67.6	2014	9 AY407014	AY407014 Pan trogl
4	1413.8	52.5	2276	3 AK033079	AK033079 Mus muscu
C 5	727.8	27.0	797	6 CD629762	CD629762 55049367J
C 6	681.8	25.3	732	6 CD629756	CD629756 55049343J
C 7	679.2	25.2	742	6 CD629754	CD629754 55049327J
C 8	656.2	24.4	717	6 CD629766	CD629766 55049391J
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C 12	600.2	22.3	658	2 BE158938	BE158938 MR0-HT040
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C 17	572.8	21.3	643	6 CD629763	CD629763 55049383H
C 18	570.2	21.2	744	6 CB244389	CB244389 UI-M-FY0-
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C 21	549.4	20.4	632	2 BB624101	BB624101 BB624101
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ALIGNMENTS

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genomic survey sequence.
ACCESSION AY407013
VERSION AY407013.1 GI:39762984
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2733)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

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ORIGIN
Query Match 97.1%; Score 2616.6; DB 9; Length 2733;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2656; Conservative 0; Mismatches 11; Indels 27; Gaps 1;

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Qy	181	TACACGAGTAGCCAGAGTCCCGCGCAACGTCAGGTACCGCGGGTGCAGAACTACCTG	240
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Db	967	ATTTCCTTTCTTGGCACTTCTGCGGCACTTCTGGCTCAGTTTGGCAATTAAGATCAA	1026
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Qy	1081	CACCTGAGGCCCTTGACACCTGACGCCCTTACCAGAAAGAACAGGGGAGCATCAAGC	1140
Db	1147	CACCTGAGGCCCTTGACACCTGACGCCCTTACCAGAAAGAACAGGGGAGCATCAAGC	1181
Qy	1141	AGTCAGAGCTTAAGTTTTAAGGAGCGAGTGGCATGGCTAGCCCGCAGGGCCAGAGTATT	1200
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Db	1240	AAGAGCCGACAAAGCCTCAGTAGGTGACAGGAGTCCCAAGCAGCGAATCACAGCCGAG	1299
Qy	1261	GGCAGTCCCAACAAAGTGCAGAGAGCTGAGAGTTCACAGCCGACCCGCTTCGGGCC	1320
Db	1300	GGCAGTCCCAACAAAGTGCAGAGAGCTGAGAGTTCACAGCCGACCCGCTTCGGGCC	1359
Qy	1321	TCGCTGCGCTCAAAGTTCTCAGCCAAAACAGTGTAGATGTGTGACACAGCCCTTGGC	1380
Db	1360	TCGCTGCGCTCAAAGTTCTCAGCCAAAACAGTGTAGATGTGTGACACAGCCCTTGGC	1419
Qy	1381	ACTGATGATGTATATGATGAAAAAGATGCCAGTGTGATGTATCAGTGGAGACCTCACC	1440
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Db	1720	ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGTTGAAAAACAGGTACAGTCC	1779
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Db	1960	TTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTCGAGTTCAATTCGAGCCCAAT	2019
Qy	1981	GAGTTAGTCCCAAGACTTTCTACGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG	2040
Db	2020	GAGTTAGTCCCAAGACTTTCTACGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG	2079
Qy	2041	GTGCCAATTAGTCAAGGGATGGCTCAGAGTGGCGCCACCAACACATTTGCAAAACCAA	2100
Db	2080	GTGCCAATTAGTCAAGGGATGGCTCAGAGTGGCGCCACCAACACATTTGCAAAACCAA	2139
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Db	2140	ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA	2199
Qy	2161	GCCTCAGAGCATCTGCCAGGCCAGAACTCTGACCCCTAACCTGAGGCTTACAGAA	2220
Db	2200	GCCTCAGAGCATCTGCCAGGCCAGAACTCTGACCCCTAACCTGAGGCTTACAGAA	2259

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QY 2281 TCARATCTCACCAGGACGTTCTATGAGGAAGCTTTGACATGGGAGGAGAACTCTG 2340
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QY 2401 ATCAGGTGCGACCGAGGAACCTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2460
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QY 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGATCATCTCAGAGCAATTTGT 2640
Db 2620 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGATCATCTCAGAGCAATTTGT 2679
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RESULT 2
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DEFINITION Mus musculus KCN05 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY407015
VERSION AY407015.1 GI:39762986
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2729)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2729)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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source
location/Qualifiers
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ORIGIN

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Matches 2363; Conservative 0; Mismatches 258; Indels 73; Gaps 3;

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QY 61 GACGCTCTGCTACTGCTGGGACACCGCGCGCCACGCTTGTGTGGCGGGCGGTGGCCTG 120
Db 169 GACGCTCTGCTACTGCTGGGACACCGCGCGCCACGCTTGTGTGGCGGGCGGTGGCCTG 228
QY 121 AGGAGAGACCCCGGGGCAAGCAGCGGGGCCCGGATGAGCTCTGCTGGGGAAGCCGCTCT 180
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QY 181 TACAGAGTACGACAGAGCTGCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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QY	1081	CACCTCAAGCGCTTGACACACCTGACGCTTACCAAGGAAGAACAGGGAAGCATCAAGC	1140
Db	1150	CATCTGAAGGCTTGCACACCTGACGCTTACCA-----	1184
QY	1141	AGTCAGAAGCTAAAGTTTAAAGAGCGAGTCGCGATCGGTAGCCCGAGGGGCGCAGATATT	1200
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Db	1303	GGCAGCCCCAACAAAGTCCAGAAAGTTGGAGCTTCAACGACCGAACCCGCTTCCAGGCC	1362
QY	1321	TCGCTGCGCCTCAAAAGTTCTTCAGCCAAAACAGTGATAGATGTGACACAGCCCTTGGC	1380
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QY	1381	ACTGATGATGTATGATGAAAAAGGATCCGAGTGTGATGTATCAGTGAAGACCTTCACC	1440
Db	1423	ATTGATGATGTGATGATGAAAGGATGCCAGTGTGAGCTCTCTGTGGAGGACCTTCACC	1482
QY	1441	CCACCCTTAAACTGTCAATTCGAGCTTATCAGAAATTTGAAATTTTCATGTTCAAAACGG	1500
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QY	2041	GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGGAGCCCAACACCATTTGCAAAACAA	2100
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Db	2136	ATAAGCGCGCACCCAAAGCAGCAGCAGCCCAACAACCTTTACAGATCCCTCTCTCTCTCTCG	2195
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Db	2196	GCATCAAGCATTTGTCCAGGCCAGAACTCTGTCTCTCAAAACCCACCGCTTTACAAGAG	2255
Qy	2221	AGCATTTCTGAGTCACCACTGCCCTGTGTGCTCCAAAGGAAAATGTTGAGTTGCACAG	2280
Db	2256	AGTATTTCTGATGTCAACCACTGCCCTGTGTGCTCCAAAGGAAAATGTTGAGTTGCACAG	2315
Qy	2281	TCAAACTCACCAAGACCGTTCATGAGGAAAAGCTTTGACATGGAGGAGAAAATCTCTG	2340
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Qy	2341	TTGCTGTCTGTCCCATGTGTGCCGAAGGACTTGGGCAAAATCTTTGTCTGTGCAAAAACCTG	2400
Db	2376	TTGTCTGTCCGCCCATGTGTGCCCAAGGATTTGGGCAAAATCTCTGTCTGTGTACAAAACCTG	2435
Qy	2401	ATCAGGTGACCGAGGAACTGAATATACAACTTTTCAGGGAGTGAGTCAAGTGCGCTCCAGA	2460
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Qy	2461	GGCAGCCAGATTTTACCCCCAAATGGAGGGAATCCAAATTTGTTTATTACTGATGAAGAG	2520
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Qy	2521	GTGGTCCCAGAGACAGACAGACATTTTGTATCCCGACCGCAGCGCTGCCAGGGAA	2580
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Qy	2641	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAATAA	2694
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DEFINITION				
ACCESSION	AY407014			
VERSION	AY407014.1	GI:39762985		
KEYWORDS	GSS.			
SOURCE	pan troglodytes (chimpanzee)			
ORGANISM	pan troglodytes			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.			
AUTHORS	1 (bases 1 to 2014) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
TITLE	Science 302 (5652), 1960-1963 (2003)			
JOURNAL	14671302			
PUBMED	2 (bases 1 to 2014)			
REFERENCE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment			
TITLE	Location/Qualifiers			
JOURNAL	1. .2014			
COMMENT				
FEATURES	source			

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Qy	91	GCCACGCTTGTGGGCGGCGGCTGGCTGAGGAGAGCGCGCGGGGCAAGCAGGGGGCC	150						
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Db	901	CTTGCTCAGGTTTGGCAATTAAGTACAAGAACCAACCCGCGAGAACTTTTGAGAAA	960						
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Db	961	AGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCTAGTTCAGCAGCTGATGAG	1020						
Qy	1051	AAATCTGTTTCCATTGCAACCTGGAAGCCACACTTTGAAGGGCTTCACACACCTGCAAGCCT	1110						
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TITLE Muramatsu, M. and Hayashizaki, Y.
JOURNAL Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Query	Best Match
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[illegible]

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LOCUS
DEFINITION CD629762 797 bp mRNA linear EST 12-JAN-2004
ACCESSION 55049367J1 FLP Homo sapiens cDNA, mRNA sequence.
VERSION CD629762.1 GI:40278028
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
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/note="Vector: pDrive Cloning Vector"

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Matches 754; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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Qy 1049 AGAAATCTGTTTCCATTCGAAACCTCGAAGCCACACTTGAAGGCCCTTGACACCTGAG-C 1107
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Best Local Similarity 98.4%; Pred. No. 46-183;
Matches 728; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

Qy 1016 TTCAGTGTGTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTCCATTGCAACTGGA 1075
Db 742 TTCAGTGTGTTGGCGTA-TTACGAGCTGATGAGAAATCTGTTCCATTGCAACTGGA 684

Qy 1076 AGCCACACTTGAAGCCTTGCACACTGCAGCCCTACCAAGAAAGAA-CAAGGGGAAGCA 1134
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Qy 1135 TCAAGCAGTCAGAAGCTAAGTTTAAAGAG-CGAGTGGCGCATGGCTAGCCCGAGGGGCA 1193
Db 623 TCAAGCAGTCAGAAGCTAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCGAGGGGCA 564

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Qy 1254 AGCCGAGGCGAGTCCACCAAGTGCAGAAAGCTGGAGCTTCAACGACCCGAAACCCGCTT 1313
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Qy 1314 CGGCGCCTCGTGCCTCAAAAGTTCTCAGCAAAACCAAGTAGATGCTGACACAGC 1373
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Qy 1494 AAAACGGAAGTTTAAAGAAACGTTACGTCCATATGATGTAAGAGATGCTATTGAACAATA 1553
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Qy 1554 TTCTGCTGTCATCTGGACATGTTGTGTAGAAATTAAGCCCTTCAAAACACGTTGATCA 1613
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Qy 1614 AATTCTTGGAAAGGGCAATCACATCAGATAAGAGCCGAGAGAAATAACAGCAGA 1673
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Qy 1674 ACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGG-TGGTCAAGGTTGAAAAACAGG 1732
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RESULT 8
CD629766/c
LOCUS CD629766 717 bp mRNA linear EST 12-JAN-2004
DEFINITION 55049391J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629766
VERSION CD629766.1 GI:40278032
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 717)
Fu.G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3150 Porter Dr., Palo Alto, CA 94304, USA
Tel.: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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Best Local Similarity 98.3%; Pred. No. 1.6e-176;
Matches 705; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

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Qy 1269 CACCAAGTGAGAGAGCTGGAGTTCAAAGCAGAACCCGCTTCCGCGCCCTCGCTGGG 1328
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Qy 1389 TGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAAGACCTCACCCACCACCT 1448
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Qy 1449 TAAACCTGTCATTCGAGCTATCAGAAATTTGAAATTTTCAATGTTGCAAAACGGAAGTTTAA 1508
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Db 237 GGAACGTTTACGTCATATGATGTAAGAGATGTCATGCAACAATTTCTGCTGGTCATCT 178

Qy 1569 GGACATGTTGTGTAGAAATTAAGCCCTTCA-AAACCGTGTGATCAAAATTTCTTGGAAAAG 1627
Db 177 GGACATGTTGTGTAGAAATTAAGCCCTTCAAAACCGTGTGATCAAAATTTCTTGGAAAAG 118

Qy 1628 GGCAAAATCACATCAGATGAAGAA-GAGCCGAGAGAAAAATAACAGCAGAACATGAGACCACA 1686
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RESULT 11
CD629752/c 724 bp mRNA linear EST 12-JAN-2004
LOCUS CD629752
DEFINITION 55049303J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629752
VERSION CD629752.1 GI:40278018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 724)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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QY 1691 ATCTCAGTATGCTCGGTGCGGTGCTGAGGTTGAAAAACAGGTACAGTCCATAGAGTCCA 1750
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DEFINITION MRO-HT0404-210200-001-c04 HT0404 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE158938
VERSION BE158938.1 GI:8621659
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 658)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2-MRO-HT0404-210
200-001-c04&t3=2000-02-21&t4=1)
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High quality sequence stop: 657.
Location/Qualifiers

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Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 22.1%; Score 594.4; DB 6; Length 599;
Best Local Similarity 99.8%; Pred. No. 8.e-159;
Matches 639; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
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RESULT 13
CD629765
LOCUS
DEFINITION 55049391H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629765

CD629765.1 GI:40278031
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 599)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1..599
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/note="Vector: pDrive Cloning Vector"

FEATURES
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Matches 595; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 14
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LOCUS
CD629760

CD629765
LOCUS
DEFINITION 55049391H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629765

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/mol_type="mRNA"
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/dev_stage="Adult"
/clone_lib="H10404"
/note="Organ: head neck; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
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Best Local Similarity 95.5%; Pred. No. 2e-160;
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Db 17 TGGCTATGGAGACAAAACCTCCCTAACTGGCTGGGAAGATTGCTTCTCAGGCTTTGC 76
Qy 891 ACTCCTTGGCATTTCTTCTTCTGCACTCTCGCGCATCTTGGCTCAGGTTTTCATT 950
Db 77 ACTCCTTGGCATTTCTTCTTCTGCACTCTCGCGCATCTTGGCTCAGGTTTTCATT 136
Qy 951 AAAAGTACAGAAACACACCGCCAGAACACTTTGAGAAAAGAGAACCCAGCTGCCAA 1010
Db 137 AAAAGTACAGAAACACACCGCCAGAACACTTTGAGAAAAGAGAACCCAGCTGCCAA 196
Qy 1011 CCTCATTCAGTGTGTGGCGTAGTTACGACGTGATGAGAAATCTGTTCCATTGCAAC 1070
Db 197 CCTCATTCAGTGTGTGGCGTAGTTACGACGTGATGAGAAATCTGTTCCATTGCAAC 256
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Db 470 CTTCCGGCCCTCGCTGGCGCTCAAAAGTTCTCAGCAAAACCCAGTAGATGCTGACAC 529
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Qy 1431 AGACCTTCAACCCACCACTTAAACCTGCTATTCAGCTATCAAGATTATGAATTTTCATGT 1490
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Qy 1491 TGCAAAACG 1499
Db 650 TGCAAAACG 658

RESULT 13
CD629765
LOCUS
DEFINITION 55049391H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629765

CD629765
LOCUS
DEFINITION 55049391H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629765

DEFINITION 55049359J1 FLP Homo sapiens cDNA, mRNA sequence.

ACCESSION CD629760

VERSION CD629760.1 GI:40278026

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 714)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput

JOURNAL extension cloning of partial genes

COMMENT Genomics 84 (1), 205-210 (2004)

CONTACT: Fu GK

INCYTE Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

TEL: 6508454102

EMAIL: gfu@incyte.com.

LOCATION/Qualifiers

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="FLP"

/note="Vector: pDrive Cloning Vector"

ORIGIN

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Best Local Similarity 96.3%; Pred. No. 3.1e-156;

Matches 643; Conservative 0; Mismatches 18; Indels 7; Gaps 4;

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QY 1122 ACAAGGGAAGCATCAAGCAGTCAGAGCTAAGTTTAAAGGCGAGTGGCATGGCTAG 1181

DB 628 AAAGGGAAGCATTCAGCAGTCAGAGCTAAGTTTAAAGGCGAGTGGCATGGCTAG 569

QY 1182 CCCAGGGGCGAGTATTAGAGCGGACAGCCCTCAGTAGTGACAGAGTCCCCAAG 1241

DB 568 CCCAGGGGCGAGTATTAGAGCGGACAGCCCTCAGTAGTGACAGAGTCCCCAAG 509

QY 1242 CACCGACATCACAGCGGAGGCGAGTCCCAACAAAGTGACAGAGCTGGAGCTTCAA-CG 1300

DB 508 CACCGACATCACAGCGGAGGCGAGTCCCAACAAAGTGACAGAGCTGGAGCTTCAA 449

QY 1301 ACCGAACCGGCTTCGGGCGCTGCTGCGCTCAAAAGTTCTCAGCCAAACACAGTGATG 1360

DB 448 ACCGAACCGGCTTCGGGCGCTGCTGCGCTCAAAAGTTCTCAGCCAAACACAGTGATG 389

QY 1361 ATGCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATG 1420

DB 388 ATGCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATG 329

QY 1421 TATCAGTGAAGACCTTCAACCCACACCTTAAACCTGCTATTCAGAGCTATCAGATTATGA 1480

DB 328 TATCAGTGAAGACCTTCAACCCACACCTTAAACCTGCTATTCAGAGCTATCAGATTATGA 269

QY 1481 AATTTTCATGTTGCAAAACCGAAGTTTAAAGGAACCGTTACGTTCCATGATGTAAGAATG 1540

DB 268 AATTTTCATGTTGCAAAACCGAAGTTTAAAGGAACCGTTACGTTCCATGATGTAAGAATG 209

QY 1541 TCATTGAACATATTCTCTGGTCTATCTGGACATGTTGTAGATTAAAGCCCTTCAA 1600

DB 208 TCATTGAACATATTCTCTGGTCTATCTGGACATGTTGTAGATTAAAGCCCTTCAA 149

QY 1601 CACGTGTTGATCAAAATCTTGGAAAGGCGCAATCACATCAGATCAAGAGAGCGAGAGA 1660

DB 148 CACGTGTTGATCAAAATCTTGGAAAGGCGCAATCACATCAGATCAAGAGAGCGAGAGA 89

QY 1661 AAATAACAGCAGAACATGAGACCCACAGACGATCTCAGTATGCTCGGTGGGTGTTCAAGG 1720

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Db 28 TGAATAACA 21

RESULT 15

LOCUS CD629751 624 bp mRNA linear EST 12-JAN-2004

DEFINITION 55049303H1 FLP Homo sapiens cDNA, mRNA sequence.

ACCESSION CD629751

VERSION CD629751.1 GI:40278017

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 624)

AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput

JOURNAL extension cloning of partial genes

COMMENT Genomics 84 (1), 205-210 (2004)

CONTACT: Fu GK

INCYTE Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

TEL: 6508454102

EMAIL: gfu@incyte.com.

LOCATION/Qualifiers

1..624

/organism="Homo sapiens"

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/clone_lib="FLP"

/note="Vector: pDrive Cloning Vector"

ORIGIN

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Best Local Similarity 97.8%; Pred. No. 8.7e-156;

Matches 614; Conservative 0; Mismatches 10; Indels 4; Gaps 2;

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DB 61 ACTTGGCTGGGAAGATTCTTCTGCAGGCTTTCGACTCTTGGCATTTCTTCTTCTGCA 120

QY 916 CTTCCTGCGGCACTTCTTGGCTCAGGTTTTCGATTAAAGTACAAGAACACACGCCAG 975

DB 121 CTTCCTGCGGCACTTCTTGGCTCAGGTTTTCGATTAAAGTACAAGAACACACGCCAG 180

QY 976 AAACACTTTGAGAAAAGAGAACCCAGCTGCCAACCTCATTCAGTGTGTTGGCGTAGT 1035

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DB 361 TTTAAGGAGCGAGTCCGATGCTAGCCCCAGGGGCCAGAGTATTTAAGAGCGGACAAAGCC 420

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Db 541 AGTTCTCAGCCAAACCAAGTGATAGATGCTGACACAG-CCTTGGCACTGATGATGT---T 596
Qy 1396 GATGAAAAGGATGCCAGTGTGATGATAT 1423
Db 597 ATGATGCAAGGATGCCCGTGTGATGATAT 624

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Job time : 8526.67 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:27:56 ; Search time 422.362 Seconds
(without alignments)
10332.249 Million cell updates/sec

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Perfect score: 2667
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2662.2	99.8	3111	4	US-09-825-147-3 Sequence 3, Appli
3	2625.2	98.4	3137	4	US-09-590-304-1 Sequence 1, Appli
4	2617.2	98.1	3074	4	US-09-813-148-1 Sequence 1, Appli
5	509.8	19.1	582	4	US-09-495-050A-303 Sequence 303, App
6	492	18.4	2196	4	US-09-949-016-1823 Sequence 1823, Ap
7	492	18.4	2335	4	US-09-492-361-1 Sequence 1, Appli
8	489.2	18.3	2273	3	US-09-177-650-88 Sequence 88, Appl
9	475.6	17.8	2169	3	US-09-105-058C-22 Sequence 22, Appl
10	465.4	17.5	896	3	US-09-105-058C-1 Sequence 1, Appli
11	452	16.9	575	4	US-09-495-050A-305 Sequence 305, App
12	427.2	16.0	2565	3	US-09-105-058C-26 Sequence 26, Appl
13	427.2	16.0	2914	3	US-09-177-650-6 Sequence 6, Appli
14	426.8	16.0	2814	3	US-09-177-650-90 Sequence 90, Appl
15	425	15.9	3287	3	US-09-105-058C-19 Sequence 19, Appl
16	423.4	15.9	3232	3	US-09-177-650-1 Sequence 1, Appli
17	423.4	15.9	3237	3	US-09-177-650-95 Sequence 95, Appl
18	421.4	15.8	900	3	US-09-105-058C-3 Sequence 3, Appli
19	420.6	15.8	900	3	US-09-105-058C-5 Sequence 5, Appli
20	363.8	13.6	930	3	US-09-105-058C-17 Sequence 17, Appl
21	334.2	12.5	735	3	US-09-105-058C-7 Sequence 7, Appli
22	276.4	10.4	284	4	US-09-495-050A-304 Sequence 304, App
23	267.8	10.0	2028	3	US-09-634-920-1 Sequence 1, Appli
24	267.8	10.0	2028	4	US-09-840-125-1 Sequence 1, Appli
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ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

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2625 AGGGAATCCAAATGTTTATATACTGATGAAGAGTGGGTCCCGAAGAGACAGACAGAC 2684
2521 ACTTTTGTATGCGCAGCCGAGGCTTGCAGGGAAGCTTGTGCAATCAGATCTCTAAGG 2580
2685 ACTTTTGTATGCGCAGCCGAGGCTTGCAGGGAAGCTTGTGCAATCAGATCTCTAAGG 2744

2581 ACTGGAAGGTACGATCATCTCAGAGCATTTGTAAGCAGGAGAAAGTACAGATGCCCTC 2640
2745 ACTGGAAGGTACGATCATCTCAGAGCATTTGTAAGCAGGAGAAAGTACAGATGCCCTC 2804
2641 AGCTTGCTCATCTCAAACTGAAATAA 2667
2805 AGCTTGCTCATCTCAAACTGAAATAA 2831
RESULT 3
US-09-590-304-1
; Sequence 1, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-09-590-304-1
Query Match 98.4%; Score 2625.2; DB 4; Length 3137;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
Qy 1 ATGAAGGATGTGAGTCGGCGCGGCGAGGGTGTCTGTAATCTCGGAGCGCCGAGGGC 60
Db 1 ATGAAGGATGTGAGTCGGCGCGGCGAGGGTGTCTGTAATCTCGGAGCGCCGAGGGC 60
Qy 61 GACGGCTGTACTGTCTGGGCAACCGCGCGCCACCGCTTGTGGCGCGCGGTGGCTG 120
Db 61 GACGGCTGTACTGTCTGGGCAACCGCGCGCCACCGCTTGTGGCGCGCGGTGGCTG 120
Qy 121 AGGAGAGCCCGCGGCGCAAGCAGGGGCGCGGATGAGCCTGTGGGAAAGCCGCTCT 180
Db 121 AGGAGAGCCCGCGGCGCAAGCAGGGGCGCGGATGAGCCTGTGGGAAAGCCGCTCT 180
Qy 181 TACAGAGTACAGAGCTCGCGCGCAACGTCAAGTACCGGCGGTGCAAGTACCTG 240
Db 181 TACAGAGTACAGAGCTCGCGCGCAACGTCAAGTACCGGCGGTGCAAGTACCTG 240
Qy 241 TACAACGTGTGGAGAGACCCCGCGCTGGCGGTTCACTACACAGCTTTCGTTTTTCTC 300
Db 241 TACAACGTGTGGAGAGACCCCGCGCTGGCGGTTCACTACACAGCTTTCGTTTTTCTC 300
Qy 301 CTCTGCTTGGTGTGATTTGTTCAGTGTTCATCATTCATTCATTCATTCATTCATTC 360
Db 301 CTCTGCTTGGTGTGATTTGTTCAGTGTTCATCATTCATTCATTCATTCATTCATTC 360
Qy 361 GCCTCAAGTGGCTTGTGATTCCTGGAGTTCGTGATGATTCGTCTTGGTGGAGTTC 420
Db 361 GCCTCAAGTGGCTTGTGATTCCTGGAGTTCGTGATGATTCGTCTTGGTGGAGTTC 420
Qy 421 ATCAATTCGAATCTGCTGCGGGTGTGTTGTCGATATAGAGGATGCAAGGAGACTG 480
Db 421 ATCAATTCGAATCTGCTGCGGGTGTGTTGTCGATATAGAGGATGCAAGGAGACTG 480
Qy 481 AGGTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTCATTCATTCATTCATTCAT 540
Db 481 AGGTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTCATTCATTCATTCATTCAT 540
Qy 541 GTTGTTCGCAAAAACCTCAGGTAATATTTTTCGCGAGCTGCACCTCAGAGTCCCGT 600
Db 541 GTTGTTCGCAAAAACCTCAGGTAATATTTTTCGCGAGCTGCACCTCAGAGTCCCGT 600

; GENERAL INFORMATION:
 ; APPLICANT: STEINMEYER, Klaus
 ; APPLICANT: LERCHE, Christian
 ; APPLICANT: SCHERER, Constanze
 ; APPLICANT: SEEBOM, Guiscard
 ; APPLICANT: BUSCH, Andreas E.
 ; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CEN
 ; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
 ; FILE REFERENCE: 38005-119
 ; CURRENT APPLICATION NUMBER: US/09/813,148
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: DE 100 13 732.6
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/194,041
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3074
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-813-148-1

Query Match 98.1%; Score 2617.2; DB 4; Length 3074;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;

Qy	1	ATGAAGATGTGGAGTCGGCGGGGAGGGTGTCTGAACTCGGCAGCGCCGAGGGG	60
Db	215	ATGAAGATGTGGAGTCGGCGGGGAGGGTGTCTGAACTCGGCAGCGCCGAGGGG	274
Qy	61	GACGGCTGTACTGTCTGGGCAACCGCGGGCCACCGCTTGGTGGCGCGCGGTGGCGTG	120
Db	275	GACGGCTGTACTGTCTGGGCAACCGCGGGCCACCGCTTGGTGGCGCGCGGTGGCGTG	334
Qy	121	AGGAGAGCGCGCGGGCAAGCAGGGGGCCGGATGAGCCCTGTGGGGAGCCGCTCTCT	180
Db	335	AGGAGAGCGCGCGGGCAAGCAGGGGGCCGGATGAGCCCTGTGGGGAGCCGCTCTCT	394
Qy	181	TACACGAGTACGAGAGCTGCGCGGCAACGCTCAAGTACCGCGGGGTGCAGAACTACCTG	240
Db	395	TACACGAGTACGAGAGCTGCGCGGCAACGCTCAAGTACCGCGGGGTGCAGAACTACCTG	454
Qy	241	TACAAAGTGTGGAGAGACCCCGCGGCTGGCGGTTTCATCTACACGCTTTTCGTTTCTC	300
Db	455	TACAAAGTGTGGAGAGACCCCGCGGCTGGCGGTTTCATCTACACGCTTTTCGTTTCTC	514
Qy	301	CTTGCTTTTGTGTGCTGATTTTGTGAGTGTTCAGTGTTCATCTACATCCCTGAGCACAAAATTG	360
Db	515	CTTGCTTTTGTGTGCTGATTTTGTGAGTGTTCAGTGTTCATCTACATCCCTGAGCACAAAATTG	574
Qy	361	GCCTCAAGTTCCTTGTATCTGAGTTCGAGTGTGCTGCTTTGTTGGTTCGAGTTC	420
Db	575	GCCTCAAGTTCCTTGTATCTGAGTTCGAGTGTGCTGCTTTGTTGGTTCGAGTTC	634
Qy	421	ATCATTCAAGTTCGCTGCGGGTGTGCTGTCGATATAGGATGCGAGGAGAGCTG	480
Db	635	ATCATTCAAGTTCGCTGCGGGTGTGCTGTCGATATAGGATGCGAGGAGAGCTG	694
Qy	481	AGGTTTGTTCGAAAGCCCTTCTGTCTTATAGATACCATTTTTCATCGCTTCAATAGCA	540
Db	695	AGGTTTGTTCGAAAGCCCTTCTGTCTTATAGATACCATTTTTCATCGCTTCAATAGCA	754
Qy	541	GTGTTTTCGAAAAAATCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAAGTTCGGT	600
Db	755	GTGTTTTCGAAAAAATCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAAGTTCGGT	814
Qy	601	TTTCCTACAGATCCTCGGATGTGCGCATGAGACCGAAGGGAGGACCTTGGAAATTAATG	660
Db	815	TTTCCTACAGATCCTCGGATGTGCGCATGAGACCGAAGGGAGGACCTTGGAAATTAATG	874
Qy	661	GGTTTCAGTGGTTTATGCTCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGT	720

; SOFTWARE: FastSeq for Windows Version 4.0		; SEQ ID NO 1823		; LENGTH: 2196	
; TYPE: DNA		; ORGANISM: Human		; US-09-949-016-1823	
Query Match		18.4%; Score 492; DB 4; Length 2196;			
Best Local Similarity		59.3%; Pred. No. 2.7e-139;			
Matches 1087; Conservative		0; Mismatches 555; Indels 192; Gaps 7;			
Qy	217	TACCGCGGGTGCAGAACTACTCTGACAACTGCTGAGAGACCCCGCGGCTGGGCGTTC	276		
Db	181	TACCGCGCGCTGCAGAACTGGGGGTACAACTGCTGGAGCGGCGCCCGGGCTGGCGCTTC	240		
Qy	277	ATCTACCAAGCTTTGGTTTCTCTGCTCTTGGTTGCTTGAATTTTGTCACTGCTTTTCT	336		
Db	241	GTCTACCAAGCTTTCTATATTTTGTGCTCTTCACTGCTGCTGCTGCTGCTGCTGCC	300		
Qy	337	ACCATCCCTGAGCACACAAATTTGGCCTTCAAGTTGCTCTTTGATCTCTGGAGTTCTGATG	396		
Db	301	ACTATCCAGGAGCACAGGAACTTGCCAAACGAGTGTCTCTCACTTTGGAATTCGTGATG	360		
Qy	397	ATTGTCGCTTTGGTTTGGAGTTCAATCATTCGAATCTGCTCGGGTTCGCTGTTGCTGA	456		
Db	361	ATCGTGGTTTTCGGCTTGGAGTACATCGTCCGGGTCTGCTCCGCGGAGTCTGTCGCGC	420		
Qy	457	TATAGAGATGCAAGGAAGACTGAGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACC	516		
Db	421	TACCGAGATGCGAGGTCGCTTCGCTTTGCCAGAAAGCCCTTCTGTGTCATCGACTTC	480		
Qy	517	ATTGTTCTTATCGCTTCAATAGCAGTGTGTTCTGCAAAACTCAGGGTAAATTTTGGCC	576		
Db	481	ATCGTGTTCGTGCTCGGTGCGCTCAATCGCGCGGGTACCCAGGGCAACATCTTGCC	540		
Qy	577	AGCTGTGCACTCAGAGTCTCGTTTCTTACAGATCTCCGATCGTGGCGATGAGACCGA	636		
Db	541	AGCTCGCGCTCGCAGCATGCGCTTCTCTGAGATCTCTGCGCATGCTGGCATGAGACCGC	600		
Qy	637	AGGGAGGACACTTGGAAATTAAGTGGTTTCAAGTGGTTTATGCTTCAAGCAAGAAATTAATC	696		
Db	601	CGCGCGGACCTGGAAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGAGCTGATC	660		
Qy	697	ACAGCTGTGTATAGGATTTTGGTTCTTATTTTCTGCTTCTGCTCTATCTGCTG	756		
Db	661	ACGCGCTGTGTATCGGGTTCCTGGTGTCTATCTTGGCTCTCTTCTGCTCTACCTGGCT	720		
Qy	757	GAAGAAGATGCCAATAAAGATTTTCTACATATGCAGATGCTCTCTGGTGGGCGCAATTT	816		
Db	721	GAGAAGAGCGCCAACTCCGACTTCTCTCTACGCGGACTCGCTCTGGTGGGAGCGATT	780		
Qy	817	ACATTGACAACTATTGGGTATGAGAGCAAACTCCCTCTAACTTGGCTGGAGATGCTT	876		
Db	781	ACATTGACAACTATCGCTATGTGACAAAGACACCGCATGCTGGCGAGGGTCTCTG	840		
Qy	877	TCGCGAGGCTTTCACCTCTCTGCACTTTCTTTCTTTGCACTTCTCTCGCGGCACTTCTGGC	936		
Db	841	CTGCTGGCTTTCGCTTCTGAGGATCTCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTG	900		
Qy	937	TCAGGTTTTCATTTAAAGTACAGAAACACCCGCGAAGAACCTTTGAGAAAGAGG	996		
Db	901	TCCGGCTTTCCTCTGAAGGTCCAGGAGCAGCAGCGGAGAGCACTTCGAGAAGCGGAGG	960		
Qy	997	AACCGAGCTGCAACCTCATCTAGTGTGTTGGGTAGTTTACGACGCTGATGAGAATCT	1056		
Db	961	ATGCGGCGCCCAACCTCATCTAGGCTGCTGGCGCTGTACTTCCACCATATGAGCCGG	1020		
Qy	1057	GTITTCATTCGAACCTGGAAGCCACACTTGAAGGCTTTGCACAC-----	1100		
Db	1021	GCCTACCTGACGCCACCTGGTACTACTATGACAGTATCTCCCATCTTCCAGAGCTG	1080		
Qy	1101	-----	1100		
Db	1081	GCCCTCTTGTGTGACACGTCGCAACGGGCGCCGCAATGGGGCCCTACGCGCCCTGGAGGTG	1140		
Qy	1101	-----	1100		
Db	1141	CGGCGGCGCGGTACCCGACGGAGCACCCCTCCCTTTACCCGCGCGTTCGCCACCTGCCAC	1200		
Qy	1101	-----CTGAGCCCTACCAATCAGAGCTAAGTTTAAAGAGGGA	1140		
Db	1201	CGGCGGCGGAGCACCTCTTCTGTCCTTGGGAAAGCAGCCGATGGGATCAAGACCGC	1260		
Qy	1141	GTGCGCATGCTAGCCAGGCGGCCAGAGTATT-----AAGAGCGCAAGACCTCAGTA	1194		
Db	1261	ATCCGATGGGAGCTTCCAGCGGGACGGGTCTTCCAGCAGCATCTGGACACTCCA	1320		
Qy	1195	GGTGAAGAGGTTCCCAAGCAGCAGCATCAGCCGAGG---GCAGTCCCAACCAAGTG	1251		
Db	1321	ACAAATCCCACTCCCAAGCAGCAGGAGTGGGTGAGGCCACCAAGCCCAACCAAGTG	1380		
Qy	1252	CAGAAGAGTGGAGCTTCAACGACCGAACCCGCTTCCGCGCCCTCGCTGCGCTCAAAAGT	1311		
Db	1381	CAAAAGAGCTGGAGCTTCAATGACCGCACCGCTTCCGCGCATCTCTGAGACTC-----	1434		
Qy	1312	TCTCAGCCAAAACAGTGTATGATGCTGACAGACCCCTTGGCAGCTGATGATATATAT	1371		
Db	1435	-----AAACCCCGCACCTCTGCTGAGGATGCC-----CCTCAGAGGAAGTAGCAGAG	1482		
Qy	1372	GAAAAGGATGCCAGTGTGATGATCAGTGGAGACCTCACCCCAACCTTAAAACTGTC	1431		
Db	1483	GAGAAGAGTACCAAGTGTGAGCTCAGGTGGAGCAGCATCATGCTCTGTGAAGACAGTC	1542		
Qy	1432	ATTTCGAGCTATCAGAAATTAATGAAATTTTCAATTTGTTGAAAAACGGAAGTTTAAAGAAAGCTTA	1491		
Db	1543	ATCGCTCCATCAGGATTTCTCAAGTTCTCTGTTGGCCAAAAGGAAATTTCAAGGAGACACTG	1602		
Qy	1492	CGTCCATATGATTAAGATGTCATGACATATTTCTGCTGCTCATCTGGACATGTTG	1551		
Db	1603	CGACCGTACGACGTGAAGGACGTCATTTGAGCAGTACTCAGCAGGCCACCTGGACATGCTG	1662		
Qy	1552	TGTAGAAATTAAGACCTTCAACACACGTTGATCAAAATTTCTTGGAAAAAGGC---AAATC	1608		
Db	1663	GGCGGATCAAGAGCTTGCAAACTCGGTGACCAAAATTTGGTGGGGCCCGGGGAC	1722		
Qy	1609	ACATCAGATAAGAGAGCCGAGAGAAATAACAGAGAACATGAGACCAAGACGATCTC	1668		
Db	1723	AGGAAGCCCGGAGAGAGGCGCACAGGGGCCCTCCGACCGGAGGTGGTGGATGAAATC	1782		
Qy	1669	AGTATGCTCGTGGGTGTCAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAAGCTG	1728		
Db	1783	AGCATGATGGGACCGGTGTCAGGTGAGAGCAGGTGCAGTCCATCGAGCACAAGCTG	1842		
Qy	1729	GACTGCTTACTAGACATCTATCAACAGGTCTTTCGGAAAGGCTCTGCTCAGCCCTCGCT	1788		
Db	1843	GACCTGCTTGTGGCTTCTATTTCGCTGCTGCTG-----GCTCTGGCACCTCGGCCAGC	1896		
Qy	1789	TTGGCTTCACTTCAGATCCACCTTTTGAATGTGTAACAGACATCTGACTATCAAGGCCCT	1848		
Db	1897	CTGGCGCGGTGCAAGTGGCGCTGTTTCCGACCCCGACATCACTTCGACTACCAAGCCCT	1956		
Qy	1849	GTGGATAGCAAGATCTTTTCGGGTTTCGCGCAAAA	1882		
Db	1957	GTGGACCAAGGAGACATCTCGTCTCCGACAGA	1990		

RESULT 7
US-09-492-361-1
; Sequence 1, Application US/09492361
; Patent No. 6794161
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127P
; CURRENT APPLICATION NUMBER: US/09/492,361

; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 1.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-09-492-361-1

Query Match 18.4%; Score 492; DB 4; Length 2335;
Best Local Similarity 59.3%; Pred. No. 2.9e-139; Mismatches 555; Indels 192; Gaps 7;
Matches 1087; Conservative 0

QY	217	TACCGCGGGTGAGAACTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGCGTTTC	276
DB	320	TACCGCGCGCTGCAGAACTGGGTCTACAACTGCTGGAGCGGCCCGCGCTGGCGTTTC	379
QY	277	ATCTACACCGCTTCCTTTCTCCTTGTCTTTGGTGTCTGTGATTTTGTGAGTTTCT	336
DB	380	GTCTACACGCTCTCATAATTTTGTGCTGTCTCAGCTGCTGTGCTGTGCTGTCTC	439
QY	337	ACCATCCCTGAGCACACAAATGGGCTCAAGTTGCTCTTGTATCTCGAGTTTCGTGATG	396
DB	440	ACTATCCAGGAGACACAGGACTTGCACAGAGTGTCTCTCATCTTGGAAATTCGTGATG	499
QY	397	ATTGTCTCTTTGGTTTGGAGTTTCATTCATTCGAAATCTGTGCTCGGGTTTCTGTTCGA	456
DB	500	ATCGTGTGTTTCGGCTTGGAGTACATCGTCCGGTCTGTGCTCGCGGATGCTGCTGCCGC	559
QY	457	TATAGAGGTGCAAGAGAGACTGAGTTTGTCTGAAAGCCCTTCTGTGTATAGATACC	516
DB	560	TACGAGGATGCGAGGTCGCTTCCGCTTTGCGAGAAAGCCCTTCTGTGTATAGATACC	619
QY	517	ATTGTTCTTATCGCTTCAATAGAGTTTGTCTTCTGCAAAACTCAGGGTAATATTTTGGC	576
DB	620	ATCGTGTCTCGTGGCTCGGTGGCGTCTATCGCGCGGGTACCCAGGGCAACATCTTCGCC	679
QY	577	ACGCTGCTACTAGAGTCTCGTTTCTTACAGATCTCTCGCATGTGCGCATGAGACCA	636
DB	680	ACGCTCGCGCTGCGAGCATGCGCTTCTCGCATCTCTCGCATGTGCGCATGAGACCGC	739
QY	637	AGGGGAGGACCTTGGAAATTAAGTGTGAGTGTGATGCTCAGACAGGAAATTAATC	696
DB	740	CGCGCGCGCACCTGGGAGCTGTGGGCTCAGTGTGCTACGCGCATAGCAAGGAGCTGATC	799
QY	697	ACAGCTTGTGTACATAGGATTTTGGTTCTTATTTTCTGTTCTTCTGTTCTATCTGGTG	756
DB	800	ACGCGCTGTGTACATCGGTTCTGTTCTGTTCTATCTTCTGTTCTTCTGTTCTACCTGGCC	859
QY	757	GAAAGGATGCCAATAAAGATTTTCTACATATGACAGTGTCTCTGTTGGGCACAAT	816
DB	860	GAGAAGGACGCCAACTCCGACTTCTCTCTACGCGGACTCGCTCTGTTGGGCGAGATT	919
QY	817	ACATTGACAACTATTGGCTATGAGACAAATCTCCCTTAATCTTGGCTGGGAGATTGCTT	876
DB	920	ACATTGACAACTATCGGCTATGTTGACAAAGACACCGCACATGGCTGGGCGAGTCTTG	979
QY	877	TCGCAAGCTTTGCACTCTCTGCAATTTCTTCTTGTGCACTTCTCTCGCGCATTTCTGGC	936
DB	980	GCTGCTTGGCTTTCGCTTACTGGGCACTCTCTTCTTGTGCTGCTGCTGCTGCTGCTG	1039
QY	937	TCAGGTTTGTGATTAAGTATCAAGAACCAACCCGCGAGAAACATCTTGGAGAAAGAGG	996
DB	1040	TCGCGCTTTGCCCTGAAGGTCCAGGAGACGACCGCGCAGAACATCTCGAGAGCGGAGG	1099
QY	997	AACCGAGTGCACCACTCATTCAGTGTGTTTGGCTAGTTTACGCACTGATGAGAAATCT	1056
DB	1100	ATGCGCGCAGCCAACTCATCCAGGCTGCTGCGGCTGTACTTCCACCGATATGAGCCGG	1159

RESULT 8

US-09-177-650-88

; Sequence 88, Application US/09177650

QY	1057	GTITTCATTTGCAACTGGAAGCCACACTTTGAAGGCCTTGCACAC	1100
DB	1160	GCTTACTGACAGCCACCTGGTACTACTATGACAGATATCTCCATCTTCCAGAGAGCTG	1219
QY	1101	-----	1100
DB	1220	GCCCTCTTTTGTAGCAGCTGCAACGCGGCCCGCAATGGGGGCTACGGCCCTTGGAGGTG	1279
QY	1101	-----	1100
DB	1280	CGGCGGCGCGGTACCCGACGAGACCCCTCCGTTACCGCCCGCTTGCACCTGCCAC	1339
QY	1101	-----CTGAGCCCTTACCAATCAGAAGCTAAGTTTAAAGAGCGCA	1140
DB	1340	CGGCGGCGGACACCTCTCTTCTGCTTGGGAAAGCAGCGGATGGGCATCAAGACCGC	1399
QY	1141	GTGCGCATGGTGTAGCCCAAGGGGCGCAGATATT-----AAGAGCCGACAAGCTCAGTA	1194
DB	1400	ATCCGATGGGAGCTCCAGCGGGGAGCGGTCTTCCAAAGCAGCAGCTGGCACCTCCA	1459
QY	1195	GGTGACAGGAGTCCCAAGCACCGACATCACAGCGAGG---GCACTCCCAACCAAGTG	1251
DB	1460	ACAATGCCACCTCCCAAGCAGCAGAGGTGGTGGGCGCACCCAGCCCCCAAGGTG	1519
QY	1252	CAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGCGCCCTCGCTGCGCTCAAAAGT	1311
DB	1520	CAAAAGAGCTGGAGCTTCAATGACCGCACCCGCTTCCGCGCATCTCTGAGACTC-----	1573
QY	1312	TCTAGCCAAACACAGTGTATGCTGACACAGCCCTTGGCAGCTGATGATGATATGAT	1371
DB	1574	-----AAACCCCGCACCTCTGCTGAGGATGCCC---CCTCAGAGGAAGTAGCAGAG	1621
QY	1372	GAAAGAGTGCAGTGTGATGATATCAGTGGAGAGACCTCACCCACCACTTAAACCTGTC	1431
DB	1622	GAGAAGAGTACAGTGTGAGCTCAGGTGGAGCAGATCATGCTCTCTGTGAAGACAGTC	1681
QY	1432	ATTGAGCTTATCAGAAATTTATGTTTGAACAAACGGAAGTTTAAAGGAAACGTTA	1491
DB	1682	ATCCGCTCATCAGGATTTCTCAAGTTCTGTTGGTGGCCAAAGGAAATTCAGGAGACATG	1741
QY	1492	CGTCCATATGATGTAAGATGTCTTGAACAAATTTCTGCTGGTCTATCTGACATGTTG	1551
DB	1742	CGACCGTACGACGTGAAGACGTCTATGAGCAGTACTCAGCAGGCGCACCTGGACATGCTG	1801
QY	1552	TGTAGATTTAAAGCCTTCAACACAGTGTGATCAAAATTTTGGAAAGGCG---AAATC	1608
DB	1802	GCCCGATCAAGAGCTGCAAACTCGGTGGACCAAAATTTGTGGTGGGGGCGCGGAC	1861
QY	1609	ACATCAGATAAAGAGCGGAGAGAAAATAACAGCAGAACATGAGACCAACAGACGATCTC	1668
DB	1862	AGGAAGCGCGGAGAAAGGCGCAAGGGGCCCTCCGACCGGAGGTGGTGGATGAATC	1921
QY	1669	AGTATGCTCGTGGGTGGTCAAGGTGTAAGAAACAGGTAACAGTCCATAGAGTCCAAAGCTG	1728
DB	1922	AGCATGATGGGACGGTGGTCAAGGTGGAGAGCAGGTGAGTCCATCGAGCACAAGCTG	1981
QY	1729	GACTGCTTACTAGACATCTATCAACAGGTCTCTCGGAAAGGCTCTGCTCAGCCCTCGCT	1788
DB	1982	GACCTGCTGTGGGTCTTATTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2035
QY	1789	TTGGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGACCTT	1848
DB	2036	CTGGGCGCGTCAAGTGGCTGTTCGACCCCGACATCACCTCCGACTACACAGCCCT	2095
QY	1849	GTGGATAGCAAGATCTTTTCGGGTTCCGCAAAA	1882
DB	2096	GTGGACCAAGAGACATCTCCGCTCTCCGACAGA	2129

Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177.650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063.147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 88
; LENGTH: 2273
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2271)
US-09-177-650-88

Query Match 18.3%; Score 489.2; DB 3; Length 2273;
Best Local Similarity 57.0%; Pred. No. 2e-138;
Matches 1020; Conservative 2; Mismatches 667; Indels 99; Gaps 4;

Qy	64	GGCTGCTACTGCTGGGACCCGGCGCCACGCTTGGTGGCGGGCGGTGGGCTGAGG	123
Db	67	GGCTTCGTGGGCTGGACCCCGGCGGCCGANTCCACCGCGCGGNCNCTACTCATC	126
Qy	124	GAGACCGCGGGGGAAGAGGGGCGCGGATGAGCTGTGGGGAAGCCCTCTCTTAC	183
Db	127	GCGGGCTCCGAGGCCCCCAAGCGCGGCANCTNTTGAACAGCGCGGACCGGGCGCG	186
Qy	184	ACGAGTAGCAGAGCTGCGGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTGTAC	243
Db	187	GGAGCGGGAAGCCCCCNWANGCAACGCCCTTCTACCGCAAGCTGCAGATTTCTCTAC	246
Qy	244	AACGCTGCTGGAGAGACCCCGGGCTGGGGTTCATCTACACGCTTCTGTTTCTCTTT	303
Db	247	AACGCTGCTAGAGCGGCCCGGGCTGCGGTTCTATCTACCGCTCTGTTCTCTCTG	306
Qy	304	GTCCTTGGTGTGATTTGTTCAGTGTCTTCTACCATCCCTGAGCACACAAAATTGGCC	363
Db	307	GTCTTCTCTGCTTGTGCTTCTGTTTCTCCACATCAAGAGGATCGAGAGAGCTCT	366
Qy	364	TCAAGTTGGCTCTTGATCTGGAGTTCGTGATGATGTCGCTTTTGGTGGAGTTTCATC	423
Db	367	GAGGGGCGCTCTACATCTTGGAAATCGTACTATCGTGGTATTCGGTGTGAGTACTTT	426
Qy	424	ATTCGAATCTGCTGCGGGTTCGTTGTGTCGATAGAGGATGCAAGGAGCTGAGG	483
Db	427	GTGAGATCTGGGCTGCAGGCTGCTGTGCGGTATCGAGGCTGAGGGCGGAGGCTCAAG	486
Qy	484	TTTGCTCGAAGCCCTCTGCTGTATAGATACATTTCTTATCGCTTCAATACAGTT	543
Db	487	TTTGGCAGGAACCGCTTCTGTGATGATATCATGGTGTGCTGATTCGCTTCCATCTGTG	546
Qy	544	GTCTTGCAGAAATCAGGGTAAATTTTGTGCAGCTCTGCACTCAGAGTCTCGGTTTC	603
Db	547	CTGGTGTGCTTCCAGGGCAATGCTTTTGCACATCTGCGCTTCGGAGCTTCGGTTTC	606
Qy	604	CTACAGATCCTCGCATGTGGCATGAGCCGGAAGGGAGGACCTTGGAAATTTCTGGT	663
Db	607	TTGCAAACTCTCGCATGATCGTATGAGCCGAGGGGTGGCACCTTGGAGCTCTTGGGA	666
Qy	664	TCAGTGGTTTATGCTCACAGCAAGGAATTAATACAGCTTGTGTACATAGATTTTGGTT	723
Db	667	TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGTATGTCCTCTGTATATGCTCTCTGC	726
Qy	724	CTTATTTTTCGTTCTTCTGTTCTATCTGGTGGAAAGGATGCGCAATAAAGAGTTTCT	783

Db	727	CTCATCTGCGCTCATTTCTGGTGTACTTTGGCAGAAAAGGGTGAATACCACTTTGAC	786
Qy	784	ACATATGAGATGCTCTCTGGTGGGCACAATTACATTGACAACTATTGGCTATGAGAC	843
Db	787	ACCTAGCAGATGCACTCTGGTGGGTCTGATCACCTCGACCACTATGGCTACGGGAG	846
Qy	844	AAACTCCCTAACTTTGGCTGGGAAGATTGCTTTCTGAGGCTTTGCACTCTCTTGGCA	903
Db	847	AAGTACCTCAGACCTTGGAAAGGGAGGCTGCTGGCAGCAGCTTTTACCTCATTTGGT	906
Qy	904	TCCTTTCTTTCACCTCTCTCGGCACTTCTGGCTCAGGTTTTCATTTAAAGTACAGAA	963
Db	907	TCGTCTTCTTCTCTCTCGGCTGCACTTTGGGATCGGCTTTGCTCTGAAAGTCCAAG	966
Qy	964	CAACACCGCCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCCAACCTCATTCAGT	1023
Db	967	CAGCATCGGCAAAAACACTTTGAGAAACCGCGGAACCTTCGCGCAGGCTCTGATC	1026
Qy	1024	GTCTGGCTAGTTACGCGAGCTGAT-----	1047
Db	1027	GCTGGAGATTCTATGCTACTTAACCTCTCAGCACCGACCTGCACTCCACGTGGCAGTAC	1086
Qy	1048	---GAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTTGAAGGCTTTGCACCTGC	1104
Db	1087	TACGAGCGNACAGTCACTGTCCCTCATGTACAGCTCAAACTCAAACTATGGGGCTCC	1146
Qy	1105	AGCCTTACC-----AATCAGAACTAAGTTTTA	1132
Db	1147	AGACTCATCCCACTCTGAACAGCTGGAGCTGCTGAGGAATCTCAAGACAAATCTGGA	1206
Qy	1133	AGAGAGGAGTGGCGATGGCTAGCCCCCAGGGGCGCAGAGTATTAAGAGCCGCAAGACCTCAG	1192
Db	1207	CTCACCTTCAGGAAGGAGCCACAGCCAGAGCCATCAACAGCCCCCGAGGCTGGCTGCC	1266
Qy	1193	TAGTGTACAGAGGTCCTCCCAAGCACCGACATCAAGC-----	1229
Db	1267	AAGGAAAGGGGTCTCCCGAGGCCAGACGGTCCCGCGTCCCGCAGTGGGATFCAGAGT	1326
Qy	1230	--CGAGGGCAGTCCCAACAAAGTGCAGAGAGCTTGAAGCTTCAACAGCCGAAACCGCTTC	1287
Db	1327	CTTGTATGACAGCCCGAGCAAGGTGCCAGAGCTTGGTGTGAGCTTGGTGTGAGCTTGGT	1386
Qy	1288	CGGCTCTGCTGGCGCTCAAAAGTTCTCAGCCAAACACAGTATAGTGTGACACAGCC	1347
Db	1387	CGCCAGGCTTTCCGCACTCAAGGGTGTGCTATCCCGCAGAAATTCAGAAAGCAAGCCTC	1446
Qy	1348	CTTGGCACTGATGATGATATATGATAAGAGATGCCAGTGTGATGATCAGTGGAAAGAC	1407
Db	1447	CCTGGGAGGACATCGTATGAGGACCAACAGAGCTGTAACTGCGAGTTTGTGACTGAAGAT	1506
Qy	1408	CTCACCCACACCTTAAACCTGCTCATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCA	1467
Db	1507	CTTACCTCTGGCTTCAAGTGTGATCAGAGCTGTGTGTATGCGGTCTTCTGTATCT	1566
Qy	1468	AAACGGAAGTTTAAAGGAACGTTACGTCATATGATGATAAGATGTCAATTGAACAATAT	1527
Db	1567	AAGCGAAGTTTCAAGAGAGTCTCGGCCATATGATGTGATGAGCTCATCGAACAGTAC	1626
Qy	1528	TCTGCTGCTCATCTGGACATGTTGTGTAGAAATTAAGAGCTTCAACAGCTGTGTGATCAA	1587
Db	1627	TCGCTGTCGACATTTGGATATGTTGTCCGCACTCAAGAGCTTCGACAGCAGAGTGGACAG	1686
Qy	1588	ATTCTTGGAAAGGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATTAACAGCAGAA	1647
Db	1687	ATTGTGGGGCGGGCCCAACAAATTAACGATTAAGGA---TCGACCAAGGGCCAGCGAA	1743
Qy	1648	CATGAGACCAAGACGATCTCAGTATGCTCGGTGGGTGTCAGGTTGAAAAACAGGTA	1707
Db	1744	ACGAGAGTGGCCCGAAGACCCAGCATGATGGAGCGGCTTGGGAAGGTGGGAAACAGGTC	1803
Qy	1708	CAGTCCATAGATCCAGCTGAGCTGCTACTAGACATCTATCAACAG 1755	

Db 1804 TTGTCATGAAAGAAAGCTCGACTTCTTGTGTGAGCATCTATACAG 1851

RESULT 9

US-09-105-058C-22
; Sequence 22, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grikoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
US-09-105-058C-22

Query Match 17.8%; Score 475.6; DB 3; Length 2169;
Best Local Similarity 57.0%; Pred. No. 2.9e-134;
Matches 1022; Conservative 0; Mismatches 664; Indels 108; Gaps 4;

QY 64 GCCTCTACTGTGGGACCCGCGCGCCACGCTTGGTGGCGCGCGTGGCTGAGG 123
DB 67 GCTTCTGTGGGCTGAGCCCGCGCGCGCTCACAGCGACGCGCGCTACTCATC 126
QY 124 GAGAGCGCGCGGCGCAAGCAGGCGCGCGGATGAGCCTGTGGGAAGCGCTCTCTTAC 183
DB 127 GCGGCTCCGAGCCCGCAAGCGCGCGCGGTTTGTAGCAAGCGCGCGCGCGG 186
QY 184 ACGAGTAGCAGAGCTGCGCGCGCAACGCTCAAGTACCGCGGGGTGAGAACTACCTGTAC 243
DB 187 GGAGCGCGGAAGCCCGCGCAAGCGCTTCTACCGCAAGCTGAGAAATTCCTCTAC 246
QY 244 AACGTCTGAGAGACCCCGCGCTGGGGTTCATCTACACGCTTTCGTTTCTCCTT 303
DB 247 AACGTCTAGAGCGCGCGCGCTGGGCTTCTACACGCTTCTACCGCTACGCTGTTCTTTA 306
QY 304 GTCTTTGGTGTGATTTTGTGAGTGTTCCTACCATCCCTGAGCACACAAATTTGGCC 363
DB 307 GTCTTCTCTGCTTGTGTTTCTGTTTTCACCATCAAGGAGTACGAGAAGAGCTCT 366
QY 364 TCAAGTGTCTTGTATCTGAGTTCGTGATGATGTGCTTGTGGTTTGGAGTTTATC 423
DB 367 GAGGGGCGCTCTACATCTGGAATTCGTGACTATCGTGTGATTCGTTGTGAGTACTTT 426
QY 424 ATTCTGAATCTGTCTCGGCTTGTCTGTCATATAGAGGATGGCAAGAGAGCTGAGG 483
DB 427 GTGAGATCTGGCTCGAGCTGCTGTCGCGGTATCGAGGCTGAGGGCGAGGCTCAAG 486
QY 484 TTTGCTCGAAGCCCTTCTGTGTATPAGATACCATTTGTTCTTATCGCTTCAATAGCAGTT 543
DB 487 TTTGCCAGGAAGCGTCTGTGTGATGATATCATGTGCTGATTGCTCCATTTGCTG 546
QY 544 GTTCTGCAAAAACCTCAGGGTATATTTTGGCATGCTGCACTCAGAAAGTCTCGGTTTC 603
DB 547 CTGGCTGCTGTTTCCAGGGCAATGTCTTTGGCAATCTGCGCTTCGAGCTTGGGTTTC 606
QY 604 CTACAGATCCTCGGATGTCGCAATGACCGAGGGAGGAGCTTGGAAATTTCTGGGT 663
DB 607 TTGCAAAATCTCGGATATCCGTATGGACCGGAGGGGTGGCACTTGGGAAGCTCTTGGGA 666

QY 664 TCAGTGGTTTATGCTCACAGCAAGAAATTAATACAGCTTGGTATACATAGGATTTTGGTT 723
DB 667 TCGGTAGTCTACGCTCACAGCAAGAGCTGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
QY 724 CTTATTTTTCGTTCTTCTGTTCTATCTGTTGGGAAAGAGATGCCAATTAAGAGTTTCTT 783
DB 727 CTCATCTCGGCTCATTTCTGTTGTTGTTGGCAGAAAGGTTGAGAATGACCACTTTGAC 786
QY 784 ACATATGAGAGTCTCTCTGTTGGGACAAATTAATACATTCACAACTATTTGGCTATGAGAC 843
DB 787 ACTACGAGATGCACTCTGTTGGGCTGATACCTGACGACCAATTTGGCTATGAGGAGAC 846
QY 844 AAACTCCCTAACTTGGCTGGGAGATTTCTTTTTCAGAGCTTTGCACTCTCTTGGCATTT 903
DB 847 AAGTACCTTCAGACCTGGAAAGGAGGCTGCTGGCAGCACCTTTACCTCTCATTTGGTGC 906
QY 904 TCTTTTCTGCACTTCTGCTGCGCATTTCTTGCTCAGTTTTCATTTAAAGTACAAAGAA 963
DB 907 TCGTTCTTTGCTTCTCTGCTGCGCATTTTGGGATCGGCTTTTCCCTGAAAGTCCAAGAG 966
QY 964 CAACACCGCAGAAACACTTTTCAGAAAGAAAGAAAGCAAGCTGCGCAACCTCTATTCAGTGT 1023
DB 967 GAGCATCGCAAAACACTTTTCAGAAAGAAAGCAAGCTGCGCAAGCTCTGATTCAGTCT 1026
QY 1024 GTTGGCGTGTATGCTGAGCACTGATGAGAAATCTGTTTCCATTCACCTGCAACCTGGAAGCCACAC 1083
DB 1027 GCTTGGAGATTTCTATGCTACTAACTCTCACGACCGACCTGCACCTCCACGTCGAGTAC 1086
QY 1084 T----- 1084
DB 1087 TAGAGCGGACAGTCACTGTCTCCCATGTACAGACTCATCCACCTCTGAACCAAGCTGGAG 1146
QY 1085 -----TGAAGSCCTTGCACACCTGC 1104
DB 1147 CTGTGAGGAATCTCAAGAGCAAAATCTGGAATCACTTCAGGAAGAGAGCCACAGCAGAG 1206
QY 1105 AGCCCTTACCAATCAGAAGCTAAGTTTAAAGAGCGAG---TGCAGTATGCTAGTACCCAGG 1161
DB 1207 CCATCAACCAAGTCAGAAGGTCAAGTTTGAAGATCGTGTCTTCTCCAGCCCGCGAGCATG 1266
QY 1162 GSCCAGAGTATTAAGAGCGGCAAGCCTCAGTATGAGTACAGAGGTCCTCCCAAGCAGCCGAC 1221
DB 1267 GCTGCAAGGAAAGAGGGGTCTCCCGAGCCCAAGAGCGTCCGCGGTCCCGCTGCGGAT 1326
QY 1222 ATCAGAGCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACAGCAGCAAC 1281
DB 1327 CAGAGTCTTGTATGACAGCCGAGCAAGGTGCCCAAGAGCTGAGGCTTTGGTACCCGAGC 1386
QY 1282 CGCTTCCGCGCTCGCTGCGCTCAAAAGTTCTCAGCCCAAAACCAAGTATAGATGCTGAC 1341
DB 1387 CGCACACGCGAGGCTTTCGCGCATCAAGGTGCTGCTATCCGCGCAGAAATTCAGAAGCAAGC 1446
QY 1342 ACAGCGCTTGGCAGTATGATGATATGATGAAAGAGTGCAGTGTGATGATGATGATGATGATG 1401
DB 1447 C---TCCCTCGGAGGAGCATCGTAGAGGACAAAGAGCTGTAACCTGCGAGTTTGTGACT 1503
QY 1402 GAAGACCTCACCCACCACTTAAACTGTCTTTCAGCTATCAGAAATTAAGAAATTTTCAT 1461
DB 1504 GAAGATCTTACCTTCCCTCGGCTCAAAGTATGATGATGATGATGATGATGATGATGATGATG 1563
QY 1462 GTTCAAAAAGGAGTTTAAAGAAAGCTTTCATATGATGATGATGATGATGATGATGATGATG 1521
DB 1564 GTATCTAAGCGAAAGTTCAAAGAGAGTCTGCGCCCATATGATGATGATGATGATGATGATG 1623
QY 1522 CAATATCTGCTGCTCATCTGCAATGTTGTAGAAATTAAGAGCTTCAAAACAGCTGTT 1581
DB 1624 CAGTACTCGGCTGAGACCTTGGATATGTTGCTCCGCTCAAGAGCTTGCAGTCCAGAGTG 1683
QY 1582 GATCAAAATTTTGGAAAGGCAATCACTCAGATAAGAGAGCGGAGAGAGAAATTAACA 1641
DB 1684 GACCAAGTTGTGGGCGGGGCCCAACAATAACGATTAAGGA---TCGCAACCAAGGCCCA 1740
QY 1642 GCAGAAATGAGACCAAGAGATCTCAGTATGCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1701

Db 1741 GCGGAAACGGAGCTGCCGAGACCCAGCATGATGGACGGCTTGGGAAGGTGGAGAAA 1800
QY 1702 CAGGTACAGTCCATAGAGTCCAGCTGAGCTGCTACTAGACATCATCAACAG 1755
Db 1801 CAGGTCTGCTCATGTAAGAAAGACTGACTTCTTGGTGAGCACTATACACAG 1854

RESULT 10
US-09-105-058C-1
; Sequence 1, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
; OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
; OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
US-09-105-058C-1

Query Match 17.5%; Score 465.4; DB 3; Length 896;
Best Local Similarity 53.7%; Pred. No. 2e-131;
Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;

QY 190 ACCGAGAGTCCGCGGCAACCTCAAGTACCGCGGGTGCAGAACTACTGTACAACTG 249
Db 13 RGSMSRCCNSYSAAGMGMAACGCCWSTACCGSMESMTSCARMTTTSWTCTACACGS 72
QY 250 CTGGAGAGACCCCGCGCTGGCGGTTCATCTACACGCTTTCGTTTTCTCTCTCTTT 309
Db 73 CTRGAGMGRCGCGGGCTGGCGGYTSMYTTACACGCTSGTGTCTCTBHTDGYVTS 132
QY 310 GGTGCTGATTTGTCAGTGTCTTCTACATCCCTGAGCACACAAAATGGCTCAAGT 369
Db 133 KSSTGCTYBTKCTGCTGTS-YKWCACAMWTCAAGGAGTAYGAGAMRKRYTCBRRGRS 191
QY 370 TGCCTTTCATCTGAGTTCGTGATGATGCTGCTTGTGTTTGGAGTTCATATCGA 429
Db 192 KSCCTYYWNTVYGARAYMKRCYATYKISRIVTYTGGHGBGAGTWYKYKTGWR 251
QY 430 ATCTGCTGCTCGGGTGTCTGTTGTCATATAGAGGATGCCAAGGAGACTGAGTTGCT 489
Db 252 ATCTGGGCGCGMTGYTSYTCGCGRTACMRWGGCTGGMGGGSGMGRCTSAAGTTGCC 311
QY 490 CGAAAGCCCTTCTGTTATAGATACATGTTCTTCTTCTCAATACAGTGTCTTCT 549
Db 312 MGAARCCVCTSTGYRTGTBAYATCTKGTGCTSATYGCCTCYHRTKSCDGTGTSKGY 371
QY 550 GCAAAACTCAGGTATATTTTTGCCAGCTCTGCACTCAGAGTCTCCGTTTCTCTACAG 609
Db 372 GYBGHWMCCAGGCAAYGYTYKGYACVTCY---CTBCGAGCYTGGSTTCTYTRCAR 428
QY 610 ATCCTCGCATGTTGGCATGAGCCGAGGGAGGCACTTGGAAATATCTGGGTTTCAGTG 669

Db 429 ATVYTRCGSATGWTSCGBATGACCCGMRGCGHGGCACTCGGAAGCTBYTGGMTCDGV 488
QY 670 GTTTATGCTCAGCAAGGAATTAATACAGCTTGTGATAGGATTTTGGTTCTTATT 729
Db 489 RTCTRYGCGYACAGCAARGACTSRTSACKGCTGTACATYGGYTTCTBWSHCTCATC 548
QY 730 TTTTCGTCTTCTCTGCTTATCTGTGGAAGGATGCCAATAAAGAGTTTCTCATAT 789
Db 549 CTYKCYTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
QY 790 GCAGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849
Db 609 GCRGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
QY 850 CCCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
Db 669 CCYMARACSTGGRAMGSGMKCTSHDGCVCVACSTTTCCTGCTGCTGCTGCTGCT 728
QY 910 TTTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
Db 729 TTYGCBCTKCCWCGDCGCATYTTGGGRTCVGGSYTKGCCCTSAARGTBCARGAGCAR 788
QY 970 CGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCCAACCCTCATTCAGTGTGTTG 1029
Db 789 MGRKARAARCACTTTGAGAAARMGGMGAABCCDGDGCGWRBCTSATYCAKCKGCTGG 848
QY 1030 CGTAGTTAGCAGCTGA 1046
Db 849 AGRTWTYATGCTACAC 865

RESULT 11
US-09-495-050A-305
; Sequence 305, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P;
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 305
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006F6
; NAME/KEY: unsure
; LOCATION: 486, 510, 552, 573
; OTHER INFORMATION: a, t, c, g, or other
US-09-495-050A-305

Query Match 16.9%; Score 452; DB 4; Length 575;
Best Local Similarity 95.0%; Pred. No. 1.8e-127;
Matches 509; Conservative 0; Mismatches 22; Indels 5; Gaps 4;

QY 1594 GGAAAGGCGCAATACATCATAGATAAGAGCGCAGAGAAAATAACGCGAGACATGAG 1653
Db 1 GGAAAGGCGCAATACATCATAGATAAGAGCGCAGAGAAAATAACGCGAGACATGAG 60
QY 1654 ACCAGACGATCTCAGTATGCTCGTGGTGTCTCAGGTTGAAACAGTACAGTCC 1713
Db 61 ACCAGACGATCTCAGTATGCTCGTGGTGTCTCAGGTTGAAACAGTACAGTCC 120
QY 1714 ATAGAGTCCAAGCTGAGCTGCTACTAGACATCTCAACAGGTCCTTCGAAAGGCTCT 1773

Db 121 ATAGATCCAAAGTGGAGTCCCTACTAGACATCTATCAACAGGTCTTCGGAAAGGTCT 180
QY 1774 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1833
Db 181 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 240
QY 1834 GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCCGACAAAACAGTGTGC 1893
Db 241 GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCCGACAAAACAGTGTGC 300
QY 1894 TTATCCAGATCAACTAGTGCACATCTCGAGAGCCCTGAGTTCATTCGAGCCCAAT 1953
Db 301 TTATCCAGATCAACTAGTGCACATCTCGAGAGCCCTGAGTTCATTCGAGCCCAAT 359
QY 1954 GAGTTCAGTCCAGACTTTCTACGGCTTAGCCCTACTATGACAGTCAAGCAACACAG 2013
Db 360 GAGTTCAGTCCAGACTTTCTA-CGGCTTAGCTTACTATGACAGTCAAGCAACACAG 417
QY 2014 GTGCCAATTAGTCAAAAGCGATGGCTCAGAGTGGCGAGCCACCAACCAATTGCAAAACCA 2073
Db 418 GTGCCAA-TAGTCAAAAGCGATGGCTCAGAGTGGCGAGCCACCAACCAATTGC-AAACCA 475
QY 2074 ATAAATACGCGCCCAAGCCAGCAGCCCAACCAACTTTACAGATCCCACTCTCTCT 2129
Db 476 ATTAATACGCGNACCCCAAGCCAGCAGCCCAACCAANTTACAGTCTCTCTCAGCTCT 531

RESULT 12
US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grikhoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KNOX POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-26

Query Match 16.0%; Score 427.2; DB 3; Length 2565;
Best Local Similarity 56.7%; Pred. No. 2.1e-119;
Matches 923; Conservative 0; Mismatches 648; Indels 57; Gaps 5;

QY 13 GAGTCGGCGCGGCGAGGTGCTGCTGAATCGGCAGCCGCGAGCGGCGACGCCCTGCTA 72
Db 43 GCGCGCGCGCGCGGCGAGGAGCGGAAAGTGGGCTGGCGCGCGCGACGTGGAGCAA 102
QY 73 CTGCTGGGACCCCGCGCGCACGCTTGGTGGCGCGCGGTGGCTGAGGGAGAGCCGC 132
Db 103 GTCACCTTGGCTCGGCGCGGAGCGGACGCAAGACGGGACCTGCTGCTGGAGGGCGC 162
QY 133 CGGGGCAAGAGGGGCGCGGATGAGCTGTGGGAAACCGCTCTTCTACAGTAGC 192
Db 163 GCGCGCGAGGCGGCGAGGAGCCCGCGAGGCTCGGGCTCTCGGCAAGACCCCG 222
QY 193 CAGAGCTGCC-----GGCGACGTCAGTACCGGGGGTGCAGAACTACCTGTAC 243
Db 223 CTGAGCGCGCGAGTCAAGAGAAACACGCGCAAGTACCGCGCATCCAACTTTGATCTAC 282

QY 244 AACGTCTGAGAGAGACCCCGCGCTGGGGTTCATCTACACAGCTTTCTGTTTTCTCCTT 303
Db 283 GAGCCCTGAGAGAGACCCCGGGCTGGGCTGCTTTTACACGCGTGTGTCTCTGATT 342
QY 304 GTCTTTGGTGTCTGATTTGTGATGTTTCTACCATCCCTGAGACACAAATTTGGCC 363
Db 343 GTCTGGGTGTCTGATTTGTGCTGCTGACACCATTCAGAGGATGATGAGACTGCTCG 402
QY 364 TCAAGTGTGCTCTGATCTGGAGTTCGATGATTTGCTGCTTTTGGAGTTTCATC 423
Db 403 GGAGACTGCTCTGTTTACTGGAGACATTTGCTATTTTTCATCTTTGGAGCGAGTTGCT 462
QY 424 ATTGCAATCTGTCTGCGGGTTGCTGTTGTCATATAGAGGATGGCAAGAGACTGAGG 483
Db 463 TTGAGGATCTGGGCTGCTGATGTTGCTCCGATACAAAGGCTGGCGGGCCGACTGAAG 522
QY 484 TTTGCTGAAAGCCCTTCTGTTATAGATACATTTGTTTCTTATCCCTTCAATAGAGTT 543
Db 523 TTTGCCAGGAAGCCCTGTCATGTTGGACATCTTTTGTGCTGATTTGCTCTGTGCGAGTG 582
QY 544 GTTCTGCAAAAACCTCAGGGTAAATATTTTGGCCAGCTGCTGCACTCAGAAAGTCTCCGTTTC 603
Db 583 GTTCTGTTGGGAAACCAAGGCAATGTTCTGGCCACT---CCCTGCAAGCCCTGCCCTTC 639
QY 604 CTACAGATCTCCGATGTTGGCATGGACCGAAGGGGAGGACCTTTGAAAATTTACTGGGT 663
Db 640 CTGAGATCTCTGGCATGCTCGGATGGACCGGAGAGGTGGCACCTTGGAGCTTTCTGGGC 699
QY 664 TCAGTGTGTTATGCTCAGAGCAAGGAAATTAATCAGAGTGTGGTACATAGAGATTTTGGTT 723
Db 700 TCAGCCATCTGTGCCACACAGCAAGAACTCATCAGGCTGTGTACATCGGTTTCTCTGACA 759
QY 724 CTTATTTTCTGCTTCTCTGCTGCTATCTGTTGGTGAAGAGATGCC----- 768
Db 760 CTCATCTTTCTTCTATTTCTGTCTACCTGTTGGTGAAGAGAGCTCCAGAGTGTGATGCA 819
QY 769 -----AATAAGAGTTTCTACATATGACAGATGCTCTCTGTTGGGGGCACA 813
Db 820 CAAGGAGAGGAGATGAAGAGAGTTTGAGACCTATGACAGTCCCTGTTGGTGGGCTG 879
QY 814 ATTACATTGACAACTATTGGCTATGGAGACAAACCTCCCTTAACTTTGGCTGGGAAGTTG 873
Db 880 ATCAGACTGGCCACCACTTTGGCTATGGAGACAAAGACACCCAAACCTGGGAAGCCGCTG 939
QY 874 CTTTCTGAGGCTTTGCACTCTCTGCACTTCTTCTTTTGGCACTTCTCTCCCGGCACTCTT 933
Db 940 ATTGCGCCACCTTTTCTTAAATGGGCTCTCTTTTGGCCCTTCCAGGGGCACTCTG 999
QY 934 GGCTCAGGTTTTCATTAAGTACAAGAAACACACCCGCGAGAAACACTTTTGAGAAAAGA 993
Db 1000 GGGTCGGGCTGGCCCTCAAGGTGAGGAGCAACACCGTCAAGACACTTTGAGAAAAGG 1059
QY 994 AGGAACCCAGCTGCCAACCCTCATTTAGTGTGTTTGGGCTAGTTAGCAGCTGATGAGAAA 1053
Db 1060 AGGAAGCCAGCTGCTGAGCTATTTCAGGCTGCTGAGGATATTGCTACCAACCCCAAC 1119
QY 1054 TCTGTTTCCATG-----CAACCTGGAAGCCACACTTTCAGAGCCCTTGCACACTGC 1104
Db 1120 AGGATTGACTGCTGGTGGGACATGGAGATTTTATGATCATGTCGTCTTTTCTTTCTTC 1179
QY 1105 AGCCCTTCAATCAGAAGCTAAGTTTAAAGGAGCGAGTGGCATGGCTAGCCCCAGGGGC 1164
Db 1180 AGGAAGAAGACAGCTGAGGAGCAGCATCCAGCCAAAGCTGGGTCTCTTGGATCGGGTTCG 1239
QY 1165 CAGAGTATTAGAGCCGACAGCCCTCAGTAGTGTGACAGAGGTCCCAAGACCCGACATC 1224
Db 1240 CTTTCTAATCTCTGCTGAGCAATACTAAAGGAAAGCTATTTCACCCCTCTGAATGTAGAT 1299
QY 1225 ACAGCCGAGGGGAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACGACCCGACCCG 1284
Db 1300 GCCATAGAGAAAGTCTCTTCTAAAGAACCAAGACCTGTTGGCTTTAAACAATAAGAGCGT 1359
QY 1285 TTCCGGCCCTCTGCTGGCTCAAAAGTTCTCAGCCAAACACAGTGTATGATGCTGACACA 1344

Db 1072 GGTCTCGGGCTGGCCCTCAAGGTGCAGGAGCAACCCGTGAGAAAGG 1131
Qy 994 AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTGGCGTAGTTCAGCAGCTATGAGAA 1053
Db 1132 AGGAAGCCAGCTGCTGAGCTCATTCAGGCTGCTGGAGGTATATGCTACCAACCCCAAC 1191
Qy 1054 TCTGTTTCCATTG-----CAACCTGGAAGCCACACTTGAAGCCCTTGACACCTGC 1104
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Db 1546 GACATGATCCCAACCTGAAGCGCGCATCCGAGCGCTCAGAAATCTCAATTCGTCCTC 1605
Qy 1465 GCAAAACGGAAGTTTAAAGAAAGCTTACGTCCATATGATGATAAGATGCTCAATGAACAA 1524
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Qy 1585 CAAATTCT 1592
Db 1726 ATGATTTT 1733

RESULT 14

US-09-177-650-90
; Sequence 90, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (202)...(2811)

US-09-177-650-90

Query Match 16.0%; Score 426.8; DB 3; Length 2814;
Best Local Similarity 56.9%; Pred No. 3e-119;
Matches 926; Conservative 3; Mismatches 640; Indels 57; Gaps 6;
Qy 15 GTGCGGCGGGGACGGGTGCTGCTGAACCTCGCACCCGCGGCGGCGGCTGAGGAGAGCGCGC 74
Db 294 GSGCGTGGCGCGAGGAGGCGAAAGTGGGGCTGGCGCGAGGAGACGTGGAGCAAGT 353
Qy 75 GCTGGGACCCGCGCGGCGCACGCTTGGTGGCGCGCGGCTGAGGAGAGCGCGCG 134
Db 354 CACCTTGGCGCTAGGGGCGGAGCGACAAAGACCCCTGCTGCTGCTGCTGAGGCGGTGG 413
Qy 135 GGGCAAGCAGGCGGCGCGGATGAGCTGCTGGGGAAGCGCTCTCTTACACAGTAGCCA 194
Db 414 CCGCAAGAGGGGAGAGAGGACCCCGAGGGCATCGGGCTCTCGGCAAGACCCCTCT 473
Qy 195 GAGCTGCC-----GGCGCAAGCTCAAGTACCGGCGGCTGAGAACTACCTGTACAA 245
Db 474 GAGCGCCCAAGTCAAGAGAGAAACAACGCAAGTACAGGCGCATCCAAACTTGTATGA 533
Qy 246 CGTGTGAGAGAGACCCCGGGCTGGCGTTCACTACACGCTTTGCTTTCTCTCTCT 305
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Qy 306 CTTTGGTGTGTTGTTGTCAGTGTCTTACCATCTCCTGAGCACACAAAATGGCCCTC 365
Db 594 CTTGGATGCTTTGATCTGGCGCTCTCACACCTTCAAGGAATATGAGACTGTGCTGG 653
Qy 366 AAGTTGCCCTTTGATCTCGAGATTCTGATGATTTCTGTTTGGAGTTTCATCAT 425
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Qy 426 TCGAATCTGCTGCGGGTGTGCTGCTGATATAGAGATGCGAAGAGAGACTGAGTT 485
Db 714 GAGGATCTGGGCTGAGGATGTTGCTGCTGATACAAAGCTGGCGTGGCGCTAAAGTT 773
Qy 486 TGCTCGAAGCCCTCTGTTTATAGATACCAATGCTTCTTATGCTTCAATAGCAGTTCT 545
Db 774 TGCCAGGAGCCCTGTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 833
Qy 546 TTCTGCAAAAACCTAGGGTAAATATTTTGCACGCTGCGACTCAGAAAGTCTCCGTTCT 605
Db 834 TGCCGTGGGAACACAGGCAATGCTTGGCCACCT--CCCTGCGAAGCTTCCGTTCT 890
Qy 606 ACAGATCTCCGATGTCGATGCGACCGAAGGGGAGGACTCTGGAATATGAGGTTCT 665
Db 891 GCAGATCTCGCATGCTTCGAATGGATAGGAGGGGTGGCACCTGGAAGCTCCTGGGCTC 950
Qy 666 AGTGGTTTATGCTCAGCAAGGAATTAATCAGCTTGGTATACATAGGATTTTGTCTCT 725
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Db 1011 CATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1070
Qy 767 -----CCAAATAAGAGTTTTTACATATGAGATGCTCTCTGTTGGGAGCAAT 815
Db 1071 AGGAGAGAGATGAAGGAGGAGTTTGGAGACCTTATGAGATGCTCTGTTGGGCGCTGAT 1130
Qy 816 TACATTGCACTATTGGCTATGAGACAAACTCCCTTAACCTTCCGCTGGGAGAGTTGCT 875
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Db 1191 TGCTGCCACCTTTCTTTAAATCGGGCTCTCTTTTGGCCCTTCCGCGAGGCACTCTTGG 1250
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Db 1251 CTCAGGCTGGCACTGAAGTTTCAAGGCTCAGGAGCAGCAGCTTTCAGAGAGAGAG 1310

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DB 1311 GAAGCAGCTGCGGAACCTATCCAGGCTGCTGGAGATATTATGCTACCAACCCCAACAG 1370
QY 1053 ATCTGTTCCATTGCAACTGGA-----AGCCACACTGAAAGGCTTGGACACACTGCGAG 1106
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DB 1551 CATAGAGAAAGCCCTTCCAAAGAGCCAAAGCCTTGGCTTAAACAATAAGAGCGTTT 1610
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QY 1347 CTTGGCACTGATGATGATATGATGAAAAGGATGCCAGTGTGATCAGTGGAGA 1406
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DB 1725 CATGATCCTTCCCTTAAAGCTGTCATCCGAGCTCAGAAATCTACAGTTCCGCTATA 1784
QY 1467 AAACGGAAGTTTAAAGAAAGCTTACGTCCTATATGATGATAAAGATGATTAAGCAATA 1526
DB 1785 TAAAAAAGTTTCAAGGAGAGCTTGGAGCCTTATGATGTGAAGATGTGATGAGCAGTA 1844
QY 1527 TTTGCTGCTCATCTGGACATGTTGTGTAGAAATTAAGAGCCTTCAACACCTGTTGATCA 1586
DB 1845 TTGCGCCGACATCTTGACATGCTTTCCAGGATAAGTACCTTACAGCAAGATAGATAT 1904
QY 1587 AATTCT 1592
DB 1905 GATTTT 1910

RESULT 15

US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:

; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin

; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19

; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-19

Query Match 15.9%; Score 425; DB 3; Length 3287;

Best Local Similarity 64.7%; Pred. No. 1.2e-118;
Matches 632; Conservative 0; Mismatches 345; Indels 0; Gaps 0;
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DB 127 GGCCTGTGTGGGCTGTGACCCCGCGCGCGGCTCCACCGGACGCGGCGCTCTCTGATC 186
QY 124 GAGAGCGCGCGGCAAGCAGGCGCGGATGAGCTGTGTGGGAAGCCGCTCTCTTAC 183
DB 187 GCGGCTCCGAGGCGCCCAAGCGCGGAGCATCTCTAGCAAAACCTCGCGGGCGGCGCG 246
QY 184 ACAGTAGCCAGAGCTGCCGCGCAACGCTCAAGTACCGGGGGTGCGAAGACTACTCTGTAC 243
DB 247 GCGCGCGGGAAGCCCCCAAGCGCAAGCCCTTACCGCAAGCTGCGAAGATTTCTCTAC 306
QY 244 AACGTGTGTGAGAGACCCCGCGGTGGCGTTCACTTACCAACGCTTTCGTTTTCTCTCT 303
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QY 304 GTCTTTGCTGTGATTTGTGAGTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGT 363
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DB 547 TTTGCGCGAAGCCGTTCTGT 606
QY 544 GTTTCTGCAAAAACCTCAGGGTAAATTTTGTGCAACGCTCTGCACCTCAGAAGTCTCCGTTTC 603
DB 607 CTGCGCGCGGCTCCAGGGCAACGCTCTTGTGCAACATCTGCGCTCCGAGCCTCGCTTC 666
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 08:10:31 ; Search time 13197.7 Seconds
(without alignments)
9791.866 Million cell updates/sec

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Perfect score: 2667
Sequence: 1 atgaaggatgtggagtcggg.....ctcatgtcaactgaaataa 2667

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416456

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: gb_htg:*
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- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2662.2	99.8	2772	6 AR565635	AR565635 Sequence
2	2662.2	99.8	2772	6 AX268474	AX268474 Sequence
3	2662.2	99.8	3111	6 AR565636	AR565636 Sequence
4	2662.2	99.8	3111	6 AX268476	AX268476 Sequence
5	2630	98.6	2694	6 AX322509	AX322509 Sequence
6	2625.2	98.4	3137	6 AR430568	AR430568 Sequence
7	2625.2	98.4	3137	6 AX056817	AX056817 Sequence
8	2625.2	98.4	3137	9 AF202977	AF202977 Homo sapi
9	2617.2	98.1	3074	6 AR393778	AR393778 Sequence
10	2617.2	98.1	3074	6 AX253254	AX253254 Sequence
11	2617.2	98.1	3074	6 AX456864	AX456864 Sequence
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13	2521	94.5	3718	6 BD275572	BD275572 Novel Hum
14	2507.6	94.0	2832	9 AF263835	AF263835 Homo sapi
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16	1548.8	58.1	1552	6 CQ720576	CQ720576 Sequence
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18	963.4	36.1	1691	9 HSA272519	HA272519 Homo sapi
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ALIGNMENTS

RESULT 1
AR565635
LOCUS AR565635
DEFINITION Sequence 1 from patent US 6767736.
ACCESSION AR565635
VERSION AR565635.1 GI:53981668
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2772)
AUTHORS Hu, Y., Kiecke, J.A., Turner, C.A. Jr., Nehls, M.C., Friedrich, G.,
Zambrowicz, B., and Sands, A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 1 27-JUL-2004;
FEATURES
source Location/Qualifiers
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LOCUS AX268474 2772 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 1 from Patent WO0175108.
ACCESSION AX268474
VERSION AX268474.1 GI:16541652
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hu,Y., Kieke,J.A., Turner,A.C., Nehls,M.C., Friedrich,G.B.,
Zambrowicz,B. and Sands,A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 0175108-A 1 11-OCT-2001;
Lexicon Genetics Incorporated (US)
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Best Local Similarity 99.9%; Pred. No. 0;
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DEFINITION Sequence 3 from patent US 6767736.
ACCESSION AR565636
VERSION AR565636.1 GI:53981669
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3111)
AUTHORS Hu, Y., Kieke, J. A., Turner, C. A. Jr., Nehls, M. C., Friedrich, G.,
Zambrowicz, B. and Sands, A. T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 3 27-JUL-2004;
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LOCUS AX322509 2694 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1 from Patent WO0192526.
ACCESSION AX322509
VERSION AX322509.1 GI:18093555
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Dworetzky,S.I., Ramanathan,C.S., Trojnecki,J.T., Boissard,C.G. and
Gribkoff,V.K.
Human kcnq5 potassium channel, methods and compositions thereof.
TITLE

JOURNAL
FEATURES
source

Patent: WO 0192526-A 1 06-DEC-2001;
Bristol-Myers Squibb Company (US)
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ORIGIN

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VERSION
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KEYWORDS
GI:12309759
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AF202977.1	TITLE	Direct Submission	
AF202977.1	JOURNAL	Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistrasse 85, Hamburg 20246, Germany	
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Aventis Pharma Deutschland GmbH (DE)

FEATURES

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Location/Qualifiers

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Lerche, C., Scherer, C.R., Seebom, G., Derst, C., Wei, A.D., Busch, A.E.
TITLE Molecular cloning and functional expression of KCNQ5, a potassium channel subunit that may contribute to neuronal M-current diversity
J. Biol. Chem. 275 (29), 22395-22400 (2000)
PUBMED 10787416
REFERENCE 2 (bases 1 to 3074)
AUTHORS Lerche, C., Scherer, C.R., Seebom, G., Derst, C., Wei, A.D., Busch, A.E.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2000) Cardiovascular Diseases, Aventis Pharma Deutschland GmbH, Building H824, Frankfurt a. M. 65926, Germany
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2855 AAGGAGGAGAAAGTACAGATCCCTCAGCTGCTCATGTCAAACTGAAATAA 2908

RESULT 13
BD275572
LOCUS BD275572 3718 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Human Voltage-Gated Potassium Channel.
ACCESSION BD275572
VERSION BD275572.1 GI:33085340
KEYWORDS JP 2002543768-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3718)
Metzker,M.L., Li,W., Petrukhin,K. and Caskey,T.C.
Novel Human Voltage-Gated Potassium Channel
Patent: JP 2002543768-A 2 24-DEC-2002;
Merck and Co Inc
OS Homo Sapiens
PN JP 2002543768-A/2
PD 24-DEC-2002
PF 10-APR-2000 JP 2000611548
PR 14-APR-1999 US 60/129274
PI michael l metzker,wen li,konstantin petrukhin,thomas c caskey
CC
FH
Key Location/Qualifiers.
Location/Qualifiers
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/db_xref="taxon:9606"
Query Match 94.5%; Score 2521; DB 6; Length 3718;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2564; Conservative 0; Mismatches 10; Indels 27; Gaps 1;
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Db |||||
78 ACTGCTGAGGACTGCGCGGTGGCTCTGAGGAGAGAGCCCGCGGCAAGCAGGGGCCCGG 137
QY 154 ATGAGCTGTCTGGGAAGCCGCTCTCTTACAGAGTAGCAGAGTCCGGGGCAACGTC 213
Db |||||
138 ATGAGCTGTCTGGGAAGCCGCTCTCTTACAGAGTAGCAGAGTCCGGGGCAACGTC 197
QY 214 AAGTACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGCTGGCG 273
Db |||||
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QY 274 TTCACTACACGCTTTGCTTTTCTCTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTT 333
Db |||||
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QY 334 TCTACCATCCCTGAGCACACAAAATGGCTTCAAGTTCCTTCTGATCCTGGAGTTCGTG 393
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Db |||||
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Db 1038 TCTGTTTCCATTGCAACTGGAAGCCACACTTGAAGGCTTTGCACACTCTGAGCCCTACC 1097
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Db 1098 AAGAAAGAACAAAGGGAAGCATCAAGCAGTCAAGAGCTAAGTTTAAAGGAGCGAGTCCGC 1157
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Db 2658 CCTCATGTCAAACTGAAATAA 2678

RESULT 14
AF263835
LOCUS 2832 bp mRNA linear PRI 01-JUN-2000
DEFINITION Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5) mRNA,
partial cds.
ACCESSION AF263835
VERSION AF263835.1 GI:8132996
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2832)
Kniazeva.M. and Han.M.
A new gene of the voltage-gated potassium channel KCNQ family,
KCNQ5, is a candidate gene for retinal disorders
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2832)

AUTHORS Kniazeva, M. and Han, M.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-2000) MDCB, University of Colorado at Boulder,
Porter Biosciences Bldg., Boulder, CO 80309, USA
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="6"
/map="6q; D6S280"
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HVKLK"

ORIGIN

Query Match 94.0%; Score 2507.6; DB 9; Length 2832;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2550; Conservative 0; Mismatches 9; Indels 27; Gaps 1;

Qy 109 GCGGTGCGCTGAGGAGAGCGCGCGGCGCAAGCAGGCGGCGCGGATGAGCTGCTGGGG 168
Db 1 GCGGTGCGCTGAGGAGAGCGCGCGGCGCAAGCAGGCGGCGGATGAGCTGCTGGGG 60

Qy 169 AAGCGCTCTTACACAGTAGCAGAGCTGCGCGGCGCAAGCTCAAGTACGCGGGGTG 228
Db 61 AAGCGCTCTTACACAGTAGCAGAGCTGCGCGGCGCAAGCTCAAGTACGCGGGGTG 120

Qy 229 CAGAACTACCTGTACAAGCTGCTGAGAGAGCCCGCGGCTGGCGTTTCATCTACCAGCT 288
Db 121 CAGAACTACCTGTACAAGCTGCTGAGAGAGCCCGCGGCTGGCGTTTCATCTACCAGCT 180

Qy 289 TTCGTTTTTCTCTTGTGTTGCTGATTTTGTTCAGTGTTCATCATCCCTGAG 348
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Qy 409 GGTTCGAGTTCATCATTCGATCTGCTCGGGTTCCTGTCGATATAGAGGATGG 468
Db 301 GGTTCGAGTTCATCATTCGATCTGCTCGGGTTCCTGTCGATATAGAGGATGG 360

Qy 469 CAAGGAGACTGAGTTCGTCGAAAGCCCTTCTGTGTATAGATACCATTTGTTTATC 528
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Qy 529 GCTTCAATAGCAGTTGTTCTGCAAAAACCTCAGGGAATAATTTTGGCACTCTGCACTC 588

Db 421 GCTTCAATAGCAGTTGTTTCTGCAAAAACCTCAGGGAATAATTTTGGCCACGCTGCACTC 480

Qy 589 AGAAGTCTCCGTTTCCCTACAGATCTCCGCAATGGTCCGATGAGCCGAGGGGAGGCACT 648

Db 481 AGAAGTCTCCGTTTCCCTACAGATCTCCGCAATGGTCCGATGAGCCGAGGGGAGGCACT 540

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Db 1441 CAATATTTCTGCTGCTCATCTGGAATGTTGTGATGATGATGATGATGATGATGATGATGATG 1500

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Qy	1702	CAGGTACAGTCCATAGAGTCCAGAGTGGAGCTGCTACTAGACATCTATCAACAGGTCCCTT	1761
Db	1621	CAGGTACAGTCCATAGAAATCCAGAGTGGACTGCTACTAGACATCTATCAACAGGTCCCTT	1680
Qy	1762	CGGAAAGGCTCTGCCTCAGCCCTCGCTTTTGGCTTTCATCTCAGATCCCACTTTTGAATGT	1821
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Db	1801	AAcAGTGGCTGCTTATCCAGATCAACTAGTGCACAATCTTCGAGAGGCTTCGAGTTCATTT	1860
Qy	1942	CTGACGCCAAATGAGTTTCAGTGCCCAAGCTTTCTTACGCCCTTAGCCCTACTATGCAcAGT	2001
Db	1861	CTGACGCCAAATGAGTTTCAGTGCCCAAGCTTTCTTACGCCCTTAGCCCTACTATGCAcAGT	1920
Qy	2002	CAGCAACACAGGTGCCAAATAGTTCAAAGCGATGGCTCAGCAGTGGCAGCAcCAACACCC	2061
Db	1921	CAGCAACACAGGTGCCAAATAGTTCAAAGCGATGGCTCAGCAGTGGCAGCAcCAACACCC	1980
Qy	2062	ATTGCAAAcCAAAATAATACGGCACCAcCAAGCCAGCAGCCCCCAcAACTTTACAGATCCCA	2121
Db	1981	ATTGCAAAcCAAAATAATACGGCACCAcCAAGCCAGCAGCCCCCAcAACTTTACAGATCCCA	2040
Qy	2122	CCTCCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAAACTCTGCAcCCTTAACCCGTCA	2181
Db	2041	CCTCCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAAACTCTGCAcCCTTAACCCGTCA	2100
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Qy	2482	ACTGATGAAGAGGTGGGTCCCGAAGAGACAGACACTTTTGTATGCCGACCGCAG	2541
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Qy	2542	CCTGCCAGGGAAGCTGCTTTGCACTCAGACTCTTAAGGACTGGAAAGGTCAcGATCATCT	2601
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Qy	2602	CAGAGCACTTTGTAAGGCAGGGAAGTACAGATGCCCTCAGCTTGGCTCATGTCAAACTG	2661
Db	2521	CAGAGCACTTTGTAAGGCAGGGAAGTACAGATGCCCTCAGCTTGGCTCATGTCAAACTG	2580
Qy	2662	AAATAA 2667	
Db	2581	AAATAA 2586	

RESULT 15	AF263836	3108 bp	mRNA	linear	ROD 01-JUN-2000
LOCUS	Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,				
DEFINITION	partial cds.				
ACCESSION	AF263836				
VERSION	AF263836.1	GI:8132998			
KEYWORDS					
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3108)				
AUTHORS	Kniazeva,M. and Han,M.				
TITLE	A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5, is a candidate gene for retinal disorders				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 3108)				
AUTHORS	Kniazeva,M. and Han,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder, Porter Biosciences Bldg., Boulder, CO 80309, USA				
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ORIGIN					
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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 08:07:42 ; Search time 1365.59 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2662.2	99.8	2772	5	AAS14653 Human ion
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5	2630	98.6	2694	6	AAS14652 Human pot
6	2626.4	98.5	3071	4	AAS14651 Human CDN
7	2625.2	98.4	3137	4	AAS14651 Human CDN
8	2617.2	98.1	3074	4	AAS14651 Human CDN
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10	2521	94.5	3718	3	AAS14651 Human pot
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21	472.2	17.7	7411	10	ADD29557 Human tum
22	472.2	17.7	7420	11	ADN38963 Cancer/an
23	472.2	17.7	7420	11	ADP65810 Human mRN
24	472.2	17.7	7420	11	ADP65731 Human pot
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28	465	17.4	548	6	ABA90234 Human ORF
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ALIGNMENTS

RESULT 1
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ID AAS14653 standard; cDNA; 2667 BP.
XX
AC AAS14653;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding a voltage gated potassium channel hKCNQ5-2.
XX
KW Human; ss; voltage-gated potassium channel; KCNQ5-2; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; splice variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..2967
FT /*tag= a
FT /product= "hKCNQ5-2"
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PN WO200170759-A1.
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XX 27-SEP-2001.
XX
XX 20-MAR-2001; 2001WO-US009328.
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XX 21-MAR-2000; 2000US-0190954P.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Jegla TJ;
XX
XX WPI; 2001-611467/70.
XX
XX P-PSDB; AAU09021.
XX
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
XX identifying a compound modulating ion flux in eukaryotic cell or cell
XX membrane expressing the protein, comprises KCNQ approximately a- subunits.
XX
XX Claim 5; Page 63-64; 78pp; English.

XX The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy) is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states. is useful for screening mutations of KCNQ5. The
CC present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-2
XX
SQ Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 U; 0 Other;
Query Match 100.0%; Score 2667; DB 4; Length 2667;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GACGCGCTGCTACTGCTGGGCAACCGCGCGCCACGCTTGGTGGCGGGCGGTGGGCTG 120
QY 121 AGGAGAGCCGCGGGGCAAGCAGGGGCGCGGATAGCTGCTGGGGAGCCGCTCTCT 180
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QY 1921 TCGAGAGGCTCAGTTTCTGACGCCAAATGAGTTGAGTCCCGCAGACTTTTCTACGG 1980
Db |||||
QY 1981 CTTAGCCCTACTATGACAGTCAAGCAACAGAGTGGCCAAATAGTCAAGCGATGGCTCA 2040
Db |||||
QY 1981 CTTAGCCCTACTATGACAGTCAAGCAACAGAGTGGCCAAATAGTCAAGCGATGGCTCA 2040
Db |||||
QY 2041 CGAGTGGCAGCCCAACCAACATTGCAACCAAAATAATACGGCAACCCAGCCAGCAGCC 2100
Db |||||
QY 2041 CGAGTGGCAGCCCAACCAACATTGCAACCAAAATAATACGGCAACCCAGCCAGCAGCC 2100
Db |||||
QY 2101 CCAACAACTTTTACAGATCCACCTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2160
Db |||||
QY 2101 CCAACAACTTTTACAGATCCACCTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2160
Db |||||
QY 2161 ACTCTGCACCTTAACCTCGAGCTTACAGGAAGCAATTTGAGTCAACACTGGCTT 2220
Db |||||
QY 2161 ACTCTGCACCTTAACCTCGAGCTTACAGGAAGCAATTTGAGTCAACACTGGCTT 2220
Db |||||
QY 2221 GTTGCTTCAAGCAAAATGTTGAGGTTGACAGTCAAAATCTCACCAGGACCGTTCTATG 2280
Db |||||
QY 2221 GTTGCTTCAAGCAAAATGTTGAGGTTGACAGTCAAAATCTCACCAGGACCGTTCTATG 2280
Db |||||
QY 2281 AGGAAAGCTTTGACATGGAGGAGAACTCTGTTGCTGTCTGTCCTATGTCCTGAGG 2340
Db |||||
QY 2281 AGGAAAGCTTTGACATGGAGGAGAACTCTGTTGCTGTCTGTCCTATGTCCTGAGG 2340
Db |||||
QY 2341 GACTTGGCAATCTTTGCTGTGCAAACTGATCAGTCAACCGAGGAACTGAATATA 2400
Db |||||
QY 2341 GACTTGGCAATCTTTGCTGTGCAAACTGATCAGTCAACCGAGGAACTGAATATA 2400
Db |||||
QY 2401 CAACCTTTGAGGAGTCAAGTCAAGTGGCTCCAGAGCAGCAAGATTTTACCCCAATGG 2460
Db |||||
QY 2401 CAACCTTTGAGGAGTCAAGTCAAGTGGCTCCAGAGCAGCAAGATTTTACCCCAATGG 2460
Db |||||
QY 2461 AGGGAATCCAAATTTGTTTATACTGATGAAGAGTGGGTCCCGAAGACAGACAGAC 2520
Db |||||
QY 2461 AGGGAATCCAAATTTGTTTATACTGATGAAGAGTGGGTCCCGAAGACAGACAGAC 2520
Db |||||
QY 2521 ACTTTTGATCGCGACCGCAGCTGCGAGGAGCTGCTTTGATCAGACTCTCTAAGG 2580
Db |||||
QY 2521 ACTTTTGATCGCGACCGCAGCTGCGAGGAGCTGCTTTGATCAGACTCTCTAAGG 2580
Db |||||
QY 2581 ACTGGAAGTCAAGTCACTCTCAGAGCATTTTGTAAAGGAGGAGAAAGTACAGATCCCTC 2640
Db |||||
QY 2581 ACTGGAAGTCAAGTCACTCTCAGAGCATTTTGTAAAGGAGGAGAAAGTACAGATCCCTC 2640
Db |||||
QY 2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
Db |||||
QY 2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
Db |||||

RESULT 2

AAH43633

ID AAH43633 standard; cDNA; 2772 BP.

XX AC AAH43633;

XX XX

DT 21-JAN-2002 (first entry)

XX

DE Human ion-channel forming protein ORF.
XX
KW Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200175108-A1.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010875.
XX
PR 03-APR-2000; 2000US-0194255P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
DR WPI; 2001-656987/75.
DR P-PSDB; AAB47678.
XX
PT New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosing or treating diseases, in drug screening, and in
PT clinical trial monitoring.
XX
PS Claim 1; Page 34-35; 41pp; English.
XX
CC The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC The protein shares structural similarity with mammalian ion channel
CC proteins, particularly voltage-gated potassium channel proteins. The
CC protein is expressed in many human cell lines including fetal brain,
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein can
CC be used in the diagnosis or treatment of diseases, in drug screening, and
CC in clinical trial monitoring. The oligonucleotides may be used as
CC hybridization probes for screening libraries, and assessing gene
CC expression patterns (particularly using a micro array or high throughput
CC chip format). The nucleic acids and novel protein can also be used in the
CC identification, selection and validation of novel molecular targets for
CC drug discovery, to screen collections of genetic material from patients
CC who have a particular medical condition, to identify mutations associated
CC with a particular disease, as a diagnostic or prognostic assay, and to
CC screen for drugs which can be used to treat symptomatic or phenotypic
CC manifestations of perturbing the normal function of novel human protein.
CC The polypeptides are further used in generating antibodies
XX
SQ Sequence 2772 BP; 715 A; 700 C; 713 G; 644 T; 0 U; 0 Other;

Query Match 99.8%; Score 2662.2; DB 5; Length 2772;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAAGGATGTGGAGTCCGGCCGGGCGAGGCTGTGCTGAACCTCGGACGCCCGAGGGGC 60
Db 106 ATGAAGGATGTGGAGTCCGGCCGGGCGAGGCTGTGCTGAACCTCGGACGCCCGAGGGGC 165
QY 61 GACGGCTCTACTGCTGGGCACCGCGCGCCAGCTTGGTGGCGCGCGGTGGCCTG 120
Db 166 GACGGCTCTACTGCTGGGCACCGCGCGCCAGCTTGGTGGCGCGCGGTGGCCTG 225
QY 121 AGGAGAGCCCGCGGGCAAGCAGGGGGCCCGGATGAGCTTGTGGGAAAGCCGCTCTCT 180
Db 226 AGGAGAGCCCGCGGGCAAGCAGGGGGCCCGGATGAGCTTGTGGGAAAGCCGCTCTCT 285
QY 181 TACACGAGTACCGAGCTGCCGCGCAACGTCGAAGTACCGCGGGTGCAGAACTACCTG 240
Db 286 TACACGAGTACCGAGCTGCCGCGCAACGTCGAAGTACCGCGGGTGCAGAACTACCTG 345
QY 241 TACACGCTGTGGAGAGACCCCGGGCTGGGGCTTCACTACCAAGCTTTCGTTTCTC 300
Db 346 TACAACTGTGGAGAGACCCCGGGCTGGGGCTTCACTACCAAGCTTTCGTTTCTC 405

Db 2566 AGGGAATCCAAATGTTTATTAATGATGAAGAGGTGGTCCCGAAGACAGACAGACAGAC 2625
QY 2521 ACTTTTGTATGCGCAGCGCAGCTCCAGGGAAGCTGCTTTGTCATCAGACTCTCTAAGG 2580
Db 2626 ACTTTTGTATGCGCAGCGCAGCTCCAGGGAAGCTGCTTTGTCATCAGACTCTCTAAGG 2685
QY 2581 ACTGGAAGGTACAGATCATCTCAGAGCAATTTGTAAGGCGAGGAGAAAGTACAGATCCCTC 2640
Db 2686 ACTGGAAGGTACAGATCATCTCAGAGCAATTTGTAAGGCGAGGAGAAAGTACAGATCCCTC 2745
QY 2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
Db 2746 AGCTTGCCTCATGTCAAACTGAAATAA 2772

RESULT 3

AAH43634
ID AAH43634 standard; cDNA; 3111 BP.
XX AC
XX AAH43634;

XX 21-JAN-2002 (first entry)

XX Human ion-channel forming protein coding sequence.

XX Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 59..2831
CDS /*tag= a
/*product= "Human ion-channel forming protein"

XX WO200175108-A1.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010875.

XX 03-APR-2000; 2000US-0194255P.

XX (LEXI-) LEXICON GENETICS INC.

XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;

XX WPI; 2001-656987/75.

XX P-PSDB; AAB47678.

XX New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosing or treating diseases, in drug screening, and in
PT clinical trial monitoring.

XX Disclosure; Page 37-38; 41pp; English.

XX The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC The protein shares structural similarity with mammalian ion channel
CC proteins, particularly voltage-gated potassium channel proteins. The
CC protein is expressed in many human cell lines including fetal brain,
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein can
CC be used in the diagnosis or treatment of diseases, in drug screening, and
CC in clinical trial monitoring. The oligonucleotides may be used as
CC hybridization probes for screening libraries, and assessing gene
CC expression patterns (particularly using a micro array or high throughput
CC chip format). The nucleic acids and novel protein can also be used in the
CC identification, selection and validation of novel molecular targets for
CC drug discovery, to screen collections of genetic material from patients
CC who have a particular medical condition, to identify mutations associated
CC with a particular disease, as a diagnostic or prognostic assay, and to
CC screen for drugs which can be used to treat symptomatic or phenotypic
CC manifestations of perturbing the normal function of novel human protein.

CC The polypeptides are further used in generating antibodies
XX SQ Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;
Query Match 99.8%; Score 2662.2; DB 5; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAAGGATGTGGAGTGGGGCGGGGCGAGGTGCTGCTGAACCTGGCAGCGCCAGGGGCG 60
Db 165 ATGAAGGATGTGGAGTGGGGCGGGGCGAGGTGCTGCTGAACCTGGCAGCGCCAGGGGCG 224
QY 61 GACGGCTGTCTACTGCTGGGCACCCGCGCCACGCTTGTGTGGCGGCGGGTGGCCCTG 120
Db 225 GACGGCTGTCTACTGCTGGGCACCCGCGCCACGCTGCTGGTGGCGGGTGGCCCTG 284
QY 121 AGGAGAGCCCGGGGCGAGCAGGGGCGCGGATGAGCTGTGGGGAAGCGCTCTCT 180
Db 285 AGGAGAGCCCGGGGCGAGCAGGGGCGCGGATGAGCTGTGGGGAAGCGCGCTCTCT 344
QY 181 TACACGAGTACGAGAGCTGCGCGCAACGCTCAAGTACCGCGGCTGCAGAACTACCTG 240
Db 345 TACACGAGTACGAGAGCTGCGCGCAACGCTCAAGTACCGCGGCTGCAGAACTACCTG 404
QY 241 TACAACGTGTGGAGAGACCCCGGGCTGGCGGTTTCATCTACCACTGCTTTGTTTTCTC 300
Db 405 TACAACGTGTGGAGAGACCCCGGGCTGGCGGTTTCATCTACCACTGCTTTGTTTTCTC 464
QY 301 CTGTCTTTGGTGTGTTGATTTGTCAAGTGTGTTTCTACCATCCCTGAGCACACAAAATTG 360
Db 465 CTGTCTTTGGTGTGTTGATTTGTCAAGTGTGTTTCTACCATCCCTGAGCACACAAAATTG 524
QY 361 GCCTCAAGTGTGCTTGTATCTCGAGTTCTGATGATTGCTCTTTGTTGGAGTTC 420
Db 525 GCCTCAAGTGTGCTTGTATCTCGAGTTCTGATGATTGCTCTTTGTTGGAGTTC 584
QY 421 ATCATTCGAATCTGCTGCGGGTTGCTGTTGTCGATATAGAGGATGCAAGGAAGACTG 480
Db 585 ATCATTCGAATCTGCTGCGGGTTGCTGTTGTCGATATAGAGGATGCAAGGAAGACTG 644
QY 481 AGTTTGTCTGAAAAGCCCTCTCTGTTATAGATACCATGTTCTTATCGCTTCAATAGCA 540
Db 645 AGTTTGTCTGAAAAGCCCTCTCTGTTATAGATACCATGTTCTTATCGCTTCAATAGCA 704
QY 541 GTTGTCTCTGCAAAAACCTCAGGGTAATAATTTTGCACGCTGCACTCAGAACTCTCCGT 600
Db 705 GTTGTCTCTGCAAAAACCTCAGGGTAATAATTTTGCACGCTGCACTCAGAACTCTCCGT 764
QY 601 TTCCTACAGATCTCCGATGCTCGCATGACCCGAGGGGAGGCACCTTGGAAATTAATCTG 660
Db 765 TTCCTACAGATCTCCGATGCTCGCATGACCCGAGGGGAGGCACCTTGGAAATTAATCTG 824
QY 661 GGTTCAGTGTGTTATGCTCAGCAGCAAGGAATTAATCAGCTTGGTACATAGGATTTTGG 720
Db 825 GGTTCAGTGTGTTATGCTCAGCAGCAAGGAATTAATCAGCTTGGTACATAGGATTTTGG 884
QY 721 GTTCTTATTTTCTGCTCTTCTCTCTCTGTTGGAAGGATGCAATAAGAGATT 780
Db 885 GTTCTTATTTTCTGCTCTTCTCTCTCTGTTGGAAGGATGCAATAAGAGATT 944
QY 781 TCTACATATGAGATGCTCTCTGTTGGGGCAATTAATCATTGACAACTATTGGCTATGGA 840
Db 945 TCTACATATGAGATGCTCTCTGTTGGGGCAATTAATCATTGACAACTATTGGCTATGGA 1004
QY 841 GACAAAACCTCCCTAACTTGTGCTGGGAAGATTGCTTTCTGAGGCTTTGCACTCTCTTGGC 900
Db 1005 GACAAAACCTCCCTAACTTGTGCTGGGAAGATTGCTTTCTGAGGCTTTTGGCACTCTCTTGGC 1064
QY 901 ATTTCTTTCTTTGCACTTCTGCTGGGCAATTTCTGCTCAGGTTTTTGGCAATAAAGTACAA 960
Db 1065 ATTTCTTTCTTTGCACTTCTGCTGGGCAATTTCTGCTCAGGTTTTTGGCAATAAAGTACAA 1124
QY 961 GAACAACACCCGCGAGAAACACTTTTGAGAAAAGAGGAACCCAGCTGCCAACCTCATTCAG 1020

Db	1125	GAACAACACCGCAGAAACACCTTTGAGAAAAGAGAACCCAGCTGCACACCTCATTCAG	1184
Qy	1021	TCGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACTGGAAGCCA	1080
Db	1185	TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACTGGAAGCCA	1244
Qy	1081	CACTTGAAGGCTTCCACACCTGCGAGCCCTACCAATCAGAAAGCTTAAGTTTAAGAGCGA	1140
Db	1245	CACTTGAAGGCTTCCACACCTGCGAGCCCTACCAATCAGAAAGCTTAAGTTTAAGAGCGA	1304
Qy	1141	GTGCGCATGCTAGCCCGAGGGCCAGAGTATTAAAGAGCGACAAAGCCTCAGTAGTGTAC	1200
Db	1305	GTGCGCATGCTAGCCCGAGGGCCAGAGTATTAAAGAGCGACAAAGCCTCAGTAGTGTAC	1364
Qy	1201	AGAGGTCCCGAAGCACCGACATCACAGCCGAGGCGAGTCCCAACAAAGTGCAGAGAGC	1260
Db	1365	AGAGGTCCCGAAGCACCGACATCACAGCCGAGGCGAGTCCCAACAAAGTGCAGAGAGC	1424
Qy	1261	TGAGGCTTCAACGACGAAACCGCTTCGCGCCCTCGCTGCGCCCTCAAAAGTTCTCAGCCA	1320
Db	1425	TGAGGCTTCAACGACGAAACCGCTTCGCGCCCTCGCTGCGCCCTCAAAAGTTCTCAGCCA	1484
Qy	1321	AAACCAAGTATAGATGCTGACACAGCCCTTGSCACTGATGATGATATGATGATAAAGGA	1380
Db	1485	AAACCAAGTATAGATGCTGACACAGCCCTTGSCACTGATGATGATGATAAAGGA	1544
Qy	1381	TGCGAGTGTGATGTATGAGTGAAGACCTCACCCACCACTTAAACCTGTCATTCGAGCT	1440
Db	1545	TGCGAGTGTGATGTATGAGTGAAGACCTCACCCACCACTTAAACCTGTCATTCGAGCT	1604
Qy	1441	ATCAGAAATATGAAATTTTCATGTTGCAAAACGGAAGTTTAAAGGAAACGTTACGTCATAT	1500
Db	1505	ATCAGAAATATGAAATTTTCATGTTGCAAAACGGAAGTTTAAAGGAAACGTTACGTCATAT	1664
Qy	1501	GATGTAAGAGTGTATGAAACATATCTGCTGCTGCTATCTGGACATCTGTGTAGAAAT	1560
Db	1665	GATGTAAGAGTGTATGAAACATATCTGCTGCTGCTATCTGGACATCTGTGTAGAAAT	1724
Qy	1561	AAAAGCCTTCAACACAGTGTGATCAAAATCTTTGGAAAAGGCAAAATCACATCAGATAAG	1620
Db	1725	AAAAGCCTTCAACACAGTGTGATCAAAATCTTTGGAAAAGGCAAAATCACATCAGATAAG	1784
Qy	1621	AAGAGCCGAGAGAAATTAACAGACAGAACATGAGACACAGACGATCTCAGTATGCTCGGT	1680
Db	1785	AAGAGCCGAGAGAAATTAACAGACAGAACATGAGACACAGACGATCTCAGTATGCTCGGT	1844
Qy	1681	CGGCTGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAAGCTGGACTGCCTACTA	1740
Db	1845	CGGCTGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAAGCTGGACTGCCTACTA	1904
Qy	1741	GACATCTATCAACAGGTCCTTCGGAAGGCTTCGCTCAGCCCTCGCTTTGGCTTCATTC	1800
Db	1905	GACATCTATCAACAGGTCCTTCGGAAGGCTTCGCTCAGCCCTCGCTTTGGCTTCATTC	1964
Qy	1801	CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA	1860
Db	1965	CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA	2024
Qy	1861	GATCTTTGGGTTCCGACAAAACAGTGGCTGCTTTATCCAGATCAACTAGTCCCAATC	1920
Db	2025	GATCTTTGGGTTCCGACAAAACAGTGGGCTGCTTTATCCAGATCAACTAGTCCCAATC	2084
Qy	1921	TCGAGAGGCTTCGAGTTTCAATCTCAGCCCAAAATGAGTTTCAAGTCCCGAGACTTTCTACGG	1980
Db	2085	TCGAGAGGCTTCGAGTTTCAATCTCAGCCCAAAATGAGTTTCAAGTCCCGAGACTTTCTACGG	2144
Qy	1981	CTTAGCCCTACTATGCAAGTCAAGCAACACAGGTGCCAATTAGTCAAGAGCATGGCTCA	2040
Db	2145	CTTAGCCCTACTATGCAAGTCAAGCAACACAGGTGCCAATTAGTCAAGAGCATGGCTCA	2204
Qy	2041	GCAGTGGCAGCCACCAACACCATTTGCAAAACCAAAATAATACGCAACCCAGCCAGCAGCC	2100
Db	2205	GCAGTGGCAGCCACCAACACCATTTGCAAAACCAAAATAATACGCAACCCAGCCAGCAGCC	2264
Qy	2101	CCAAACACTTTTACAGATCCACCTCTCTCCAGCCATCAAGACATCTGCCAGGCCAGAA	2160
Db	2265	CCAAACACTTTTACAGATCCACCTCTCTCCAGCCATCAAGACATCTGCCAGGCCAGAA	2324
Qy	2161	ACTCTGACACCTTAACCTTCAGGCTTTACAGGAAGCAATTTCTGAGTCTACACCTGCCTT	2220
Db	2325	ACTCTGACACCTTAACCTTCAGGCTTTACAGGAAGCAATTTCTGAGTCTACACCTGCCTT	2384
Qy	2221	GTTCCTTCCAAAGAAATGTTTCAGGTTGACAGTCAAAATCTCACAAGGACCGTTCTATG	2280
Db	2385	GTTCCTTCCAAAGAAATGTTTCAGGTTGACAGTCAAAATCTCACAAGGACCGTTCTATG	2444
Qy	2281	AGGAAAAGCTTTTGACATGGGAGGAGAACTCTGTTCTGTCTGTCCCATGTGTGCCGAAG	2340
Db	2445	AGGAAAAGCTTTTGACATGGGAGGAGAACTCTGTTCTGTCTGTCCCATGTGTGCCGAAG	2504
Qy	2341	GACTTGGGCAAAATCTTTGCTGTGCAAAACCTTCAGTTCGACCGAGGAACTGAAATATA	2400
Db	2505	GACTTGGGCAAAATCTTTGCTGTGCAAAACCTTCAGTTCGACCGAGGAACTGAAATATA	2564
Qy	2401	CAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGAGCAAGATTTTACCCAAATGG	2460
Db	2565	CAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGAGCAAGATTTTACCCAAATGG	2624
Qy	2461	AGGGAATCCAAATTTGTTTATACTGATGAAGAGTGGTCCCAAGAGACAGACAGACAGAC	2520
Db	2625	AGGGAATCCAAATTTGTTTATACTGATGAAGAGTGGTCCCAAGAGACAGACAGACAGAC	2684
Qy	2521	ACTTTTGTATGCCGACCGCAGCTGCCAGGGAAGCTTTCATCAGACTCTCTAAGG	2580
Db	2685	ACTTTTGTATGCCGACCGCAGCTGCCAGGGAAGCTTTCATCAGACTCTCTAAGG	2744
Qy	2581	ACTGGAAGGTCAAGATCATCTCAGAGCATTTGTAAGCAGAGGAAAGTACAGATGCCCTC	2640
Db	2745	ACTGGAAGGTCAAGATCATCTCAGAGCATTTGTAAGCAGAGGAAAGTACAGATGCCCTC	2804
Qy	2641	AGCTTGCCTCATGTCAAACTGAAATAA	2667
Db	2805	AGCTTGCCTCATGTCAAACTGAAATAA	2831
RESULT 4			
AAS14652			
ID	AAS14652 standard; cdNA; 2694 BP.		
AC	AAS14652;		
XX			
DT	(first entry)		
XX			
DE	Human cdNA encoding a voltage gated potassium channel hKCNQ5-1.		
XX			
KW			

QY	1534	GGTCATCTGGACATGTTGTGTAGAAATTAAGCCTTAAACACAGTGTGTGATCAAAATCTTT	1593
Db	1561	GGTCATCTGGACATGTTGTGTAGAAATTAAGCCTTAAACACAGTGTGTGATCAAAATCTTT	1620
QY	1594	GGAAAGGGCAATACATCAGATAGAAAGAGCGGAGAGAAATACACAGAACATGAG	1653
Db	1621	GGAAAGGGCAATACATCAGATAGAAAGAGCGGAGAGAAATACACAGAACATGAG	1680
QY	1654	ACCACAGACATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAACACAGGTACAGTCC	1713
Db	1681	ACCACAGACATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAACACAGGTACAGTCC	1740
QY	1714	ATAGAGTCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCTTCGGAAGGCTCT	1773
Db	1741	ATAGAGTCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCTTCGGAAGGCTCT	1800
QY	1774	GCCTCAGCCTCGCTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT	1833
Db	1801	GCCTCAGCCTCGCTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT	1860
QY	1834	GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCGACACAAACAGTGGGTGC	1893
Db	1861	GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCGACACAAACAGTGGGTGC	1920
QY	1894	TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTCGAGTTCAATCTGAGCCAAAT	1953
Db	1921	TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTCGAGTTCAATCTGAGCCAAAT	1980
QY	1954	GAGTTCAGTCCAGACATTTCTAGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG	2013
Db	1981	GAGTTCAGTCCAGACATTTCTAGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG	2040
QY	2014	GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCCAGCCAAACACATTTGCAACAA	2073
Db	2041	GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCCAGCCAAACACATTTGCAACAA	2100
QY	2074	ATAAATACGCCACCAAGCAGCAGCCCAACACTTTACAGATCCACCTCTCTCCCA	2133
Db	2101	ATAAATACGCCACCAAGCAGCAGCCCAACACTTTACAGATCCACCTCTCTCTCCCA	2160
QY	2134	GCATCAAGCATCTGCCAGGCCAGAAACTCTGACCCCTAACCCCTGCGAGGTTACAGGAA	2193
Db	2161	GCATCAAGCATCTGCCAGGCCAGAAACTCTGACCCCTAACCCCTGCGAGGTTACAGGAA	2220
QY	2194	AGCATTTCTGAGTCAACCTGCTTGTGCTTCCAGGAAATGTTTCAGGTTGCAAG	2253
Db	2221	AGCATTTCTGAGTCAACCTGCTTGTGCTTCCAGGAAATGTTTCAGGTTGCAAG	2280
QY	2254	TCAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2313
Db	2281	TCAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2340
QY	2314	TTGCTGCTGCTGCCATGTCGGAAGGACTTTGGGCAAACTTTGCTGTGCAAAACCTG	2373
Db	2341	TTGCTGCTGCTGCCATGTCGGAAGGACTTTGGGCAAACTTTGCTGTGCAAAACCTG	2400
QY	2374	ATCAGTTCAGCAGGAACTGAATATACACTTTTTCAGGAGTGAAGTGGCTCCAGA	2433
Db	2401	ATCAGTTCAGCAGGAACTGAATATACACTTTTTCAGGAGTGAAGTGGCTCCAGA	2460
QY	2434	GGCAGCCAAAGTTTTTACCCCAATGAGGGAATCCAAATGTTTATTAATGATGAAGAG	2493
Db	2461	GGCAGCCAAAGTTTTTACCCCAATGAGGGAATCCAAATGTTTATTAATGATGAAGAG	2520
QY	2494	GTGGGTCCGAGAGACAGACAGACATTTTGTATGCGCACCCGAGCTGCGCAGGAA	2553
Db	2521	GTGGGTCCGAGAGACAGACAGACATTTTGTATGCGCACCCGAGCTGCGCAGGAA	2580
QY	2554	GCTGCCCTTTCATCAGACTCTTATAGGACTGGAAGTCAAGTCAATCTCAGAGCAATTTGT	2613
Db	2581	GCTGCCCTTTCATCAGACTCTTATAGGACTGGAAGTCAAGTCAATCTCAGAGCAATTTGT	2640
QY	2614	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGCTCAAACTGAATATAA	2667
Db	2641	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGCTCAAACTGAATATAA	2694
RESULT 5			
ID	AAD27192	AAD27192 standard; cDNA; 2694 BP.	
XX	AC	AAD27192;	
XX	DT	09-APR-2002 (first entry)	
XX	XX	Human potassium channel polypeptide, KCNQ5 cDNA.	
DE	XX	Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;	
XX	XX	dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;	
KW	XX	multiple sclerosis; MS; Parkinson's disease; ataxia; depression;	
KW	XX	anxiety disorder; bipolar disorder; sleep disorder; eating disorder;	
KW	XX	addiction; myokymia; Alzheimer's disease; age-associated memory loss;	
KW	XX	learning deficiency; cognitive disorder; motor disease; neuron disease;	
KW	XX	neurophysiological disorder; neuropsychological disorder; asthma;	
KW	XX	neuron cell death; brain tumor; gene therapy; antisense therapy;	
KW	XX	synaptic transmission; electrical excitability; ss.	
OS	XX	Homo sapiens.	
XX	XX	Location/Qualifiers	
PH	XX	1..2694	
FT	XX	/*tag= a	
FT	XX	/product= "Human KCNQ5 protein"	
XX	XX	W0200192526-A1.	
XX	XX	06-DEC-2001.	
XX	XX	24-MAY-2001; 2001WO-US017314.	
XX	XX	26-MAY-2000; 2000US-0207389P.	
XX	XX	(BRIM) BRISTOL-MYERS SQUIBB CO.	
XX	XX	Dworetzky SI, Ramanathan CS, Trojnecki JT, Boissard CG;	
PI	XX	Gribkoff VK;	
XX	XX	WPI: 2002-122069/16.	
DR	XX	P-PSDB; AAE16599.	
XX	XX	Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding	
PT	XX	it, for diagnosing, treating and identifying modulators useful in	
PT	XX	treating neurological, neurophysiological and neuropsychological	
XX	XX	diseases.	
PS	XX	Claim 3; Fig 1; 128pp; English.	
XX	XX	The invention relates to potassium channel polypeptides referred to as	
XX	XX	KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5	
CC	XX	polypeptides are useful for identifying compounds that modulate their	
CC	XX	biological activity. The compounds identified and KCNQ5 polynucleotides	
CC	XX	are useful for treating acute and chronic pain, migraine, acute stroke,	
CC	XX	dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),	
CC	XX	multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,	
CC	XX	depression, bipolar disorders, sleep disorders, eating disorders,	
CC	XX	addiction, myokymia, Alzheimer's disease, age-associated memory loss, The	
CC	XX	learning deficiencies, cognitive disorders and motor neuron diseases. The	
CC	XX	nucleic acid molecules of the invention are further useful for treating	
CC	XX	neurophysiological, neuropsychological disorders, asthma, neuron cell	
CC	XX	death and brain tumors. They are also used in gene therapy and antisense	
CC	XX	therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical	
CC	XX	excitability in the brain and are useful for generating antibodies. They	
CC	XX	are also useful to affinity purify biological effectors from biological	
CC	XX	materials e.g. disease tissues or cells. The present sequence is human	
CC	XX	KCNQ5 cDNA	

XX	SQ	Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;
	Query Match	98.6%; Score 2630; DB 6; Length 2694;
	Best Local Similarity	99.0%; Pred. No. 0;
	Matches 2667; Conservative	0; Mismatches 0; Indels 27; Gaps 1;
Qy	1	ATGAAGGATGTGGAGTCCGGCCGGGCGAGGGTGTCTGAACTCGGAGCGCCAGGGGC 60
Db	1	ATGAAGGATGTGGAGTCCGGCCGGGCGAGGGTGTCTGAACTCGGAGCGCCAGGGGC 60
Qy	61	GACGGCTGTACTCTTGGGCACCGCGCGGCCACGCTTGGTGGCGGGCGGTGGCTG 120
Db	61	GACGGCTGTACTCTTGGGCACCGCGCGGCCACGCTTGGTGGCGGGCGGTGGCTG 120
Qy	121	AGGAGAGCCCGCCGGGCGAAGCAGGGGGCCCGGATGAGCCCTGCTGGGGAAAGCCGCTCTCT 180
Db	121	AGGAGAGCCCGCCGGGCGAAGCAGGGGGCCCGGATGAGCCCTGCTGGGGAAAGCCGCTCTCT 180
Qy	181	TACACGAGTAGCCAGAGTCCGCGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG 240
Db	181	TACACGAGTAGCCAGAGTCCGCGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG 240
Qy	241	TACAACTGTCTGGAGAGACCCCGCGCTGGCGGTTCACTACCAAGCTTTTGGTTTTTCTC 300
Db	241	TACAACTGTCTGGAGAGACCCCGCGCTGGCGGTTCACTACCAAGCTTTTGGTTTTTCTC 300
Qy	301	CTTGCTTTTGGTGTCTTGAATTTTGTCAAGTGTTTTCTACCACTCCCTGAGCACACAAAATTG 360
Db	301	CTTGCTTTTGGTGTCTTGAATTTTGTCAAGTGTTTTCTACCACTCCCTGAGCACACAAAATTG 360
Qy	361	GCCTCAAAGTTGCCCTCTTTGATCTCTGGAGTTCGTGATGATTTGCTTTTGGTGGAGTTC 420
Db	361	GCCTCAAAGTTGCCCTCTTTGATCTCTGGAGTTCGTGATGATTTGCTTTTGGTGGAGTTC 420
Qy	421	ATCATTCGAATCTGGTCTCGGGTTGCTTTGTTCGATATAGAGATGGCAAGAGACTG 480
Db	421	ATCATTCGAATCTGGTCTCGGGTTGCTTTGTTCGATATAGAGATGGCAAGAGAGACTG 480
Qy	481	AGGTTTCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db	481	AGGTTTCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Qy	541	GTTGTTTCTGCAAAAACCTCAGGGTAAATATTTTGGCACGTCGCACTCAGAAGTCTCCGT 600
Db	541	GTTGTTTCTGCAAAAACCTCAGGGTAAATATTTTGGCACGTCGCACTCAGAAGTCTCCGT 600
Qy	601	TTCCTACAGATCTCCGCAATGGTCGCAATGGAACGAAAGGGAGGCACTTGGAAATTAAGT 660
Db	601	TTCCTACAGATCTCCGCAATGGTCGCAATGGAACGAAAGGGAGGCACTTGGAAATTAAGT 660
Qy	661	GGTTCAGTGGTTATGCTCAGCAAGGAATTATACAGCTTGGTACATAGGATTTTTCG 720
Db	661	GGTTCAGTGGTTATGCTCAGCAAGGAATTATACAGCTTGGTACATAGGATTTTTCG 720
Qy	721	GTTCTTATTTTTTTCGCTCTTTCTTGTCTATCTGGTGGAAAGGATGCCAATAAAGAGTTT 780
Db	721	GTTCTTATTTTTTTCGCTCTTTCTTGTCTATCTGGTGGAAAGGATGCCAATAAAGAGTTT 780
Qy	781	TCTACATATGAGATGCTCTCTGTGTGGGCACAATTAATACATGACAACTATTTGGCTATGGA 840
Db	781	TCTACATATGAGATGCTCTCTGTGTGGGCACAATTAATACATGACAACTATTTGGCTATGGA 840
Qy	841	GACAAAACCCCTAACTTGGCTGGGAAGATGCTTTCTCGAGGCTTTCACCTCTTGGC 900
Db	841	GACAAAACCCCTAACTTGGCTGGGAAGATGCTTTCTCGAGGCTTTCACCTCTTGGC 900
Qy	901	ATTTCTTTCTTTGCACTTCTTCGCGGCAATCTTGGCTCAGGTTTTTGCAATTAAGAATCAAA 960
Db	901	ATTTCTTTCTTTGCACTTCTTCGCGGCAATCTTGGCTCAGGTTTTTGCAATTAAGAATCAAA 960
Qy	961	GAAACAACCGCCAGAAACACTTTTGAGAAAGAGGAACCCAGCTGCCAACCTCAATTCAG 1020

QY 2074 ATAAATACGGACCCAGCAGCAGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2133
 Db 2101 ATAAATACGGACCCAGCAGCAGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2160
 QY 2134 GCCATCAAGCATCTGCCAGGCCAGAACTCTGCACCTTAACCTGCAGGCTTACAGGAA 2193
 Db 2161 GCCATCAAGCATCTGCCAGGCCAGAACTCTGCACCTTAACCTGCAGGCTTACAGGAA 2220
 QY 2194 AGCAATTTCTGACGTCACCACTGCTTTGTCCTCCCAAGGAAATGTTTCAAGTTGCACAG 2253
 Db 2221 AGCAATTTCTGACGTCACCACTGCTTTGTCCTCCCAAGGAAATGTTTCAAGTTGCACAG 2280
 QY 2254 TCAAATCTCAACAGGACCGTTCTTATGAGGAAAGCTTTTCAATGCGAGGAGAACTCTG 2313
 Db 2281 TCAAATCTCAACAGGACCGTTCTTATGAGGAAAGCTTTTCAATGCGAGGAGAACTCTG 2340
 QY 2314 TTGTCTGTCTGCCATGTTGCCAAGGACTTGGGCAAACTTTTGTCTGTGCAAACTCTG 2373
 Db 2341 TTGTCTGTCTGCCATGTTGCCAAGGACTTGGGCAAACTTTTGTCTGTGCAAACTCTG 2400
 QY 2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTGGCTCCAGA 2433
 Db 2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTGGCTCCAGA 2460
 QY 2434 GGCAGCCAAAGATTTTACCCCAATGAGGAAATGCCAAATGTTTATTAATGATGAAGAG 2493
 Db 2461 GGCAGCCAAAGATTTTACCCCAATGAGGAAATGCCAAATGTTTATTAATGATGAAGAG 2520
 QY 2494 GTGGGTCGAGAGACAGACAGACTTTTTCATGCGCAGCGAGCTTCCAGGAGAA 2553
 Db 2521 GTGGGTCGAGAGACAGACAGACTTTTTCATGCGCAGCGAGCTTCCAGGAGAA 2580
 QY 2554 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2613
 Db 2581 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
 QY 2614 AAGCAGAGAGAAAGTACAGATGCCCTTACGCTTGCCTCATGTCAAACTGAATAA 2667
 Db 2641 AAGCAGAGAGAAAGTACAGATGCCCTTACGCTTGCCTCATGTCAAACTGAATAA 2694

RESULT 6
 AAS14651
 ID AAS14651 standard; cDNA; 3071 BP.
 AC AAS14651;
 XX 18-DEC-2001 (first entry)
 DE Human cDNA for voltage gated potassium channel hKCNQ5.
 XX Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
 KW pain; gene therapy.
 XX Homo sapiens.
 XX WO200170759-A1.
 PN 27-SEP-2001.
 XX 20-MAR-2001; 2001WO-US009328.
 PF 21-MAR-2000; 2000US-0190954P.
 PR (ICAG-) ICAGEN INC.
 PA Jegla TJ;
 XX WPI; 2001-611467/70.
 XX DR

XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ approximately a- subunits.
 XX Claim 5; Page 61-62; 78pp; English.
 XX The invention relates to an isolated polypeptide comprising an alpha-
 CC subunit of a KCNQ potassium channel, with a subsequence having 65%
 CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
 CC and forms a KCNQ potassium channel having the characteristic of voltage-
 CC gating with at least an additional KCNQ alpha-subunit. Also included in
 CC the scope of the invention are the nucleic acids encoding hKCNQ5
 CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
 CC vectors encoding them, antibodies against them, the use of 3-dimensional
 CC computer modelling to identify molecules that bind to a KCNQ containing
 CC potassium channel and modulate ion flux through the channel. The KCNQ
 CC polypeptide is useful for identifying a compound that increases or
 CC decreases ion flux through a potassium channel expressed in an eukaryotic
 CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
 CC used in gene therapy) is useful as a pharmaceutical agent for treating
 CC diseases involving abnormal ion flux, such as disorders of the central
 CC nervous system, such as epilepsy, migraines, hearing and vision problems,
 CC psychotic disorders, seizures, learning and memory disorders, stroke and
 CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
 CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
 CC computer databases to find variants of the sequence which are associated
 CC with disease states, is useful for screening mutations of KCNQ5. The
 CC present sequence is a representative cDNA for hKCNQ5
 XX Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 0 U; 1 Other;
 SQ Query Match 98.5%; Score 2626.4; DB 4; Length 3071;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;
 QY 1 ATCAAGAGATGTGAGTGGGCGCGGCGGAGGTGCTGCTGAACCTCGCAGCGCAGGGC 60
 Db 10 ATCAAGAGATGTGAGTGGGCGCGGCGGAGGTGCTGCTGAACCTCGCAGCGCAGGGC 69
 QY 61 GACGGCTGCTACTGCTGGGCACCCCGCGGCGGAGGTGCTGCTGAACCTCGCAGCGCAGGGC 120
 Db 70 GACGGCTGCTACTGCTGGGCACCCCGCGGCGGAGGTGCTGCTGAACCTCGCAGCGCAGGGC 129
 QY 121 AGGAGAGCGCGCGGCGGAGGTGCTGCTGAACCTCGCAGCGCAGGGCAGCGCTCTCT 180
 Db 130 AGGAGAGCGCGCGGCGGAGGTGCTGCTGAACCTCGCAGCGCAGGGCAGCGCTCTCT 189
 QY 181 TACACGAGTAGCAGAGCTGCCCGCGGAGGTGCTGCTGAACCTCGCAGCGCAGGGCAGCGCT 240
 Db 190 TACACGAGTAGCAGAGCTGCCCGCGGAGGTGCTGCTGAACCTCGCAGCGCAGGGCAGCGCT 249
 QY 241 TACACGAGTAGCAGAGCTGCCCGCGGAGGTGCTGCTGAACCTCGCAGCGCAGGGCAGCGCT 300
 Db 250 TACACGAGTAGCAGAGCTGCCCGCGGAGGTGCTGCTGAACCTCGCAGCGCAGGGCAGCGCT 309
 QY 301 CTGTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 Db 310 CTGTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 369
 QY 361 GCCTCAAGTTGCCTCTTTGATCTCGGAGTTCGTGATGATGATGATGATGATGATGATGATGAT 420
 Db 370 GCCTCAAGTTGCCTCTTTGATCTCGGAGTTCGTGATGATGATGATGATGATGATGATGATGAT 429
 QY 421 ATCAATCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 Db 430 ATCAATCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 489
 QY 481 AGGTTTGTCTGAAAGCCCTTCTGTTTATAGATACCATTTCTTATCGTTCGTTCAATAGCA 540
 Db 490 AGGTTTGTCTGAAAGCCCTTCTGTTTATAGATACCATTTCTTATCGTTCGTTCAATAGCA 549
 QY 541 GTTGTCTTCTGCAAAACTCAGGGTAAATATTTTGGCAGCTGCTGCAAGTCTCCGT 600

[illegible]

Db	1630	GGAAAAAGGGCAAATCA	CATCAGATATAAGAGAGCCGAGAGAAAAATAACAGCAGAACATGAG	1689
Qy	1654	ACCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC		1713
Db	1690	ACCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC		1749
Qy	1714	ATAGAGTCCAAGCTGGAGTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT		1773
Db	1750	ATAGAAATCCAAGCTGGAGTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT		1809
Qy	1774	GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCCACCTTTTGAATGTGAACAGACATCT		1833
Db	1810	GCCTCAGCCCTCGCTTTGGCTTCAATCCAGTCCCACCTTTTGAATGTGAACAGACATCT		1869
Qy	1834	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCCGCACAAAAACAGTGGCTGC		1893
Db	1870	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCCGCACAAAAACAGTGGCTGC		1929
Qy	1894	TTATCCAGATCAACTAGTGTGCCAATCTCGAGAGGCGTGCAGTTTCATTTCTGACGCCAAAT		1953
Db	1930	TTATCCAGATCAACTAGTGTGCCAATCTCGAGAGGCGTGCAGTTTCATTTCTGACGCCAAAT		1989
Qy	1954	GAGTTCAGTGGCCAGACTTTCTACGGCGCTTAGCGCTACTATGACACAGTCAAGCAACACAG		2013
Db	1990	GAGTTCAGTGGCCAGACTTTCTACGGCGCTTAGCGCTACTATGACACAGTCAAGCAACACAG		2049
Qy	2014	GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCAA		2073
Db	2050	GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCAA		2109
Qy	2074	ATAAATACGGCACCCCAAGCCAGCAGCGCCCAACAACTTTTACAGATCCCACTCTCTCCCA		2133
Db	2110	ATAAATACGGCACCCCAAGCCAGCAGCGCCCAACAACTTTTACAGATCCCACTCTCTCCCA		2169
Qy	2134	GCCATCAAGCATCTGCCCGCAGCAAAACTCTGCAACCTTAACCTGCGGCTTACAGGAA		2193
Db	2170	GCCATCAAGCATCTGCCCGCAGCAAAACTCTGCAACCTTAACCTGCGGCTTACAGGAA		2229
Qy	2194	AGCATTTCTGACGTCCACACTCGCTTGTGGCTTCCAAAGGAAAATGTTTCAGGTTGCACAG		2253
Db	2230	AGCATTTCTGACGTCCACACTCGCTTGTGGCTTCCAAAGGAAAATGTTTCAGGTTGCACAG		2289
Qy	2254	TCAAATCTCAACGAGCCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAACTCTG		2313
Db	2290	TCAAATCTCAACGAGCCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAACTCTG		2349
Qy	2314	TTGTCTGTCTGTCCATGTGCGAAGGACTTGGGCAAACTCTTTGTCTGTGCAAAAACCTG		2373
Db	2350	TTGTCTGTCTGTCCATGTGCGCAAGGACTTGGGCAAACTCTTTGTCTGTGCAAAAACCTG		2409
Qy	2374	ATCAGGTCGACCGAGGAACGTATATACAACTTTTCAGGGAGTCAAGTCAAGTGCCTCCAGA		2433
Db	2410	ATCAGGTCGACCGAGGAACGTATATACAACTTTTCAGGGAGTCAAGTCAAGTGCCTCCAGA		2469
Qy	2434	GGCAGCCCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTTATACTGATGAAGAG		2493
Db	2470	GGCAGCCCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTTATACTGATGAAGAG		2529
Qy	2494	GTGGGTCCCGAAGACAGACAGACATCTTTTGTATGTCGCGCACCGCAGCCTGCCAGGGAA		2553
Db	2530	GTGGGTCCCGAAGACAGACAGACATCTTTTGTATGTCGCGCACCGCAGCCTGCCAGGGAA		2589
Qy	2554	GCTGCCTTTGCATCAGACTCTTAAGGACTGGAAGGTTCAGATCACTCTCAGAGCATTTGT		2613
Db	2590	GCTGCCTTTGCATCAGACTCTTAAGGACTGGAAGGTTCAGATCACTCTCAGAGCATTTGT		2649
Qy	2614	AAGCGAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACCTGAATAA		2667
Db	2650	AAGCGAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACCTGAATAA		2703

RESULT 7
AAC85414

ID	AAC85414	standard; cDNA; 3137 BP.	QY	121	AGGAGAGCGCGCGGCAAGCAGCGGGCCCGATGAGCTGTGGGGAAGCCGCTCTCT	180
XX			DB	121	AGGAGAGCGCGCGGCAAGCAGCGGGCCCGATGAGCTGTGGGGAAGCCGCTCTCT	180
AC	AAC85414;		QY	181	TACACGAGTAGCCAGAGCTGCCGGCGCAACGCTCAAGTACCGCGGGTGCAGAGTACCTG	240
XX			DB	181	TACACGAGTAGCCAGAGCTGCCGGCGCAACGCTCAAGTACCGCGGGTGCAGAGTACCTG	240
DT	20-APR-2001	(first entry)	QY	241	TACAAAGTGTGGAGAGACCCCGCGCTGGCGCTTCATCTACCAAGCTTTGCTTTTCTC	300
XX			DB	241	TACAAAGTGTGGAGAGACCCCGCGCTGGCGCTTCATCTACCAAGCTTTGCTTTTCTC	300
DE	Human KCNQ5	potassium channel subunit coding sequence.	QY	301	CTTGTCTTTGGTGTCTTCAATTTTGTCAAGTGTCTTCTACCAATCCCTGAGACACAAAATTG	360
XX			DB	301	CTTGTCTTTGGTGTCTTCAATTTTGTCAAGTGTCTTCTACCAATCCCTGAGACACAAAATTG	360
KW	Human; KCNQ5;	heteromeric channel; chromosome 6; Parkinson's disease; central nervous system; CNS; Alzheimer's disease; anxiety; ataxia; CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia; compulsive behaviour; dementia; depression; Huntington's disease; mania; memory impairment; memory dysfunction; spinal cord damage; phobia; pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy; ds.	QY	361	GCCTCAAGTTGCTCTTGATCTCTGGAGTTCTGTGATGATGTCGTTTGGTTCGAGTTC	420
XX			DB	361	GCCTCAAGTTGCTCTTGATCTCTGGAGTTCTGTGATGATGTCGTTTGGTTCGAGTTC	420
OS	Homo sapiens.		QY	421	ATCATTTGGAATCTGCTGCGGTTGCTGTGTGATATAGAGGATGCAAGGAGACTG	480
XX			DB	421	ATCATTTGGAATCTGCTGCGGTTGCTGTGTGATATAGAGGATGCAAGGAGACTG	480
PH	Key	Location/Qualifiers	QY	481	AGGTTTGTCTCGAAAGCCCTTCTGTATATAGATACCATTTGTTTATCGCTTCAATGCA	540
XX			DB	481	AGGTTTGTCTCGAAAGCCCTTCTGTATATAGATACCATTTGTTTATCGCTTCAATGCA	540
FT	CD5	1..2694	QY	541	GTGTCTTCTGCAAAAGCTCAGGTTTATATTTTGGCAGCTCTGCACTCAGAGTCTCGT	600
FT	/*tag= a		DB	541	GTGTCTTCTGCAAAAGCTCAGGTTTATATTTTGGCAGCTCTGCACTCAGAGTCTCGT	600
FT	/product= "KCNQ5 subunit"		QY	601	TTCTTACAGATCTCTCGCATGCTGCGCATGGTGGACCGAAGGGAGGCACTTGGAAATCTG	660
XX	WO200077035-A2.		DB	601	TTCTTACAGATCTCTCGCATGCTGCGCATGGTGGACCGAAGGGAGGCACTTGGAAATCTG	660
XX	21-DEC-2000.		QY	661	GGTTCAAGTGGTTATGCTCACAGCAGGAAATTAATCACAAGCTTGGTACATAGATTTTG	720
XX			DB	661	GGTTCAAGTGGTTATGCTCACAGCAGGAAATTAATCACAAGCTTGGTACATAGATTTTG	720
XX	WPI: 2001-080678/09.		QY	721	GTTCCTTATTTTTCGTTCTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	780
XX	P-PSDB; AAB47046.		DB	721	GTTCCTTATTTTTCGTTCTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	780
XX	Novel genes encoding KCNQ5 potassium channel subunits, useful for treating Alzheimer's disease, anxiety, ataxia, stroke, dementia, depression, Huntington's disease, schizophrenia and Parkinson's disease.		QY	781	TCTACATATGACAGATGCTCTCTGTTGGGCAAGATTTGCTTCTGCAAGCTTTGCACTTCCTTGGC	840
XX	Claim 2; Page 44-48; 50pp; English.		DB	781	TCTACATATGACAGATGCTCTCTGTTGGGCAAGATTTGCTTCTGCAAGCTTTGCACTTCCTTGGC	840
XX	This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms heteromeric channels with other KCNQ channel subunits, in particular KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of chromosome 6 (6q14). Chemicals which have the ability to bind to KCNQ5 are useful for diagnosis, treatment, prevention or alleviation of diseases related to diseases or adverse conditions of the central nervous system (CNS), including affective disorders, Alzheimer's disease, anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative illness, cognitive deficits, compulsive behaviour, dementia, depression, Huntington's disease, mania, memory impairment, memory disorders, memory dysfunction, motion disorders, motor disorders, neurodegenerative diseases, Parkinson's disease and Parkinson-like motor disorders, phobias, pick's disease, psychosis, schizophrenia, spinal cord damage, stroke, tremor, seizures, convulsions and epilepsy		QY	841	GACAAAGTCTCCCTTAACTTGGCTGGCAAGATTTGCTTCTGCAAGCTTTGCACTTCCTTGGC	900
XX			DB	841	GACAAAGTCTCCCTTAACTTGGCTGGCAAGATTTGCTTCTGCAAGCTTTGCACTTCCTTGGC	900
XX			QY	901	ATTTCCTTTCTTTCGCTTCTGCGGCAATTTGCTTGGCTCAGGTTTGGATTAAGTACAA	960
XX			DB	901	ATTTCCTTTCTTTCGCTTCTGCGGCAATTTGCTTGGCTCAGGTTTGGATTAAGTACAA	960
XX			QY	961	GAAACAACCGCCAGAAACACTTTGAAAAGAGAAAGCAAGCCAGCTGCCAACCTCAATCAG	1020
XX			DB	961	GAAACAACCGCCAGAAACACTTTGAAAAGAGAAAGCAAGCCAGCTGCCAACCTCAATCAG	1020
XX			QY	1021	TGCTGTTGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA	1080
XX			DB	1021	TGCTGTTGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA	1080
XX			QY	1081	CACCTGAAGGCTTGGCACTCTGAGGCTTACCA-----1115	1115
XX			DB	1081	CACCTGAAGGCTTGGCACTCTGAGGCTTACCA-----1115	1115
XX			QY	1116	--TCAGAGCTAAAGTTTAAAGGAGCGAGTGGCATGCTAGCCCCAGGGCCAGAGTATT	1173
XX			DB	1141	AGTCAGAGCTAAAGTTTAAAGGAGCGAGTGGCATGCTAGCCCCAGGGCCAGAGTATT	1200
XX			QY	1174	AAGAGCCGCAAGCCCTCAGTAGGTGACAGGAGGTCCCAAGCACCACATCACAGCCGAG	1233
XX			DB			

Query Match 98.4%; Score 2625.2; DB 4; Length 3137;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

QY 1 ATGAAGATGTGAGTGGCGCGGCGAGGCTGCTGTAAGTGGCAGCCGCGGCGG 60
DB 1 ATGAAGATGTGAGTGGCGCGGCGAGGCTGCTGTAAGTGGCAGCCGCGGCGG 60

QY 61 GACGGCTGTACTGTGGCACCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 120
DB 61 GACGGCTGTACTGTGGCACCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 120

[illegible]

Db	2281	TCAAACTCTCACCAGGACCGTTCTATGAGAAAGCTTTGACATGGAGGAGAAACTCTG	2340
Qy	2314	TTGTCTCTCTGCCATCGTGGCGAAGGACTTGGGCAAAATCTTTTGTCTGTGCAAAACCTG	2373
Db	2341	TTGTCTCTCTGCCATCGTGGCGAAGGACTTGGGCAAAATCTTTTGTCTGTGCAAAACCTG	2400
Qy	2374	ATCAGGTCGACCGAGGAACCTGAATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2433
Db	2401	ATCAGGTCGACCGAGGAACCTGAATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2460
Qy	2434	GGCAGCCCAAGATTTTATCCCCCAATGGAGGGAATCCAAATGTTTATAACTGATGAAGAG	2493
Db	2461	GGCAGCCCAAGATTTTATCCCCCAATGGAGGGAATCCAAATGTTTATAACTGATGAAGAG	2520
Qy	2494	GTGGTCCCGAAGACAGAGACAGACACATTTTGTATGCCGACCGAGCCTGCCAGGGAA	2553
Db	2521	GTGGTCCCGAAGACAGAGACAGACACATTTTGTATGCCGACCGAGCCTGCCAGGGAA	2580
Qy	2554	GCTGCCTTTTGCATCAGACTCTTAAGGACTTGGAAGGTACAGATCATCTCAGAGCATTTGT	2613
Db	2581	GCTGCCTTTTGCATCAGACTCTTAAGGACTTGGAAGGTACAGATCATCTCAGAGCATTTGT	2640
Qy	2614	AAGCGAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACCTGAATAA	2667
Db	2641	AAGCGAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACCTGAATAA	2694

RESULT 8

RESOL1 8
AAH49499
ID AAH49499 standard: DNA: 3074 BP.

AA
AC
AAH49499:

11-DEC-2001 (first entry)

AA
DE
Human KCNO5 DNA.

XX KCNQ5; potassium channel protein; human; neurological; cardiovascular;
KW anticonvulsant; excitability modulator; membrane potential; neuron;
KW voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
KW screening; central nervous system disease; cardiovascular disease; ds.

XX
OS
Homo sapiens.

	Key	Location/Qualifiers
XX	CDS	110 2908
FH		
FT		

```
FT /*tag= a
FT /product= "KCNO5"
FT
```

XX
PN DE10013732-A1XX
27-SEP-2001XX
DE 21-MAR-2000:

0
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5
6
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W
X
Y
Z

[illegible]

XX

DR P-PSDB; AAB86979.

PT New DNA sequence encoding potassium

PT system and cardiovascular diseases.

PS Claim 2a: Page 9-10: 20pp: German:

XX This invention describes a novel DNA sequence (I) encoding: (i) a

CC

CC polypeptide (II) with potassium channel KCNQ5 activity; (II) a
CC polypeptide with the amino acid (aa) sequence of KCNQ5. The products of

CC the invention have neurological, cardiovascular and anticonvulsant
CC activity and act as modulators of the voltage-dependent K_{CNQ5} potassium
CC channel, a key regulator of membrane potential and modulator of
CC excitability of electrically activated cells such as neurons and
CC cardiomyocytes. K_{CNQ5} may be implicated in some forms of epilepsy. (II)
CC are used to screen for compounds that modulate the activity of K_{CNQ5},
CC potentially useful for treating central nervous system (e.g. epilepsy),
CC and cardiovascular diseases. This sequence encodes the human potassium
CC channel K_{CNQ5} protein described in the invention
XX
SQ Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 U; 0 Other;

Query Match 98.1%; Score 2617.2; DB 4; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;

QY 1 ATGAGGATGCGAGTCGGGCGGGGCGAGGCTGCTGTAACCTCGGAGCGCGCAGGGGC 60
DB 215 ATGAGGATGCGAGTCGGGCGGGGCGAGGCTGCTGTAACCTCGGAGCGCGCAGGGGC 274

QY 61 GACGGCTGCTACTGCTGGGCAACCGCGCGGCCACGCTTGGTGGCGCGCGGTGGCGTG 120
DB 275 GACGGCTGCTACTGCTGGGCAACCGCGCGGCCACGCTTGGTGGCGCGCGGTGGCGTG 334

QY 121 AGGAGAGCGCGGGGCAACGAGCGGGCGCGGATGAGCTGCTGGGGAAGCGCTCTCT 180
DB 335 AGGAGAGCGCGGGGCAACGAGCGGGCGCGGATGAGCTGCTGGGGAAGCGCTCTCT 394

QY 181 TACACGAGTACGAGCTGCGCGGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG 240
DB 395 TACACGAGTACGAGCTGCGCGGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG 454

QY 241 TACACGAGTACGAGCGCGCGGCGGCTGCTACCTACCGCTTTCGTTTCTC 300
DB 455 TACACGAGTACGAGCGCGCGGCGGCTGCTACCTACCGCTTTCGTTTCTC 514

QY 301 CTTGCTTTGGTGTGATTTGCTGAGTGTTCAGTGTTCCTACCTCGGAGCACAAAATTG 360
DB 515 CTTGCTTTGGTGTGATTTGCTGAGTGTTCAGTGTTCCTACCTCGGAGCACAAAATTG 574

QY 361 GCCTCAAGTTGGCTTTCGAGTTCGAGTTCGATGATTTGCTTTCGAGTTC 420
DB 575 GCCTCAAGTTGGCTTTCGAGTTCGAGTTCGATGATTTGCTTTCGAGTTC 634

QY 421 ATCATTCGAACTGCTGCGGGTTCGTTGCTCGATAGAGATGCGAGGAGACTG 480
DB 635 ATCATTCGAACTGCTGCGGGTTCGTTGCTCGATAGAGATGCGAGGAGACTG 694

QY 481 AGGTTTGTCTGAAAGCCCTTCTGCTATAGATACATTTGTTTCCTTCCTCAATAGCA 540
DB 695 AGGTTTGTCTGAAAGCCCTTCTGCTATAGATACATTTGTTTCCTTCCTCAATAGCA 754

QY 541 GTTGTTCGAAAAAATCAGGGTAATAATTTTGGCCAGCTGCACTCAGAACTCCGT 600
DB 755 GTTGTTCGAAAAAATCAGGGTAATAATTTTGGCCAGCTGCACTCAGAACTCCGT 814

QY 601 TTCCTACAGATCCTCGGATGTCGATGAGCGGAGGAGGCACTTGGAAATTAATG 660
DB 815 TTCCTACAGATCCTCGGATGTCGATGAGCGGAGGAGGCACTTGGAAATTAATG 874

QY 661 GTTTCAGTGTGTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 720
DB 875 GTTTCAGTGTGTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 934

QY 721 GTTTCATATTTTTCGCTTTCTGCTATCTGCTGGGAAAGGATGCCAATAAGAGTTT 780
DB 935 GTTTCATATTTTTCGCTTTCTGCTATCTGCTGGGAAAGGATGCCAATAAGAGTTT 994

QY 781 TCTACATATGCAATGCTCTCTGCTGGGCAAAATTTACATTTGCAAACTATTGGCTATGGA 840
DB 995 TCTACATATGCAATGCTCTCTGCTGGGCAAAATTTACATTTGCAAACTATTGGCTATGGA 1054

QY 841 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTCGACTCCTTGGC 900

DB 1055 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTCGACTCCTTGGC 1114
QY 901 ATTTCTTTTTCGCACTTCCCTGCGCGCATTTCTGGCTCAGGTTTGGCAATTAAGAGTCAA 960
DB 1115 ATTTCTTTTTCGCACTTCCCTGCGCGCATTTCTGGCTCAGGTTTGGCAATTAAGAGTCAA 1174
QY 961 GAACACACCGCCGAGAACACTTTTCAGAAAAAGAGAACCCAGCTGCCAATCTATTGAG 1020
DB 1175 GAACACACCGCCGAGAACACTTTTCAGAAAAAGAGAACCCAGCTGCCAATCTATTGAG 1234
QY 1021 TGTGTTTGGCTAGTTTACGACGCTGATGAGAAATCTGTTTTCATTTGCAACCTGGAGGCA 1080
DB 1235 TGTGTTTGGCTAGTTTACGACGCTGATGAGAAATCTGTTTTCATTTGCAACCTGGAGGCA 1294
QY 1081 CACTTGAAGGCTTTCGACACCTGCGAGCCCTACCA----- 1115
DB 1295 CACTTGAAGGCTTTCGACACCTGCGAGCCCTACCAAGAAAGAAACAAGGGGAAGCATCAAGC 1354
QY 1116 --TCAGAACTAACTTTTAAAGGAGCGAGTGCAGCTAGCCGCCAGGGGCGCAGAGTATT 1173
DB 1355 AGTCAGAACTAACTTTTAAAGGAGCGAGTGCAGCTAGCCGCCAGGGGCGCAGAGTATT 1414
QY 1174 AAGAGCCGCAACAGCTTCACTAGTGCAGAGAGTCCCAAGCAACCGACATCAGCCGAG 1233
DB 1415 AAGAGCCGCAACAGCTTCACTAGTGCAGAGAGTCCCAAGCAACCGACATCAGCCGAG 1474
QY 1234 GGAGTCCCAACCAAGTGCAGAGAGTCCCAAGCAACCGACATCAGCCGAG 1293
DB 1475 GGCAGTCCCAACCAAGTGCAGAGAGTCCCAAGCAACCGACATCAGCCGAG 1534
QY 1294 TCGCTCGCTCAAAAAGTTCTCAGCCAAAACAGTATAGATGCTGACACAGCCCTTGGC 1353
DB 1535 TCGCTCGCTCAAAAAGTTCTCAGCCAAAACAGTATAGATGCTGACACAGCCCTTGGC 1594
QY 1354 ACTGATGATGATATGATGAAAAAGGATGCGAGTGTGATGATGATGATGATGATGATGAT 1413
DB 1595 ACTGATGATGATATGATGAAAAAGGATGCGAGTGTGATGATGATGATGATGATGATGAT 1654
QY 1414 CCACCACTTAAACTGCTTCACTGAGCTATCAGAAATTTGAAATTTTCAATTTTCAATTTTCA 1473
DB 1655 CCACCACTTAAACTGCTTCACTGAGCTATCAGAAATTTGAAATTTTCAATTTTCAATTTTCA 1714
QY 1474 AAGTTAAAGGAAACGTTTACGTCATATGATGATGATGATGATGATGATGATGATGATGAT 1533
DB 1715 AAGTTAAAGGAAACATTTACGTCATATGATGATGATGATGATGATGATGATGATGATGAT 1774
QY 1534 GGTCACTGACATGTTGTTAGAAATTTAAAGCTTTCAAAACAGCTGTTGATCAAAATTTCTT 1593
DB 1775 GGTCACTGACATGTTGTTAGAAATTTAAAGCTTTCAAAACAGCTGTTGATCAAAATTTCTT 1834
QY 1594 GGAAGAGGGCAAAATCAGATCAGATAAGAGAGCGGAGAGAAAAATAACAGAGAACATGAG 1653
DB 1835 GGAAGAGGGCAAAATCAGATCAGATAAGAGAGCGGAGAGAAAAATAACAGAGAACATGAG 1894
QY 1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGCTCAGGTTGCAAAACAGAGTACAGTCC 1713
DB 1895 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGCTCAGGTTGCAAAACAGAGTACAGTCC 1954
QY 1714 ATAGAGTCCAGAGCTGAGCTGCTTACTAGACATCTATCAACAGAGTCTTTCGGAAGGCTCT 1773
DB 1955 ATAGAAATCCAGCTGAGCTGCTTACTAGACATCTATCAACAGAGTCTTTCGGAAGGCTCT 2014
QY 1774 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATTTGAACAGACATCT 1833
DB 2015 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATTTGAACAGACATCT 2074
QY 1834 GACTATCAAGCCCTGCTGGATAGCAAGATCTTTTCGGGTTCCGCAAAAACAGTGGGCTGC 1893
DB 2075 GACTATCAAGCCCTGCTGGATAGCAAGATCTTTTCGGGTTCCGCAAAAACAGTGGGCTGC 2134
QY 1894 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCTCGAGTTCATTTCTGACGCCAAAT 1953

QY	301	CTTGTCTTTGGTTCGCTGATTTTGTTCAGTGTCTTTTCTACCATCCTCGAGCACACAAAATTG	360	1354	ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAGACCTCACC	1413
Db	515	CTTGTCTTTGGTTCGCTGATTTTGTTCAGTGTCTTTTCTACCATCCTCGAGCACACAAAATTG	574	1595	ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAGACCTCACC	1654
QY	361	GCCTCAAGTTCCTCTTGTATCTCGAGTTCGTGATGATGTCTTTCGTTTGGATTC	420	1414	CCACCACCTTAAACCTGTCATTCGAGCTATCAGAAATATGAAATTCATGTTGCAAAACGG	1473
Db	575	GCCTCAAGTTCCTCTTGTATCTCGAGTTCGTGATGATGTCTTTCGTTTGGATTC	634	1655	CCACCACCTTAAACCTGTCATTCGAGCTATCAGAAATATGAAATTCATGTTGCAAAACGG	1714
QY	421	ATCATTCGAATCTGCTCGGGTTCGTGTTCGATATAGAGATGGCAAGGAAGACTG	480	1474	AAGTTTAAAGGAAACGTTTACGTCATATGATCTAAAGATGTCATTGAAACAATATTTCTGCT	1533
Db	635	ATCATTCGAATCTGCTCGGGTTCGTGTTCGATATAGAGATGGCAAGGAAGACTG	694	1715	AAGTTTAAAGGAAACGTTTACGTCATATGATCTAAAGATGTCATTGAAACAATATTTCTGCT	1774
QY	481	AGGTTTCTGCTCGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	540	1534	GGTCACTCTGGACATGTTCTGTAGAAATTAAGACCTTCAACACAGCTGTTGATCAAAATCTT	1593
Db	695	AGGTTTCTGCTCGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	754	1775	GGTCACTCTGGACATGTTCTGTAGAAATTAAGACCTTCAACACAGCTGTTGATCAAAATCTT	1834
QY	541	GTGTTTCTGCAAAAACCTCAGGTAATATTTTGGCAGGTCCTGACCTCAGAACTCTCCGT	600	1594	GGAAAAGGGCAAAATCACAATCAGATAGAAAGCCGAGAGAAATAACAGCAGAAACATGAG	1653
Db	755	GTGTTTCTGCAAAAACCTCAGGTAATATTTTGGCAGGTCCTGACCTCAGAACTCTCCGT	814	1835	GGAAAAGGGCAAAATCACAATCAGATAGAAAGCCGAGAGAAATAACAGCAGAAACATGAG	1894
QY	601	TTCTACAGATCTCCGATGCTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTAAGT	660	1654	ACCACAGACGATCTCAGTATGCTCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1713
Db	815	TTCTACAGATCTCCGATGCTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTAAGT	874	1895	ACCACAGACGATCTCAGTATGCTCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1954
QY	661	GGTTCAAGTTCCTGCTCAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTG	720	1714	ATAGAGTCCAAAGTCCGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	1773
Db	875	GGTTCAAGTTCCTGCTCAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTG	934	1955	ATAGAAATCCAAAGTCCGACTGCTCTTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	2014
QY	721	GTCTCTAATTTTTCGTCCTTCTGTCATCTGCTGGAAAGGATGCAATTAAGAGTTT	780	1774	GGCTCAGCCCTCGCTTGGCTTCAATCCAGATCCACACCTTTTGAATGTGAACAGACATCT	1833
Db	935	GTCTCTAATTTTTCGTCCTTCTGTCATCTGCTGGAAAGGATGCAATTAAGAGTTT	994	2015	GGCTCAGCCCTCGCTTGGCTTCAATCCAGATCCACACCTTTTGAATGTGAACAGACATCT	2074
QY	781	TCTACATATGAGATGCTCTCTGCTGGGCAACAATACATGACAACTATTTGGCTATGGA	840	1834	GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGCAACAAAGTGGCTGC	1893
Db	995	TCTACATATGAGATGCTCTCTGCTGGGCAACAATACATGACAACTATTTGGCTATGGA	1054	2075	GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGCAACAAAGTGGCTGC	2134
QY	841	GACAAAACCTCCCTAACCTTGGCTGGAGATGCTTCTGCGAGCTTTGCACTCCTTGGC	900	1894	TTATCCAGATCAACTAGTCCCAACATCTCGAGAGCCCTGCACTTCTAGGCGCAAAAT	1953
Db	1055	GACAAAACCTCCCTAACCTTGGCTGGAGATGCTTCTGCGAGCTTTGCACTCCTTGGC	1114	2135	TTATCCAGATCAACTAGTCCCAACATCTCGAGAGCCCTGCACTTCTAGGCGCAAAAT	2194
QY	901	ATTTCTTTTCTTGGCACTTCTGCGCGCATCTTGGCTCAGGTTTGGCAATTAAGATCAA	960	1954	GAGTTCAAGTCCGAGACTTTTCTACGGCTTACGCCCTTACTATGCACAGTCAAGCAACAG	2013
Db	1115	ATTTCTTTTCTTGGCACTTCTGCGCGCATCTTGGCTCAGGTTTGGCAATTAAGATCAA	1174	2195	GAGTTCAAGTCCGAGACTTTTCTACGGCTTACGCCCTTACTATGCACAGTCAAGCAACAG	2254
QY	961	GAAACAACCGCAGAAACACTTTGAGAAAAGAGGAAACCCAGCTGCCAACCTCATTCAG	1020	2014	GTCCCAATTTAGTCAAAAGCGATGGCTCAGCAGTGGGAGCCCAACCAACCAATTCGAACCAA	2073
Db	1175	GAAACAACCGCAGAAACACTTTGAGAAAAGAGGAAACCCAGCTGCCAACCTCATTCAG	1234	2255	GTCCCAATTTAGTCAAAAGCGATGGCTCAGCAGTGGGAGCCCAACCAACCAATTCGAACCAA	2314
QY	1021	TGTGTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA	1080	2074	ATAAATACGGCACCCCAAGCCAGCCCAACCACTTTTACAGATCCCACTCTCTCCCA	2133
Db	1235	TGTGTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA	1294	2315	ATAAATACGGCACCCCAAGCCAGCCCAACCACTTTTACAGATCCCACTCTCTCCCA	2374
QY	1081	CACTTTGAAGGCTTGCACACCTGACGCTTACCAA-----	1115	2134	GCCATCAAGCATCTGCCAGGCGAGAAACTCTGACCCCTAACCCCTGAGGCTTACAGGAA	2193
Db	1295	CACTTTGAAGGCTTGCACACCTGACGCTTACCAA-----	1354	2375	GCCATCAAGCATCTGCCAGGCGAGAAACTCTGACCCCTAACCCCTGAGGCTTACAGGAA	2434
QY	1116	--TCGAAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGCCAGAGTATT	1173	2194	AGCATTTCTGACCTCACCACCTCTGTCCTTGGCTCCCAAGGAAATGTTTACAGTTGACAG	2253
Db	1355	AGTCAGAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGCCAGAGTATT	1414	2435	AGCATTTCTGACCTCACCACCTCTGTCCTTGGCTCCCAAGGAAATGTTTACAGTTGACAG	2494
QY	1174	AAGAGCCGACAAGCCCTCAGTAGTGACAGGAGGTCCCAAGCACCGACATCAACGCCAG	1233	2254	TCAAATCTCACCAGGAGCCCTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTG	2313
Db	1415	AAGAGCCGACAAGCCCTCAGTAGTGACAGGAGGTCCCAAGCACCGACATCAACGCCAG	1474	2495	TCAAATCTCACCAGGAGCCCTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTG	2554
QY	1234	GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGTTCAACGACCGAACCGGCTTCGGGCC	1293	2314	TTGTCCTGCTGTCCCATGGTGCAGAGGACTTGGGCAAAATCTTTGCTGTGCAAAACCTG	2373
Db	1475	GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGTTCAACGACCGAACCGGCTTCGGGCC	1534	2555	TTGTCCTGCTGTCCCATGGTGCAGAGGACTTGGGCAAAATCTTTGCTGTGCAAAACCTG	2614
QY	1294	TGCTGGGCTCAAAAGTTCTCAGCCAAACACAGTATAGTGTGACACAGCCCTTGGC	1353	2374	ATCAGTTCGACCCGAGGAACTGAATATACAACTTTTACGGGAGTCAAGTGGCTCCAGA	2433
Db	1535	TGCTGGGCTCAAAAGTTCTCAGCCAAACACAGTATAGTGTGACACAGCCCTTGGC	1594	2615	ATCAGTTCGACCCGAGGAACTGAATATACAACTTTTACGGGAGTCAAGTGGCTCCAGA	2674
				2434	GGCAGCCAAAGATTTTACCCTCAAAATGGAGGAAATCCAAATTTGTTTATACTGATGAAGAG	2493

Db 2675 GGCGAGCAAGATTTTACCCCAATGAGGGAATCAAAATGTTTATAACTGATGAAGAG 2734
QY 2494 GTGGGTCCGGAAGACAGACAGACACATTTTGTATGCGCGACCGCAGCTGCGCAGGAA 2553
Db 2735 GTGGGTCCGGAAGACAGACAGACACATTTTGTATGCGCGACCGCAGCTGCGCAGGAA 2794
QY 2554 GTGGCTTTTGCATCAGACTCTCTTAAGGACTGGAAGGTGACGATCATCTCAGAGCAATTTGT 2613
Db 2795 GCTGCCCTTTGCATCAGACTCTCTTAAGGACTGGAAGGTGACGATCATCTCAGAGCAATTTGT 2854
QY 2614 AAGGACAGGAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAAACTGAAATTA 2667
Db 2855 AAGGACAGGAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAAACTGAAATTA 2908

RESULT 10

AAC64371
ID AAC64371 standard; cDNA; 3718 BP.

XX AAC64371;

XX 07-FEB-2001 (first entry)

XX Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.

XX Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW Salla disease; ophthalmological; auditory; central nervous system;
KW cardioactive; anticonvulsant; gastrointestinal; muscular active;
KW age-related macular degeneration; macular degeneration; deafness;
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW gastrointestinal disorder; ss.

XX Homo sapiens.

XX WO200061606-A1.

XX 19-OCT-2000.

XX 10-APR-2000; 2000WO-US009587.

XX 14-APR-1999; 99US-0129274P.

XX (MERI) MERCK & CO INC.

XX Petrukhin K, Caskey CT, Li W, Metzker ML;

XX WPI; 2000-647417/62.

XX P-PSDB; AAB24241.

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT inhibitors and activators which can treat e.g. Stargardt-like macular
PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.

XX Claim 3; Fig 2; 99pp; English.

XX The present sequence encodes the human KCNQ5 (also called KCN6q) protein,
CC which is a voltage-gated potassium channel protein. Human KCNQ5 has
CC ophthalmological, auditory, central nervous system (CNS), cardioactive,
CC anticonvulsant, gastrointestinal and muscular active activities.
CC Sequences and methods from the present invention are useful for
CC identifying activators or inhibitors of KCNQ5 protein. These activators
CC and inhibitors are useful for treating Stargardt-like macular dystrophy,
CC cone-rod dystrophy, Salla disease, age-related macular degeneration,
CC other forms of macular degeneration, deafness, epilepsy, and different
CC forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC Stargardt-like macular dystrophy and cone-rod dystrophies are located at
CC chromosome 6q

SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;

Query Match

94.5%; Score 2521; DB 3; Length 3718;

Best Local Similarity 98.6%; Pred. No. 0;
Matches 2564; Conservative 0; Mismatches 10; Indels 27; Gaps 1;
QY 94 AGCTTTGTTGGCGCGGCTGCGCTGAGGAGAGCCGCGGGGCAAGCAGGGGCGCGG 153
Db 78 ACTGCTGAGACTGCGGCGGTGCGCTTGTAGGAGAGCCGCGGGGCAAGCAGGGGCGCGG 137
QY 154 ATGAGCTGCTCGGGGAAGCCGCTCTCTTACAGAGTAGCAGAGCTGCCGGGCAACGTC 213
Db 138 ATGAGCTGCTCGGGGAAGCCGCTCTCTTACAGAGTAGCAGAGCTGCCGGGCAACGTC 197
QY 214 AAGTACCGCGGCTGAGAACTACCTGTACAACTGTCTGGAGAGACCCCGCGGCTGGCGG 273
Db 198 AAGTACCGCGGCTGAGAACTACCTGTACAACTGTCTGGAGAGACCCCGCGGCTGGCGG 257
QY 274 TTCTATCTACACGCTTTGCTTTTCTCTTGTCTTTGTTGTTGTTGTTGTTGTTGTTGTT 333
Db 258 TTCTATCTACACGCTTTGCTTTTCTCTTGTCTTTGTTGTTGTTGTTGTTGTTGTTGTT 317
QY 334 TCTACATCCCTGAGCACACAAAATTGGCTCAAGTTGCTCTTGTATCTCGAGTTGCTG 393
Db 318 TCTACATCCCTGAGCACACAAAATTGGCTCAAGTTGCTCTTGTATCTCGAGTTGCTG 377
QY 394 ATGATTGCTCTTTGTTTGGAGTTCAATTCGAACTCTGTTGCGGGTCTGTTGTTGTTGTT 453
Db 378 ATGATTGCTCTTTGTTTGGAGTTCAATTCGAACTCTGTTGCGGGTCTGTTGTTGTTGTT 437
QY 454 CCATATAGAGGATGCAAGGAGACTGAGTTTGTCTCGAAAGCCCTTCTGTTGTTATAGAT 513
Db 438 CCATATAGAGGATGCAAGGAGACTGAGTTTGTCTCGAAAGCCCTTCTGTTGTTATAGAT 497
QY 514 ACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACCTCAGGGTAAATTTT 573
Db 498 ACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACCTCAGGGTAAATTTT 557
QY 574 GCCAGTCTGCACTCAGAACTCTCGTTTCTTACAGATCTCCGATGTTGCGCATGGAC 633
Db 558 GCCAGTCTGCACTCAGAACTCTCGTTTCTTACAGATCTCCGATGTTGCGCATGGAC 617
QY 634 CGAAGGAGGACACTTGGAATTAAGTCTGAGTTCAGTGGTTTATGCTCAGCAAGGAATTA 693
Db 618 CGAAGGAGGACACTTGGAATTAAGTCTGAGTTCAGTGGTTTATGCTCAGCAAGGAATTA 677
QY 694 ATCAGAGCTTGGTACATAGGATTTTGTCTTATTTTCTGTTCTCTTCTGTTCTATCTG 753
Db 678 ATCAGAGCTTGGTACATAGGATTTTGTCTTATTTTCTGTTCTCTTCTGTTCTATCTG 737
QY 754 GTGAAAAGGATGCCAATAAAGAGTTTCTACATATGAGATGCTCTCTGTTGGGCGACA 813
Db 738 GTGAAAAGGATGCCAATAAAGAGTTTCTACATATGAGATGCTCTCTGTTGGGCGACA 797
QY 814 ATTCATTTGACAACTATTGGCTATGAGACAAACTCCCTTAACCTTGGCTGGGAAGATTG 873
Db 798 ATTCATTTGACAACTATTGGCTATGAGACAAACTCCCTTAACCTTGGCTGGGAAGATTG 857
QY 874 TTTTCTGAGGCTTTGCACTCTCTTGGCAATTTCTTTTGTGCACTTCTCTCCGCGCATTC 933
Db 858 TTTTCTGAGGCTTTGCACTCTCTTGGCAATTTCTTTTGTGCACTTCTCTCCGCGCATTC 917
QY 934 GGCTCAGGTTTGTCAATTAAGTACAGAAACAAACCCGCGAGAAACACTTTGAGAAAAAGA 993
Db 918 GGCTCAGGTTTGTCAATTAAGTACAGAAACAAACCCGCGAGAAACACTTTGAGAAAAAGA 977
QY 994 AGGACCCAGCTGCCAACCCTCAATTCAGTGTGTTTGGCGTAGTTACGCGAGCTCATGAGAA 1053
Db 978 AGGACCCAGCTGCCAACCCTCAATTCAGTGTGTTTGGCGTAGTTACGCGAGCTCATGAGAA 1037
QY 1054 TCTGTTTCCATTGCAACCTGGAAGCCACACTTTGAAAGGCTTGCACACCTGCGACCTACC 1113
Db 1038 TCTGTTTCCATTGCAACCTGGAAGCCACACTTTGAAAGGCTTGCACACCTGCGACCTACC 1097
QY 1114 AA-----TCAGAACTTAAGTTTAAAGGAGGAGTGCGC 1146
||

Db	1098	AAGAAAGAACAGAGGGAAGCATCAACAGCTCAGAAGCTAAGTTTTAAGGACGAGTGC	1157
Qy	1147	ATCGCTAGCCCCAGGGCCAGAGTATTAAAGCCGCAAGCCTCAGTAGGTGACAGGAGG	1206
Db	1158	ATGGCTAGCCCCAGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGG	1217
Qy	1207	TCCCCAAAGCACCGACATCACAGCCGAGGGCAGTCCACCANAAGTGCAGAAAGCTGGAGC	1266
Db	1218	TCCCCAAAGCACCGACATCACAGCCGAGGGCAGTCCACCANAAGTGCAGAAAGCTGGAGC	1277
Qy	1267	TTCAAGCAGCGAACC	1326
Db	1278	TTCAAGCAGCGAACC	1337
Qy	1327	GTGATAGATGCTGACACAGCCCTTGGCAGCTGATGATGTATATGAAAGAGATGCCAG	1386
Db	1338	GTGATAGATGCTGACACAGCCCTTGGCAGCTGATGATGTATATGAAAGAGATGCCAG	1397
Qy	1387	TGTGATGCTATCAGTGGGAAGACCTCACCCACCACTTTAAACCTGTCAATCGAGCTATCAGA	1446
Db	1398	TGTGATGCTATCAGTGGGAAGACCTCACCCACCACTTTAAACCTGTCAATCGAGCTATCAGA	1457
Qy	1447	ATTATGAAATTTTCATGTTGCAAAACGGAAAGTTTAAAGAAAACGGTTACGTCCATATGATGTA	1506
Db	1458	ATTATGAAATTTTCATGTTGCAAAACGGAAAGTTTAAAGAAAACGGTTACGTCCATATGATGTA	1517
Qy	1507	AAAGATGCTCAATGCAACAAATATTCGTGGTGCATCTGGACATGTTGTGTAGAAATTAAGAGC	1566
Db	1518	AAAGATGCTCAATGCAACAAATATTCGTGGTGCATCTGGACATGTTGTGTAGAAATTAAGAGC	1577
Qy	1567	CTTCAAACACGCTGTTGATCAAAATTTTGGAAAAAGGGCAATCAATCAGATTAAGAAAGC	1626
Db	1578	CTTCAAACACGCTGTTGATCAAAATTTTGGAAAAAGGGCAATCAATCAGATTAAGAAAGC	1637
Qy	1627	CGAGAGAAAATTAACAGACAGAACATGAGACACACAGACGATCTCAGTAGTCTCGGTCCGGTG	1686
Db	1638	CGAGAGAAAATTAACAGACAGAACATGAGACACACAGACGATCTCAGTAGTCTCGGTCCGGTG	1697
Qy	1687	GTCAAGGTTTGAATAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTTACTAGACATC	1746
Db	1698	GTCAAGGTTTGAATAACAGGTACAGTCCATAGATCCAAGCTGCCTTACTAGACATC	1757
Qy	1747	TATCAACAGAGTCTCTGGAAAGGCTGCTCAGCCCTCGCTTTGGCTTCATTTCCAGATC	1806
Db	1758	TATCAACAGAGTCTCTGGAAAGGCTGCTCAGCCCTCGCTTTGGCTTCATTTCCAGATC	1817
Qy	1807	CCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATACAAAGATCTTT	1866
Db	1818	CCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATACAAAGATCTTT	1877
Qy	1867	TCGGGTTCCGACAAAACAGTGGCTGCTTATCCAGATCAA	1926
Db	1878	TCGGGTTCCGACAAAACAGTGGCTGCTTATCCAGATCAA	1937
Qy	1927	GGCTGCAAGTTTCATTTGACCGCAAAATCAGTTCAGTCCAGACCTTTCTACGGCTTAGC	1986
Db	1938	GGCTGCAAGTTTCATTTGACCGCAAAATCAGTTCAGTCCAGACCTTTCTACGGCTTAGC	1997
Qy	1987	CCTACTATGCAAGTCAAGCAACACAGGTGCAAT	2046
Db	1998	CCTACTATGCAAGTCAAGCAACACAGGTGCAAT	2057
Qy	2047	GGAGCCCAACACCATTTGCAAA	2106
Db	2058	GGAGCCCAACACCATTTGCAAA	2117
Qy	2107	ACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCAGGCAGAACTCTG	2166
Db	2118	ACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCAGGCAGAACTCTG	2177
Qy	2167	CACCTTAACCTGCAAGGCTTACAGAAAGCATTTCTGACGTACGACCTGCCTGTTGTC	2226
Db	2178	CACCTTAACCTGCAAGGCTTACAGAAAGCATTTCTGACGTACGACCTTTGTTGTTGCC	2237

RESULT 11

RESOLUTION
AAC64370

AAC64370
ID AAC64370 standard: DNA: 125910 BP.

AAC6
ID
vv

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AAC6

XX

DT 07-F

100

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Huma

XX DE HUMA

XY	YY
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KW Human

KW Star

KW Sall

KW card

KW age-

KW epil

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kw
yy
gas

XXV

OS Homc

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PN WO20

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PD 19-C

[illegible]

10-2
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yy
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14	8
XIX	9

PR 14-7

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PA (MEF)

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PI Petr

XXI

WPT
WPT

DR	WPI, %
DR	P-DC

DR P-PS

XX

Claim 3; Fig 1; 99pp; English.

The present sequence represents the human KCNQ5 (also called KCM6q) gene, which encodes a voltage-gated potassium channel protein. Human KCNQ5 has ophthalmological, auditory, central nervous system (CNS), cardioactive, anticonvulsant, gastrointestinal and muscular active activities. Sequences and methods from the present invention are useful for identifying activators or inhibitors of KCNQ5 protein. These activators and inhibitors are useful for treating Stargardt-like macular dystrophy, cone-rod dystrophy, Salla disease, age-related macular degeneration, other forms of macular degeneration, deafness, epilepsy, and different forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders. Stargardt-like macular dystrophy and cone-rod dystrophies are located at chromosome 6q

Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 0 U; 72 Other;

Query Match 36.1%; Score 963.4; DB 3; Length 125910;

Best Local Similarity 99.9%; Pred. No. 6.6e-272;

Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1703	AGGTACAGTCCATAGATCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTC	1762
DB	123624	AGGTACAGTCCATAGATCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTC	123683
QY	1763	GGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTG	1822
DB	123684	GGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTG	123743
QY	1823	AACAGCATCTGATATCAATCAAGCCCTGTGATAGCAAGATCTTTCGGTTCGACAAA	1882
DB	123744	AACAGCATCTGATATCAATCAAGCCCTGTGATAGCAAGATCTTTCGGTTCGACAAA	123803
QY	1883	ACAGTGGCTGCTTATCCAGATCAATAGTGCACCAATCTCGAGAGCCCTGCAGTTCATTC	1942
DB	123804	ACAGTGGCTGCTTATCCAGATCAATAGTGCACCAATCTCGAGAGCCCTGCAGTTCATTC	123863
QY	1943	TGACGCCAAATGAGTTCAGTGCCCAAGATCTTACGCGCTTAGCCCTACTATGCACAGTC	2002
DB	123864	TGACGCCAAATGAGTTCAGTGCCCAAGATCTTACGCGCTTAGCCCTACTATGCACAGTC	123923
QY	2003	AGCAACACAGTGGCAATAGTCAAGGATGGCTCAGAGTGGCGAGCCACCAACACCA	2062
DB	123924	AGCAACACAGTGGCAATAGTCAAGGATGGCTCAGAGTGGCGAGCCACCAACACCA	123983
QY	2063	TTGCAACCAATAATACGGCACCAAGCCAGCAGCCCAACAACTTTACAGATCCAC	2122
DB	123984	TTGCAACCAATAATACGGCACCAAGCCAGCAGCCCAACAACTTTACAGATCCAC	124043
QY	2123	CTCCTCTCCAGCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTAACCCCTGCAG	2182
DB	124044	CTCCTCTCCAGCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTAACCCCTGCAG	124103
QY	2183	GCTTACAGAAAGCATTTCTGACGTCCACCCCTGCTTGGCTTCCCAAGGAAATGTC	2242
DB	124104	GCTTACAGAAAGCATTTCTGACGTCCACCCCTGCTTGGCTTCCCAAGGAAATGTC	124163
QY	2243	AGTTTGCACAGTCAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGAG	2302
DB	124164	AGTTTGCACAGTCAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGAG	124223
QY	2303	GAGAACTCTGTGTCTGTCTCCATGGTGGCGAAGCATTTGGGCAAACTTTTGTCTG	2362
DB	124224	GAGAACTCTGTGTCTGTCTCCATGGTGGCGAAGCATTTGGGCAAACTTTTGTCTG	124283
QY	2363	TGCAAACTGTATCAGTTCAGCCAGGAACTGAATATACAACTTTTCAGGAGTGAAGTCAA	2422
DB	124284	TGCAAACTGTATCAGTTCAGCCAGGAACTGAATATACAACTTTTCAGGAGTGAAGTCAA	124343
QY	2423	GTGGCTCCAGGCGCCAGATTTTACCCCAATGAGGGAATCCAAATGTTTATAA	2482
DB	124344	GTGGCTCCAGGCGCCAGATTTTACCCCAATGAGGGAATCCAAATGTTTATAA	124403

QY	2483	CTGATGAAGAGTGGTCCCGAAGAGACAGACAGACACACTTTTGTATGCCGACCGCAGC	2542
DB	124404	CTGATGAAGAGTGGTCCCGAAGAGACAGACAGACACACTTTTGTATGCCGACCGCAGC	124463
QY	2543	CTGCCAGGAAGCTGCTCTTTCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTC	2602
DB	124464	CTGCCAGGAAGCTGCTCTTTCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTC	124523
QY	2603	AGAGCATTTGTAAGGACAGGAGAAAGTACAGATGCTCAGCTTGCTCTATGTCAAACTCA	2662
DB	124524	AGAGCATTTGTAAGGACAGGAGAAAGTACAGATGCTCAGCTTGCTCTATGTCAAACTCA	124583
QY	2663	AATAA 2667	
DB	124584	AATAA 124588	
RESULT 12			
ACA04855			
ID	ACA04855	standard; cDNA; 582 BP.	
XX	ACA04855;		
XX	28-MAY-2003	(first entry)	
XX	cDNA encoding human membrane associated protein fragment #303.		
XX	Human; ss; gene; microarray; membrane-associated protein; neuropathology;		
KW	immunopathology; pancreatic disease; cancer; diabetes; hyperlipidaemia;		
KW	pancreatic cholera; Alzheimer's disease; Huntington's disease; sarcoma;		
KW	fibrocystic disease; leukaemia; adenocarcinoma; AIDS; allergy; anaemia;		
XX	asthma; gout; dementia.		
OS	Homo sapiens.		
XX	US6492505-B1.		
XX	10-DEC-2002.		
XX	31-JAN-2000; 2000US-00495050.		
XX	01-FEB-1999; 99US-0118318P.		
XX	(INCY-) INCYTE GENOMICS INC.		
XX	Reddy R, Guegler KJ, Au-Young J;		
XX	WPI; 2003-327324/31.		
XX	Combination for research/diagnostic applications and for monitoring		
PT	treatment of e.g., cancer, comprises polynucleotides comprising a		
PT	fragment of gene encoding membrane-associated proteins, receptors or ion		
PT	channels.		
XX	Claim 1; Fig 2; 147pp; English.		
XX	The invention relates to a combination comprising several polynucleotide		
CC	sequences comprising a fragment of gene encoding membrane-associated		
CC	proteins, receptors or ion channels. The combination is useful as a		
CC	probe, for research and diagnostic applications, for monitoring the		
CC	expression of several expressed polynucleotides, in the diagnosis and		
CC	monitoring of treatment of pancreatic disease, cancer, immunopathology or		
CC	neuropathology, for investigating an individual's predisposition to the		
CC	above disease, in genetic or gene expression analysis of polynucleotide		
CC	sequences, to investigate cellular responses to infection or drug		
CC	treatment, as hybridisable array elements in a microarray, to purify a		
CC	subpopulation of mRNAs, cDNAs or genomic fragments in a sample, in		
CC	diagnostics, prognostics and treatment regimens, in drug discovery and		
CC	development, in toxicological and carcinogenicity studies, and in		
CC	forensics or pharmacogenomics, to monitor the progression of disease, to		
CC	monitor the efficacy of treatment, to diagnose the conditions of the		
CC	pancreas e.g. diabetes, pancreatic cholera, hyperlipidaemia or		
CC	fibrocystic disease, to diagnose a cancer e.g. leukaemia, adenocarcinoma		

or sarcoma, to diagnose immunopathologies e.g. AIDS, allergies, anaemia, athma or gout, to diagnose neuropathologies e.g. Alzheimer's disease, dementia or Huntington's disease, to rapidly screen large numbers of candidate drug molecules and as query sequences against GenBank, SwissProt, BLOCKS and PRINTS databases. The combination is employed to fine tune the treatment regimen and thus the expression patterns associated with undesirable side effects are avoided. The present sequence represents a cDNA encoding a fragment of gene encoding human membrane-associated proteins, receptors or ion channels

Sequence 582 BP; 180 A; 157 C; 125 G; 120 T; 0 U; 0 Other;

Query Match 19.1%; Score 509.8; DB 8; Length 582;
Best Local Similarity 99.4%; Pred. No. 2.4e-139;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

1594 GGAAGGCGCAATCATCATAGTAAGAGCGCGAGAGAAATACAGCAGAACATGAG 1653
1 GGAAGGCGCAATCATCATAGTAAGAGCGCGAGAGAAATACAGCAGAACATGAG 60

1654 ACCACAGGATCTCAGTATCTCGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1713
61 ACCACAGGATCTCAGTATCTCGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 120

1714 ATAGAGTCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCTTCGGAAGGCTCT 1773
121 ATAGATCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCTTCGGAAGGCTCT 180

1774 GCTCAGGCTCGCTTGGCTTCATCCAGATCCCACTTTTGAATGTGAACACATCT 1833
181 GCTCAGGCTCGCTTGGCTTCATCCAGATCCCACTTTTGAATGTGAACACATCT 240

1834 GACTATCAAGGCTGTGGATAGCAAGATCTTTTCGGGTTCCGACAAACAGTGGCTGC 1893
241 GACTATCAAGGCTGTGGATAGCAAGATCTTTTCGGGTTCCGACAAACAGTGGCTGC 300

1894 TTATCAGATCAACTAGTGCCAAATCTCGAGAGCGCTGAGTTCATCTCAGCCCAAT 1953
301 TTATCAGATCAACTAGTGCCAAATCTCGAGAGCGCTGAGTTCATCTCAGCCCAAT 360

1954 GAGTTCAGTCCAGACTTTCTACGGCTTACGCTTACTATGACAGTCAAGCAACACAG 2013
361 GAGTTCAGTCCAGACTTTCTACGGCTTACGCTTACTATGACAGTCAAGCAACACAG 420

2014 GTGCCAATTAGTCAAGGATGGCTCAGAGTGGAGCCACCAACACCATTCGAACCAA 2073
421 GTGCCAATTAGTCAAGGATGGCTCAGAGTGGAGCCACCAACACCATTCGAACCAA 480

2074 ATAAATACGGACCCCAAGCCAGCGCCCAACCAACTTTTACAGATC 2118
481 ATAAATACGGACCCCAAGCCAGCG-CCCAACCACTTTTACAGATC 524

RESULT 13
AAA47618
ID AAA47618 standard; cDNA; 2335 BP.
XX
AC AAA47618;
XX
08-NOV-2000 (first entry)
XX
DE KCNQ4 Potassium channel gene.
XX
KW KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;
KW deafness; probes; treatment; therapy; transgenic animal; antibody;
KW agonist; antagonist; tinnitus; hearing loss; neonatal deafness;
KW presbycusis; affective disorder; Alzheimer's disease; anxiety; ataxia;
KW cognitive deficits; compulsive behavior; dementia; depression;
KW Huntington's disease; mania; memory impairment; motor disorders;
KW neurodegenerative disease; Parkinson's disease; pick's disease;
KW psychosis; schizophrenia; spinal cord damage; stroke; tremor; ds.
XX
OS Homo sapiens.

Key Location/Qualifiers
CDS 83..2170
/*tag= a
/product= "KCNQ4 Potassium channel polypeptide"

WO200044786-A1.
XX
03-AUG-2000.
XX
19-JAN-2000; 2000WO-DK000024.
XX
26-JAN-1999; 99DK-00000076.
XX
19-MAY-1999; 99DK-00000693.
XX
(NEUR-) NEUROSEARCH AS.
XX
Jentsch TJ;
XX
WPI: 2000-548813/50.
XX
P-PSDB; AAB01476.
XX
Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's diseases.
XX
Claim 1; Page 43-48; 65pp; English.
XX
Mutations in 3 known genes of the KCNQ branch of the potassium channel gene family underlie inherited cardiac arrhythmias, neonatal epilepsy and in some cases associated with deafness. KCNQ4 has been mapped to the DFN2 locus for autosomal dominant hearing loss, and a dominant negative KCNQ4 mutation that causes deafness in a DFN2 pedigree has been identified. KCNQ4 is the first potassium channel gene underlying non-syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4 protein and the protein itself may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate KCNQ4 expression. The nucleotides may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples and to identify mutations within them, and hence which patients may be in need of restorative therapy. They may also be used to study the expression and function of KCNQ4 polypeptides and their role in metabolism, for example through the production of transgenic animals. The KCNQ4 polypeptides may be used as (agonists and antagonists) of KCNQ4 expression and activity. The anti-KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate KCNQ4 expression and activity. They may be used in this way to treat tinnitus, loss of hearing (especially progressive hearing loss, neonatal deafness and presbycusis (deafness of the elderly)) and disease or adverse conditions of the central nervous system (CNS) such as affective disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative illness, cognitive deficits, compulsive behavior, dementia, depression, Huntington's disease, mania, memory impairment, motor disorders and dysfunctions, motion disorders, Parkinson-like motor disorders, phobias, pick's disease, psychosis, schizophrenia, spinal cord damage, stroke and/or tremor. Conversely, antisense nucleic acid molecules may be administered to down regulate KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing their expression

Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Query Match 18.4%; Score 492; DB 3; Length 2335;
Best Local Similarity 59.3%; Pred. No. 1e-133;
Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;

217 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
218 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
219 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
220 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
221 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
222 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
223 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
224 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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226 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
227 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
228 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
229 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
230 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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238 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
239 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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242 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
243 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
244 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
245 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
246 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
247 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
248 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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264 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
265 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
266 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
267 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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269 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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272 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
273 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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281 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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284 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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305 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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307 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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309 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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319 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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327 TACCGCGCGGTGCAGAACTACTCTGACAACTGCTGAGAGAGACCCCGCGGTGGCGTTC 276
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PR	15-MAR-2002;	2002US-0364529P.	Db	440	ACTATCCAGGAGCACCCAGGAACCTTGCCAAACGAGTGTCTCTCATCTTGGAAATTCGTGATG	499
PR	19-APR-2002;	2002US-0373861P.	Qy	397	ATTGTGCTTTTGGTTTGGAGTTTCAATTCGAAATCTGCTCGCGGTTGCTGTTGTGCA	456
PR	29-JUN-2002;	2002US-0376287P.	Db	500	ATCGTGGTTTTCGGCTTGGAGTACATCGTCCGGGTTCGGTCCGCGGATGCTGCTGCCGC	559
PR	24-JUN-2002;	2002US-0390971P.	Qy	457	TATAGAGGATGCAAGAGAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTGTTTATAGATACC	516
PR	03-JUL-2002;	2002US-03941130P.	Db	560	TACCGAGGATGGCAGGTCGCTCCGCTTGGCAGAAAGCCCTTCTGTGTCATCGACTTC	619
PR	10-JUL-2002;	2002US-0394797P.	Qy	517	ATTGTTCTTATCGCTTCAATAGCAGTTGTTCTGCAAAAACCTCAGGGTATATTTTGGC	576
PR	21-AUG-2002;	2002US-0404904P.	Db	620	ATCGTGTTCGTGGCTCGGTGCGGTATCGCGCGGGTACCCAGGGCAACATCTTCGCC	679
PR	04-SEP-2002;	2002US-0408070P.	Qy	577	ACGTCTGCACTCAGAACTCTCGTTTCTTACAGATCCTCCGATGCTGCGCATGGCCATGACCA	636
PR	06-NOV-2002;	2002US-0424300P.	Db	680	ACGTCCGCGTGGCAGCATGCGCTTCTTGCAGATCTCTGGCATGGTGGCATGGACCGC	739
PR	05-DEC-2002;	2002US-0431042P.	Qy	637	AGGGAGGACATTTGGAAATTAATCTGGGTTTCACTGGGTTTATGCTCACAGCAAGAAATTAATC	696
PR	05-DEC-2002;	2002US-0431079P.	Db	740	CGCGCGGCACCTGGAAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGAGCTGATC	799
XX	(MILL-) MILLENNIUM PHARM INC.		Qy	697	ACAGTTGGTACATAGGATTTTGGTTCTTATTTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTT	756
XX	Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;		Db	800	ACGCTTGGTACATCGGGTTCCTGGTGTCTATCTTCGCTTCTTCTTCTTCTTCTTCTTCTTCTT	859
PI	Stagliano N, Perodin J, Rodrigue-Way A;		Qy	757	GAAGAGATGCCAATAAAGATTTTCTACATATGAGATGCTCTCTGGTGGGGCACAAT	816
PI	WPI; 2003-731468/69.		Db	860	GAGAAGACCCCAACTCCGACTTCTCTCTAGCCGACTGCTCTCTGTTGGGGACGATT	919
DR	P-PSDB; ADE31699.		Qy	817	ACATTGACAACTATTTGGCTATGAGACAAACCTCCCTTAACCTTGGCTGGGAAGATTGCTT	876
XX	Identifying a compound capable of treating a cardiovascular disorder		Db	920	ACATTGACAACTATTTGGCTATGAGACAAACCTCCCTTAACCTTGGCTGGGAAGATTGCTT	979
XX	(e.g. atherosclerosis) comprises assaying the ability of the compound to		Qy	877	TCGCGAGCTTTCGACTCTCTTGGCTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	936
PT	modulate the expression or activity of e.g. 1682, 6169 or 6193		Db	980	GCTGCTGGCTTCGCTTACTTGGGCTATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1039
PT	polypeptide or nucleic acid.		Qy	937	TCAGTTTTCGATTAAGATFACAGAACACACCGCCAGAAACACTTTTGAGAAAAGAG	996
PS	Disclosure; SEQ ID NO 55; 328pp; English.		Db	1040	TCGGCTTTCGCTTGAAGTCCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1099
CC	The invention relates to a method for identifying a compound capable of		Qy	997	AACCCAGCTGCCAACCTTCACTTATGAGTGTGTTGGGTAGTTTACGAGCTGATGAGAAATCT	1056
CC	treating a cardiovascular disorder. The present invention identifies the		Db	1100	ATGCGGCGAGCAACCTTATCCAGGCTGCTGGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTT	1159
CC	differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,		Qy	1057	GTTCCTTCACTTGAAGCCACACTTGAAGCCCTTGCACAC	1100
CC	43726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,		Db	1160	GCCTTACCTGACGACCTGTTACTTATGACAGTATCTTCTTCTTCTTCTTCTTCTTCTTCTT	1219
CC	33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484,		Qy	1101	-----	1100
CC	345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,		Db	1220	GCCCTCTTGTGAGCAGTGAACCGGCGCAATGGGGCTTACGCGCCCTTGGAGGTG	1279
CC	2868, 283, 2534, 9464, 17799, 26686, 43848, 32135, 13208, 2914, 51130,		Qy	1101	-----	1100
CC	19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or		Db	1280	CGCGGGCGCGGTACCCGAGCAGCACCTTCCGTTTACCGCCCGTGTGCCACCTGCCAC	1339
CC	6585 genes in cardiovascular disease states. The methods are useful in		Qy	1101	-----CTGCAGCCCTTACCAATCAGAACTTAAGTTTTPAAGAGCGCA	1140
CC	diagnosing, preventing and treating cardiovascular disorders, such as		Db	1340	CGCGGGGAGCAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1399
CC	atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,		Qy	1141	GTGCGCATGTTAGCCCGCAGGGCCAGAGTATTT-----AAGAGCCGACAGCTTCAGTA	1194
CC	restenosis, arterial inflammation, vascular wall remodeling, coronary		Db	1400	ATCCGATGGGAGCTCCCGAGCGGACCGGTCTCTTCCAGAGCAGCTGGCACCTTCCA	1459
CC	microembolism, tachycardia, bradycardia, pressure overload, aortic		Qy	1195	GGTACAGGAGGTCCCAAGCACACGACATCACACCGAGG---GCAGTCCCAACAAAGTG	1251
CC	bending, coronary artery ligation, vascular heart disease, valvular		Db	1460	ACAATGCCACCTTCCCAAGCAGCAGCAGCTGGGTGGGTCAGCCACCCACCAAGTG	1519
CC	disease, including but not limited to, valvular degeneration caused by		Qy	1252	CAGAAGAGCTGGAGCTTCAACGACCGAAACCGCTTTCGGGCCCTCGTGGCTCCTAAAGT	1311
CC	calcification, rheumatic heart disease, endocarditis, or complications of		Db	1520	CAANAGAGCTGGAGCTTCAATGACCGCACCGCTTCCGGGCTCTCTGAGACTC-----	1573
CC	artificial valves; atrial fibrillation, long-QT syndrome, congestive					
CC	heart failure, sinus node dysfunction, atrial flutter, pericardial disease,					
CC	hypertension, atrial fibrillation, pericardial effusion and pericarditis;					
CC	including but not limited to, pericardial effusion or idiopathic					
CC	cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic					
CC	cardiomyopathy, myocardial infarction, coronary artery disease, coronary					
CC	artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and					
CC	cardiovascular developmental disorders. The methods may also be used for					
CC	identifying compounds that modulate cardiovascular disorders. Sequences					
CC	given in ADE31644-ADE31769 represent the genes and proteins that may be					
CC	regulated by a compound of the invention.					
XX	Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;					
SQ						
	Query Match	18.4%; Score 492; DB 10; Length 2335;				
	Best Local Similarity	59.3%; Pred. NO. 1e-133;				
	Matches 1087; Conservative	0; Mismatches 555; Indels 192; Gaps 7;				
Qy	217	TACCGGGGTGAGAACTACCTGTACACGCTGAGAGACCCCGCGGCTGGCGTTC	276			
Db	320	TACCGGGGTGAGAACTACCTGTACACGCTGAGAGACCCCGCGGCTGGCGTTC	379			
Qy	277	ATCTACACGCTTTCGTTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	336			
Db	380	GTCTACACGCTTTCATATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	439			
Qy	337	ACCATCCCTGAGCACAAATTTGGCTTCAAGTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	396			

Tue Apr 12 17:15:11 2005

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Db 667 TCGGTAGTCTACGCTCAGCAGGAAGTGGTACTGCTGGTACATTTGGCTTCTCTGC 726
Qy 724 CTTATTTTCTCTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 783
Db 727 CTCATCTTGGCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 786
Qy 784 ACATATGAGATGCTCTCTGCTGGGACAAATTAATTGACAACTATTTGCTATGAGAC 843
Db 787 ACCTAGCAGATGCACTCTGCTGGGCTGTGATCACTCCCTGACGACATTTGGCTACGGGAC 846
Qy 844 AAACTCCCTTAACTTGGCTGGGAGATTGCTTCTGAGGCTTTGCACTCTCTTGGCAT 903
Db 847 AAGTACCTCAGACCTGAAACGGGAGGCTGCTGGAGGACCTTTACCTCATTTGGTGC 906
Qy 904 TCTTTCTTTGCACTTCTCTGCGGATCTTGGCTCAGTTTGGATTTGAATTAAGTACAAGAA 963
Db 907 TCGTTCTTTGCTCTTCCGCTGGCATTTTGGGATCCGGCTTTGGCTGAAAGTCCAAGAG 966
Qy 964 CAACACCGCAGAAACACTTTGAGAAAGAGGACCCAGCTGCCAACCTCATTCAGTGT 1023
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Qy 1024 GTTGGCGTAGTTACGCACTGAT----- 1047
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Qy 1648 CATGAGACCAGACAGATCTCAGTATGCTCGTGGTGGTCAAGCTTGAACAAACAGTA 1707
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Job time : 1388.59 secs

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 10:31:37 ; Search time 1484.49 Seconds
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Title: US-09-810-796-3

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2662.2	99.8	2772	18	US-10-803-268-1
4	2662.2	99.8	3111	9	US-09-825-147-3
5	2662.2	99.8	3111	18	US-10-803-268-3
6	2630	98.6	2694	9	US-09-866-020-1
7	2630	98.6	2694	9	US-09-810-796-2
8	2630	98.6	2694	19	US-10-948-493-1
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13	492	18.4	2335	17	US-10-353-690-55	Sequence 55, Appl
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15	489.2	18.3	2273	16	US-10-096-578-88	Sequence 88, Appl
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17	475.6	17.8	2169	14	US-10-131-685-22	Sequence 22, Appl
18	472.2	17.7	7411	18	US-10-335-053-6	Sequence 6, Appli
19	472.2	17.7	7420	17	US-10-295-027-281	Sequence 281, App
20	472.2	17.7	7420	18	US-10-643-795A-75	Sequence 75, Appl
21	472.2	17.7	7420	19	US-10-948-518-75	Sequence 75, Appl
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25	465	17.4	548	10	US-09-826-734-269	Sequence 269, App
26	452	16.9	575	15	US-10-313-542-305	Sequence 305, App
27	445.2	16.7	5595	18	US-10-820-307-8	Sequence 8, Appli
28	427.4	16.0	1848	18	US-10-744-796-5	Sequence 5, Appli
29	427.2	16.0	2565	13	US-10-128-870-26	Sequence 26, Appl
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38	424.2	15.9	4512	15	US-10-084-817-334	Sequence 334, App
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40	423.4	15.9	1425	10	US-09-960-706-511	Sequence 511, App
41	423.4	15.9	1425	10	US-09-873-319-313	Sequence 313, App
42	423.4	15.9	1425	16	US-10-116-712-662	Sequence 662, App
43	423.4	15.9	1878	18	US-10-744-796-3	Sequence 3, Appli
44	423.4	15.9	1932	18	US-10-744-796-1	Sequence 1, Appli
45	423.4	15.9	2619	15	US-10-345-680-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

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Best Local Similarity 100.0%; Pred. No. 0;
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[illegible]

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; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. US20020042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
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; ORGANISM: homo sapiens
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; Sequence 1, Application US/10803268				
; Publication No. US20040157259A1				
; GENERAL INFORMATION:				
; APPLICANT: Hu, Yi				
; APPLICANT: Kieke, James Alvin				
; APPLICANT: Turner, C. Alexander Jr.				
; APPLICANT: Nehls, Michael C.				
; APPLICANT: Friedrich, Glenn				
; APPLICANT: Zambrowicz, Brian				
; APPLICANT: Sands, Arthur T.				
; TITLE OF INVENTION: Novel Human Ion Channel Protein and				
; TITLE OF INVENTION: Polynucleotides Encoding the Same				
; FILE REFERENCE: LEX-0160-USA				
; CURRENT APPLICATION NUMBER: US/10/803,268				
; CURRENT FILING DATE: 2004-03-18				
; PRIOR APPLICATION NUMBER: US/09/825,147				
; PRIOR FILING DATE: 2001-04-03				
; PRIOR APPLICATION NUMBER: US 60/194,255				
; PRIOR FILING DATE: 2000-04-03				
; NUMBER OF SEQ ID NOS: 3				
; SOFTWARE: FastSeq for Windows Version 4.0				
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; TYPE: DNA				
; ORGANISM: homo sapiens				
US-10-803-268-1				
Query Match 99.8%; Score 2662.2; DB 18; Length 2772;				
Best Local Similarity 99.9%; Pred. No. 0;				
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1	ATGAAGGATGTGGAGTCCGGGCGGGGCGAGGGTGTCTGTGAACCTCGGCAGCGCCAGGGGC	60	
Db	106	ATGAAGGATGTGGAGTCCGGGCGGGGCGAGGGTGTCTGTGAACCTCGGCAGCGCCAGGGGC	165	
QY	61	GACGGCTGTACTCTGGGCACCCGGCGGCCACGGTTGGTGGCGGGCGGTGGCCCTG	120	
Db	166	GACGGCTGTACTCTGGGCACCCGGCGGCCACGGTTGGTGGCGGGCGGTGGCCCTG	225	
QY	121	AGCGAGAGCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGTCTGGGGAAGCCGCTCTCT	180	
Db	226	AGCGAGAGCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGTCTGGGGAAGCCGCTCTCT	285	
QY	181	TACAGAGTAGCAGACTCCGGCGCAACCTCAAGTACCCGGCGGTGCAGAACTACCTG	240	
Db	286	TACAGAGTAGCAGACTCCGGCGCAACCTCAAGTACCCGGCGGTGCAGAACTACCTG	345	

QY	1261	TGGAGCTTCAACGACCGAACCCGCTTCGGGCCCTCGCTCGCCCTCAAAAGTTCTCAGCCA	1320
Db	1366	TGGAGCTTCAACGACCGAACCCGCTTCGGGCCCTCGCTCGCCCTCAAAAGTTCTCAGCCA	1425
QY	1321	AAACCAAGTATAGATGCTGCACACAGCCCTTGGCACTGATGATGATATGATGAAAAAGGA	1380
Db	1426	AAACCAAGTATAGATGCTGCACACAGCCCTTGGCACTGATGATGATATGATGAAAAAGGA	1485
QY	1381	TGCCAGTGTGATGATCACTGAGGAACACCTCACCCACCACTTAAAACTGTCTATTCGAGCT	1440
Db	1486	TGCCAGTGTGATGATCACTGAGGAACACCTCACCCACCACTTAAAACTGTCTATTCGAGCT	1545
QY	1441	ATCAGAAATTATGAAATTTTCATGTTGCAAAACGGAAGTTTAAAGAAACGTTACGTCCCATAT	1500
Db	1546	ATCAGAAATTATGAAATTTTCATGTTGCAAAACGGAAGTTTAAAGAAACGTTACGTCCCATAT	1605
QY	1501	GATGTAAGAGATGTCATTCGAAACAAATATTCGTCTGCTCATCTGGACATCTGTGTAGAAATT	1560
Db	1606	GATGTAAGAGATGTCATTCGAAACAAATATTCGTCTGCTCATCTGGACATCTGTGTAGAAATT	1665
QY	1561	AAAAGCCTTCAAAACACGCTGTTGATCAAAATCTTTGGAAAGGGCAAAATCACATCAGATAAG	1620
Db	1666	AAAAGCCTTCAAAACACGCTGTTGATCAAAATCTTTGGAAAGGGCAAAATCACATCAGATAAG	1725
QY	1621	AAGAGCCGAGAGAAATATACAGCAGAAACATGAGACACAGACGATCTCAGTATGTCGGT	1680
Db	1726	AAGAGCCGAGAGAAATATACAGCAGAAACATGAGACACAGACGATCTCAGTATGTCGGT	1785
QY	1681	CGGTGCTCAAGGTTGAAAAACAGGTACAGTCAATAGATCCAAAGCCTGTGGATAGCAAA	1740
Db	1786	CGGTGCTCAAGGTTGAAAAACAGGTACAGTCAATAGATCCAAAGCCTGTGGATAGCAAA	1845
QY	1741	GACATCTATCAACAGGTCCTTTCCGAAAGGCTCGCCTCAGCCCTCGCTTTGGCTTCAATTC	1800
Db	1846	GACATCTATCAACAGGTCCTTTCCGAAAGGCTCGCCTCAGCCCTCGCTTTGGCTTCAATTC	1905
QY	1801	CAGATCCCACCTTTTGAATGTGAACGACATCTGACTATCAAAAGCCTGTGGATAGCAAA	1860
Db	1906	CAGATCCCACCTTTTGAATGTGAACGACATCTGACTATCAAAAGCCTGTGGATAGCAAA	1965
QY	1861	GATCTTTGCGGTTCCGACAAACAGTGGCTGCTTATCCAGATCAACTAGTGCACATC	1920
Db	1966	GATCTTTGCGGTTCCGACAAACAGTGGCTGCTTATCCAGATCAACTAGTGCACATC	2025
QY	1921	TCGAGAGGCTGCAAGTTCAATTCGACGCCAAATGAGTTCAAGTCCACAGACTTTCTACGG	1980
Db	2026	TCGAGAGGCTGCAAGTTCAATTCGACGCCAAATGAGTTCAAGTCCACAGACTTTCTACGG	2085
QY	1981	CTTAGCCCTACTATGCAAGTCAAGAAACACAGTGCCTTATCAAGCGATGGCTCA	2040
Db	2086	CTTAGCCCTACTATGCAAGTCAAGAAACACAGTGCCTTATCAAGCGATGGCTCA	2145
QY	2041	GCAGTGGCAGCCACCAACACCATTTGCAAAACCAATAAATAGCGACCCAGCCAGCGC	2100
Db	2146	GCAGTGGCAGCCACCAACACCATTTGCAAAACCAATAAATAGCGACCCAGCCAGCGC	2205
QY	2101	CCAAACACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA	2160
Db	2206	CCAAACACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA	2265
QY	2161	ACTCTGCAACCTTAACCCCTGAGGCTTACAGGAAAGCATTTCTGACGTCAACACTGCTTT	2220
Db	2266	ACTCTGCAACCTTAACCCCTGAGGCTTACAGGAAAGCATTTCTGACGTCAACACTGCTTT	2325
QY	2221	GTTGCTCCAAAGGAAATGTTCAAGTTGCAAGTCAAAATCTCACCAGGACCGTCTATG	2280
Db	2326	GTTGCTCCAAAGGAAATGTTCAAGTTGCAAGTCAAAATCTCACCAGGACCGTCTATG	2385
QY	2281	AGGAAAGCTTTGACATGGAGGAGAACTCTGTTGCTGCTCTGTCCTCATGTTGCCGAG	2340
Db	2386	AGGAAAGCTTTGACATGGAGGAGAACTCTGTTGCTGCTCTGTCCTCATGTTGCCGAG	2445

QY	241	TACAACGTCGTGGAGAGACCCCGCGCTGGCGCTTCATCTACCAACGCTTTCGTTTTCTC	300
Db	346	TACAACGTCGTGGAGAGACCCCGCGCTGGCGCTTCATCTACCAACGCTTTCGTTTTCTC	405
QY	301	CTTGCTTTGGTGGCTGATTTTGTGTCAGTGTGTTTCTACCATCCCTGAGACACAAATTTG	360
Db	406	CTTGCTTTGGTGGCTGATTTTGTGTCAGTGTGTTTCTACCATCCCTGAGACACAAATTTG	465
QY	361	GCCTCAAGTTGCTCTTGATCCCTGGAGTTGTCGATGATTCGTCTTTGGTTGGAGTTC	420
Db	466	GCCTCAAGTTGCTCTTGATCCCTGGAGTTGTCGATGATTCGTCTTTGGTTGGAGTTC	525
QY	421	ATCATTTGCAATCTGGTCTGCGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGCTG	480
Db	526	ATCATTTGCAATCTGGTCTGCGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGCTG	585
QY	481	AGTTTTCGTCGAAAGCCCTTCTGTTTATAGATACCATTTGTTATCGCTTCAATAGCA	540
Db	586	AGTTTTCGTCGAAAGCCCTTCTGTTTATAGATACCATTTGTTATCGCTTCAATAGCA	645
QY	541	GTGTTTCTGCAAAACTCAGGGTAATATTTTGGCCACGTCCTGACATCAGAGTCTCCGT	600
Db	646	GTGTTTCTGCAAAACTCAGGGTAATATTTTGGCCACGTCCTGACATCAGAGTCTCCGT	705
QY	601	TTCTACAGATCCTCCGATGTCGTCATGGACCGAAGGGAGGCACTTGGAAATTTACTG	660
Db	706	TTCTACAGATCCTCCGATGTCGTCATGGACCGAAGGGAGGCACTTGGAAATTTACTG	765
QY	661	GGTTCAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATTTTGG	720
Db	766	GGTTCAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATTTTGG	825
QY	721	GTTCCTATTTTTCGTCCTTCTGTCATCTGGTGGAAAGATGCCAATAAGAGTTT	780
Db	826	GTTCCTATTTTTCGTCCTTCTGTCATCTGGTGGAAAGATGCCAATAAGAGTTT	885
QY	781	TCTACATATCGAGATCTCTCTGGTGGGCACAAATTTACATTTGCAACTATTGGCTATGGA	840
Db	886	TCTACATATCGAGATCTCTCTGGTGGGCACAAATTTACATTTGCAACTATTGGCTATGGA	945
QY	841	GACAAACTCCCTAACTGGCTGGGAAGATTCGTTTCTGAGGCTTTCGATCTCCTGGC	900
Db	946	GACAAACTCCCTAACTGGCTGGGAAGATTCGTTTCTGAGGCTTTCGATCTCCTGGC	1005
QY	901	ATTCTTTCTTTCGACTCTCCTCGGCATTTCTGGCTCAGGTTTTCATTTAAAGTACAA	960
Db	1006	ATTCTTTCTTTCGACTCTCCTCGGCATTTCTGGCTCAGGTTTTCATTTAAAGTACAA	1065
QY	961	GAACAAACCCGCGAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCCAACCTCATTTAG	1020
Db	1066	GAACAAACCCGCGAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCCAACCTCATTTAG	1125
QY	1021	TGTGTTGGGTAGTTACGAGCTGATGAGAAATCTGTTTTCATTTGCAACCTGGAGGCA	1080
Db	1126	TGTGTTGGGTAGTTACGAGCTGATGAGAAATCTGTTTTCATTTGCAACCTGGAGGCA	1185
QY	1081	CACTTGAAGGCTTGCACACCTGCAGCCCTACCAATCAGAACTAAGTTTAAAGAGGGA	1140
Db	1186	CACTTGAAGGCTTGCACACCTGCAGCCCTACCAATCAGAACTAAGTTTAAAGAGGGA	1245
QY	1141	GTGCGCATGGCTAGCCCGGAGGCGCAGAGTATTAGAGCCGACAAAGCCCTCAGTAGGTGAC	1200
Db	1246	GTGCGCATGGCTAGCCCGGAGGCGCAGAGTATTAGAGCCGACAAAGCCCTCAGTAGGTGAC	1305
QY	1201	AGGAGTCCCGAAGCACCGACATCACAGCCGAGGAGTCCCAACCAAGTGAGAGAGC	1260
Db	1306	AGGAGTCCCGAAGCACCGACATCACAGCCGAGGAGTCCCAACCAAGTGAGAGAGC	1365
QY	1261	TGAGGCTTCAACGACCGAACCGCTTTCGCGCCCTCGCTCGGCTCAAAAGTTCTCAGCCA	1320
Db	1366	TGAGGCTTCAACGACCGAACCGCTTTCGCGCCCTCGCTCGGCTCAAAAGTTCTCAGCCA	1425
QY	1321	AAACCAAGTATAGATCTGACACAGCCCTTGGCACTGATGATGATATATGATGAAAAAGGA	1380
Db	1426	AAACCAAGTATAGATCTGACACAGCCCTTGGCACTGATGATGATATATGATGAAAAAGGA	1485
QY	1381	TGCCAGTGTGATGTATCAGTGGAGAGACCTCACCCACCACTTTAAACCTGTCAATCAGCT	1440
Db	1486	TGCCAGTGTGATGTATCAGTGGAGAGACCTCACCCACCACTTTAAACCTGTCAATCAGCT	1545
QY	1441	ATCAGAAATTTATCAAAATTTTCATGTTCCAAAACCGGAAGTTTAAAGGAACGTTAGCTCCATAT	1500
Db	1546	ATCAGAAATTTATCAAAATTTTCATGTTCCAAAACCGGAAGTTTAAAGGAACGTTAGCTCCATAT	1605
QY	1501	GATGTAAGAGATGTCTATTGAAACAAATTTCTGCTGGTCACTCGACATGTTGTGTAATTT	1560
Db	1606	GATGTAAGAGATGTCTATTGAAACAAATTTCTGCTGGTCACTCGACATGTTGTGTAATTT	1665
QY	1561	AAAAAGCTTCAAAACAGTGTTCATCAAAATTTCTTGGAAAAGGGCAATCAATCAGATAAG	1620
Db	1666	AAAAAGCTTCAAAACAGTGTTCATCAAAATTTCTTGGAAAAGGGCAATCAATCAGATAAG	1725
QY	1621	AAGAGCCGAGAGAAAATAACAGCAGAAATAGAGACACAGACGATCTCAGTAGTCTCGGT	1680
Db	1726	AAGAGCCGAGAGAAAATAACAGCAGAAATAGAGACACAGACGATCTCAGTAGTCTCGGT	1785
QY	1681	CGGTTGGTCAAGTTTGAATAATGTGAAACAGGTACAGTCCATAGAGTCCAAAGCTGACTCTA	1740
Db	1786	CGGTTGGTCAAGTTTGAATAATGTGAAACAGGTACAGTCCATAGAGTCCAAAGCTGACTCTA	1845
QY	1741	GACATCTATCAACAGGTCCTTCGAAAAGGCTCTGCTCAGCCCTGCTTTGGTTCATTTTC	1800
Db	1846	GACATCTATCAACAGGTCCTTCGAAAAGGCTCTGCTCAGCCCTGCTTTGGTTCATTTTC	1905
QY	1801	CAGATCCCAACCTTTTGAATGTGAAACAGACATCTGACTACTCAAAAGCCCTGTGGATAGCAA	1860
Db	1906	CAGATCCCAACCTTTTGAATGTGAAACAGACATCTGACTACTCAAAAGCCCTGTGGATAGCAA	1965
QY	1861	GATCTTTTCGGGTTCCGCAAAACAGTGGCTCTTATCCAGATCAACTAGTGCACATC	1920
Db	1966	GATCTTTTCGGGTTCCGCAAAACAGTGGCTCTTATCCAGATCAACTAGTGCACATC	2025
QY	1921	TGAGAGGCTGTCAGTTTCAATTTGAGCCCAATAGATTCAGTGGCCAGACTTTTCTACGGG	1980
Db	2026	TGAGAGGCTGTCAGTTTCAATTTGAGCCCAATAGATTCAGTGGCCAGACTTTTCTACGGG	2085
QY	1981	CTTAGCCCTACTATGACAGTCAAGCAACAGAGTGCCTTCTGAGCCCAATAGTCAAGCCATG	2040
Db	2086	CTTAGCCCTACTATGACAGTCAAGCAACAGAGTGCCTTCTGAGCCCAATAGTCAAGCCATG	2145
QY	2041	GCAGTGGCAGCCCAACCAACCATTTGCAAAACCAATTAATAACGCAACCAAGCCAGCAGCC	2100
Db	2146	GCAGTGGCAGCCCAACCAACCATTTGCAAAACCAATTAATAACGCAACCAAGCCAGCAGCC	2205
QY	2101	CCAAACAACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCCAGGCCAGAA	2160
Db	2206	CCAAACAACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCCAGGCCAGAA	2265
QY	2161	ACTCTGACCCCTAACCCCTGAGGCTTACAGGAAGCAATTTCTGAGTCAACCACTGCTT	2220
Db	2266	ACTCTGACCCCTAACCCCTGAGGCTTACAGGAAGCAATTTCTGAGTCAACCACTGCTT	2325
QY	2221	GTTCCTCCAAAGGAAATGTTTCAGGTTGCAAGTCAAAATCTCACCAGGACCGCTTCTATG	2280
Db	2326	GTTCCTCCAAAGGAAATGTTTCAGGTTGCAAGTCAAAATCTCACCAGGACCGCTTCTATG	2385
QY	2281	AGGAAAGCTTTGACATGGAGGAGAACTCTGTTGTCTGTCTGTCTGTCCATGTGTGGCGAAG	2340
Db	2386	AGGAAAGCTTTGACATGGAGGAGAACTCTGTTGTCTGTCTGTCTGTCCATGTGTGGCGAAG	2445
QY	2341	GACTTTGGGCAAACTTTCTGTGTGCAAAACCTGATCAGGTGCACCGAGAACTGTAATATA	2400
Db	2446	GACTTTGGGCAAACTTTCTGTGTGCAAAACCTGATCAGGTGCACCGAGAACTGTAATATA	2505
QY	2401	CAACTTTTCAGGAGTGTAGTCAAGTGGCTCCAGAGGCGACCAAGATTTTTTACCCCAATGG	2460

Db 2506 CAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGCGCAGCAAGATTTTACCCCAAAATGG 2565
 Qy 2461 AGGGAATCCAAATTTTAACTGATGAAGAGTGGTCCCGAAGAGCAGAGACAGAC 2520
 Db 2566 AGGGAATCCAAATTTTAACTGATGAAGAGTGGTCCCGAAGAGCAGAGACAGAC 2525
 Qy 2521 ACTTTTGATCGCGACCGCAGCCTGCCAGGGAAGCTGCTTTTGATCAGACTCTCTTAAGG 2580
 Db 2626 ACTTTTGATCGCGACCGCAGCCTGCCAGGGAAGCTGCTTTTGATCAGACTCTCTTAAGG 2685
 Qy 2581 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAAGCAGAGAAAGTACAGATGCCCTC 2640
 Db 2686 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAAGCAGAGAAAGTACAGATGCCCTC 2745
 Qy 2641 AGCTTGCCTCATGTCAAACTGAATAA 2667
 Db 2746 AGCTTGCCTCATGTCAAACTGAATAA 2772

RESULT 4

US-09-825-147-3
 ; Sequence 3, Application US/09825147
 ; Patent No. US20020042505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kieke, James Alvin
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael C.
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0160-USA
 ; CURRENT APPLICATION NUMBER: US/09/825,147
 ; CURRENT FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/194,255
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 3111
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-09-825-147-3

Query Match 99.8%; Score 2662.2; DB 9; Length 3111;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ATGAAGGATGTGAGTCGGCGCGGGCAGGGTCTGCTGAACTCGGCAGCCCGCAGGGGC 60
 Db 165 ATGAAGGATGTGAGTCGGCGCGGGCAGGGTCTGCTGAACTCGGCAGCCCGCAGGGGC 224
 Qy 61 GACGGCTGTACTGTGGCACCCGCGGGCAGCCTGGTGGCGGGCGGGTGGCCTG 120
 Db 225 GACGGCTGTACTGTGGCACCCGCGGGCAGCCTGGTGGCGGGCGGGTGGCCTG 284
 Qy 121 AGGAGAGCGCGCGGGCAAGCAGCGGGCGCCGATGAGCCTGTGGGGAGCGGCTCTCT 180
 Db 285 AGGAGAGCGCGCGGGCAAGCAGCGGGCGCCGATGAGCCTGTGGGGAGCGGCTCTCT 344
 Qy 181 TACAGAGTAGCAGACTCGCGGCAAGCTCAAGTACCGGGGTGCAAGACTACCTG 240
 Db 345 TACAGAGTAGCAGACTCGCGGCAAGCTCAAGTACCGGGGTGCAAGACTACCTG 404
 Qy 241 TACAACGTGTGGAGAGACCCCGGGTGGCGGTTCATCTACACGCTTTTCGTTTTTCTC 300
 Db 405 TACAACGTGTGGAGAGACCCCGGGTGGCGGTTCATCTACACGCTTTTCGTTTTTCTC 464
 Qy 301 CTTGCTTTGGTGTGATTTTGTAGTTTCTACCATCTCCCTGAGCAGCAAAATG 360

Db 465 CTTGCTTTGGTGTGATTTTGTGCTGCTTCTACCATCTCCCTGAGCAGCAAAATG 524
 Qy 361 GCCTCAAGTTGCTCTTGATATCTGAGTCTGATGATGCTGCTTTGGTTGAGTTG 420
 Db 525 GCCTCAAGTTGCTCTTGATATCTGAGTCTGATGATGCTGCTTTGGTTGAGTTG 584
 Qy 421 ATCATTGGAATCTGCTGCGGTTGCTGTTGTCGATATAGAGATGGCAAGAGACTG 480
 Db 585 ATCATTGGAATCTGCTGCGGTTGCTGTTGTCGATATAGAGATGGCAAGAGACTG 644
 Qy 481 AGGTTTGTCTGAAAGCCCTTCTGTTATAGATACATTTGTTCTTATGCTTCAATAGCA 540
 Db 645 AGGTTTGTCTGAAAGCCCTTCTGTTATAGATACATTTGTTCTTATGCTTCAATAGCA 704
 Qy 541 GTTGTCTTGCAGAAACTCAGGGTAATTTTTCACAGCTGCTGCACTCAGAACTCTCGT 600
 Db 705 GTTGTCTTGCAGAAACTCAGGGTAATTTTTCACAGCTGCTGCACTCAGAACTCTCGT 764
 Qy 601 TTCTTACAGATCTCCGATGGTGGCATGGACCGAAGGGGAGGCATTTGGAATTTACTG 660
 Db 765 TTCTTACAGATCTCCGATGGTGGCATGGACCGAAGGGGAGGCATTTGGAATTTACTG 824
 Qy 661 GGTTCAGTGGTTATGCTCAGACAGGAATTAATCAGAGCTTGGTACATAGATTTTGG 720
 Db 825 GGTTCAGTGGTTATGCTCAGACAGGAATTAATCAGAGCTTGGTACATAGATTTTGG 884
 Qy 721 GTTCTTATTTTTCGTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 780
 Db 885 GTTCTTATTTTTCGTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 944
 Qy 781 TCTACATATGAGATGCTCTGTTGGGGCAATTTACATTTGACATTTGGCTATGGA 840
 Db 945 TCTACATATGAGATGCTCTGTTGGGGCAATTTACATTTGACATTTGGCTATGGA 1004
 Qy 841 GACAAACTCTCCCTTAACTTGGCTGGGAAGATTTCTTCTGAGGCTTTGCACTCTTGGC 900
 Db 1005 GACAAACTCTCCCTTAACTTGGCTGGGAAGATTTCTTCTGAGGCTTTGCACTCTTGGC 1064
 Qy 901 ATTTCTTTTCTTGGCTCTGCGGCATTTCTGGCTCAGTTTGGCTTGAATTAAGTACAA 960
 Db 1065 ATTTCTTTTCTTGGCTCTGCGGCATTTCTGGCTCAGTTTGGCTTGAATTAAGTACAA 1124
 Qy 961 GAACAAACCCGCGAGAACTTTGAGAAAGAGAACCCAGCTGCAACCTCATTTCAG 1020
 Db 1125 GAACAAACCCGCGAGAACTTTGAGAAAGAGAACCCAGCTGCAACCTCATTTCAG 1184
 Qy 1021 TGTGTTTGGCTAGTTACGAGCTGTAGAGAAATCTGTTTCCATTTGCAACTGGAAGCCA 1080
 Db 1185 TGTGTTTGGCTAGTTACGAGCTGTAGAGAAATCTGTTTCCATTTGCAACTGGAAGCCA 1244
 Qy 1081 CACTTGAAGGCTTTGCACTGAGCCCTACCATCAGAACTTAAGTTTAAGGAGCGA 1140
 Db 1245 CACTTGAAGGCTTTGCACTGAGCCCTACCAATCAGAACTTAAGTTTAAGGAGCGA 1304
 Qy 1141 GTGCGCATGCTAGCCCGGCGCAGAGTATTAAAGAGCGCAGAACTCAGTAGGTGAC 1200
 Db 1305 GTGCGCATGCTAGCCCGGCGCAGAGTATTAAAGAGCGCAGAACTCAGTAGGTGAC 1364
 Qy 1201 AGGAGTCCCCAAGCAGCAGCATCAGCCGAGGGCAGTCCCAAAAGTGCAGAGAGC 1260
 Db 1365 AGGAGTCCCCAAGCAGCAGCATCAGCCGAGGGCAGTCCCAAAAGTGCAGAGAGC 1424
 Qy 1261 TGGAGCTTCAACGACCGAACCCGCTTCGGCCCTCGCTCGCCCTCAAAAGTTCTCAGCCA 1320
 Db 1425 TGGAGCTTCAACGACCGAACCCGCTTCGGCCCTCGCTCGCCCTCAAAAGTTCTCAGCCA 1484
 Qy 1321 AAACAGGTGATAGTGTGACACAGCCCTTGGCACTGATGATGATATGATGAAAAAGGA 1380
 Db 1485 AAACAGGTGATAGTGTGACACAGCCCTTGGCACTGATGATGATATGATGAAAAAGGA 1544
 Qy 1381 TGCCAGTGTGATGATGATGAGTGAAGACCTCAGCCCAACCTTAAACCTGATTCGAGCT 1440
 Db 1545 TGCCAGTGTGATGATGATGAGTGAAGACCTCAGCCCAACCTTAAACCTGATTCGAGCT 1604

1441 ATCAGAAATATGAAATTTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTTACGTCCATAT 1500
1605 ATCAGAAATATGAAATTTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTTACGTCCATAT 1664
1501 GATGTAAGAGATGTCATGAAACAAATATTCGTGCTGTCATCTGACATGTTGTGTAAT 1560
1665 GATGTAAGAGATGTCATGAAACAAATATTCGTGCTGTCATCTGACATGTTGTGTAAT 1724
1561 AAAAGCCTTCAAAACAGTGTGATCAAAATTCCTTGGAAAGGGCAATCAATCAGATAAG 1620
1725 AAAAGCCTTCAAAACAGTGTGATCAAAATTCCTTGGAAAGGGCAATCAATCAGATAAG 1784
1621 AAGAGCCGAGAGAAAAATAACAGCAGAACATGAGACCAACAGACGATCTCAGTATGCTCGT 1680
1785 AAGAGCCGAGAGAAAAATAACAGCAGAACATGAGACCAACAGACGATCTCAGTATGCTCGT 1844
1681 CGGGTGGTCAAGTTGAAAAAAGGTACAGTACATAGAGTCCAAAGTGGAGTCCCTACTA 1740
1845 CGGGTGGTCAAGTTGAAAAAAGGTACAGTACATAGAGTCCAAAGTGGAGTCCCTACTA 1904
1741 GACATCTATCAACAGGTCTTCGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCATTC 1800
1905 GACATCTATCAACAGGTCTTCGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCATTC 1964
1801 CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATGACAAA 1860
1965 CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATGACAAA 2024
1861 GATCTTTTGGGTTCCGCAACAAAACAGTGGTGTCTTATCAGATCAACTAGTGCCAAATC 1920
2025 GATCTTTTGGGTTCCGCAACAAAACAGTGGTGTCTTATCAGATCAACTAGTGCCAAATC 2084
1921 TCAGAGAGGCTGCAGTTTCTGAGCCAAATAGTTCAGTGCAGCTTCTACGG 1980
2085 TCAGAGAGGCTGCAGTTTCTGAGCCAAATAGTTCAGTGCAGCTTCTACGG 2144
1981 CTTAGCCCTACTATGACAGTCAAGCAACACAGAGTGCCTAATAGTCAAAAGCGATGCTCA 2040
2145 CTTAGCCCTACTATGACAGTCAAGCAACACAGAGTGCCTAATAGTCAAAAGCGATGCTCA 2204
2041 GCAGTGGGACCAACCAACCATTTGCAAAACCAATTAATAGCGCACCAAGCCAGCAGCC 2100
2205 GCAGTGGGACCAACCAACCATTTGCAAAACCAATTAATAGCGCACCAAGCCAGCAGCC 2264
2101 CCAACAACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGCCAGAA 2160
2265 CCAACAACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGCCAGAA 2324
2161 ACTCTGACCCCTAACCCCTGAGGCTTACAGGAAGCATTTTGAACCTCACCCTGCTT 2220
2325 ACTCTGACCCCTAACCCCTGAGGCTTACAGGAAGCATTTTGAACCTCACCCTGCTT 2384
2221 GTTGCTTCAAGGAAATGTTTCAAGTTGACAGTCAAAATCTCAAGGACGCTTCTATG 2280
2385 GTTGCTTCAAGGAAATGTTTCAAGTTGACAGTCAAAATCTCAAGGACGCTTCTATG 2444
2281 AGGAAAGCTTTGACATGGGAGAGAACTCTGTTGCTGCTGCTCCATGTCGCGAG 2340
2445 AGGAAAGCTTTGACATGGGAGAGAACTCTGTTGCTGCTGCTCCATGTCGCGAG 2504
2341 GACTTGGGCAATCTTTGCTGTGCAAAACCTGATCAGGTGCAACGAGGAACTGAATATA 2400
2505 GACTTGGGCAATCTTTGCTGTGCAAAACCTGATCAGGTGCAACGAGGAACTGAATATA 2564
2401 CAATTTTCAAGGAGTCAAGTGGCTCCAGAGGAGCAAGATTTTACCCCAATGG 2460
2565 CAATTTTCAAGGAGTCAAGTGGCTCCAGAGGAGCAAGATTTTACCCCAATGG 2624
2461 AGGGAATCCAAATGTTTATTAATGATGAAGTGGTCCGAGAGACAGACAGAC 2520
2625 AGGGAATCCAAATGTTTATTAATGATGAAGTGGTCCGAGAGACAGACAGAC 2684

2521 ACTTTTGATGCGCACCCGAGCTGCGAGGAAGTGCCTTTGTCATCAGACTCTCTAAGG 2580
2685 ACTTTTGATGCGCACCCGAGCTGCGAGGAAGTGCCTTTGTCATCAGACTCTCTAAGG 2744
2581 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAGGCAAGGAGAAAGTACAGATGCCCTC 2640
2745 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAGGCAAGGAGAAAGTACAGATGCCCTC 2804
2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
2805 AGCTTGCCTCATGTCAAACTGAAATAA 2831

RESULT 5

US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kiehl, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Query Match 99.8%; Score 2662.2; DB 18; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGAAGGATGTGAGTCCGGCCGGGCGAGGGTGTGCTGCTGAACTCGGCAGCCGCGAGGGC 60
165 ATGAAGGATGTGAGTCCGGCCGGGCGAGGGTGTGCTGCTGAACTCGGCAGCCGCGAGGGC 224
61 GACGCTGTACTGCTGGGCAACCGCGGCGACGCTTGTGGCGGGCGGCGGTGGCCCTG 120
225 GACGCTGTACTGCTGGGCAACCGCGGCGACGCTGCTGGGCGGGCGGCGGTGGCCCTG 284
121 AGGAGAGCGCGCGGCGCAAGCAGGGGCGCGGATGAGCTGCTGGGGAAGCGGCTCTCT 180
285 AGGAGAGCGCGCGGCGCAAGCAGGGGCGCGGATGAGCTGCTGGGGAAGCGGCTCTCT 344
181 TACAGAGTAGCAGAGTCCGGGCGCAACGTCAGTACCGGGGGTGCAGAACTACCTG 240
345 TACAGAGTAGCAGAGTCCGGGCGCAACGTCAGTACCGGGGGTGCAGAACTACCTG 404
241 TACAACGTGCTGAGAGAGACCCCGGCGGTTCATCTACACGCTTTTCTGTTTCTC 300
405 TACAACGTGCTGAGAGAGACCCCGGCGGTTCATCTACACGCTTTTCTGTTTCTC 464
301 CTTGCTTTGTTGTTGATTTTGTAGTGTTCCTACCATCCCTGAGCACACAAATTTG 360
465 CTTGCTTTGTTGTTGATTTTGTAGTGTTCCTACCATCCCTGAGCACACAAATTTG 524
361 GCCTCAAGTTGCTCTTGAATCTCGAGTTCTGATGATGTCTTGTGTTTGGAGTTC 420
525 GCCTCAAGTTGCTCTTGAATCTCGAGTTCTGATGATGTCTTGTGTTTGGAGTTC 584

Db 2745 ACTGGAAGGTACAGATCATCTCAGAGCAATTTGTAAGGCAGGAGAGAAAGTACAGATGCCTC 2804
Qy 2641 AGCTTCCTCATGTCAAACTGAAATAA 2667
Db 2805 AGCTTCCTCATGTCAAACTGAAATAA 2831

RESULT 6

US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNO5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-020-1

Query Match 98.6%; Score 2630; DB 9; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;
Qy 1 ATGAAGGATGTGGAGTCGGGCGGGGACGGGTGCTGTAACCTCGGACGCGCCAGGGGC 60
Db 1 ATGAAGGATGTGGAGTCGGGCGGGGACGGGTGCTGTAACCTCGGACGCGCCAGGGGC 60
Qy 61 GACGGCTCTACTGCTGGGACCCCGCGGGGACCGCTTGGTGGCGGGCGGCGGCTG 120
Db 61 GACGGCTCTACTGCTGGGACCCCGCGGGGACCGCTTGGTGGCGGGCGGCGGCTG 120
Qy 121 AGGGAGAGCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGGAAGCCGCTCTCT 180
Db 121 AGGGAGAGCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGGAAGCCGCTCTCT 180
Qy 181 TACACAGTAGCCAGAGCTGCCGGGCAACGTCACAGTACCGGGGTGCAGAACTACCTG 240
Db 181 TACACAGTAGCCAGAGCTGCCGGGCAACGTCACAGTACCGGGGTGCAGAACTACCTG 240
Qy 241 TACACAGTCTGAGAGACCCCGGGGTCGCTTACCTACGCTTTCGTTTTC 300
Db 241 TACACAGTCTGAGAGACCCCGGGGTCGCTTACCTACGCTTTCGTTTTC 300
Qy 301 CTGTGCTTTGGTGTGATTTTGTTCAGTGTGTTTCTACCATCCCTGAGCACAAATTTG 360
Db 301 CTGTGCTTTGGTGTGATTTTGTTCAGTGTGTTTCTACCATCCCTGAGCACAAATTTG 360
Qy 361 GCCTCAAGTGTCTCTTGATCTCGGATTCGTCGATGATTCGCTTGTGGAGTTC 420
Db 361 GCCTCAAGTGTCTCTTGATCTCGGATTCGTCGATGATTCGCTTGTGGAGTTC 420
Qy 421 ATCATTCGAATCTGCTCGGGGTGCTGTTGTCATATAGAGATGGAAGAGACTG 480
Db 421 ATCATTCGAATCTGCTCGGGGTGCTGTTGTCATATAGAGATGGAAGAGACTG 480
Qy 481 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATGTTCTTATCGCTTCAATAGCA 540
Db 481 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATGTTCTTATCGCTTCAATAGCA 540

Qy 541 GTTGTCTTCTGAAAACTCAGGGTAATAATATTTTGGCACGCTGTGCACTCAGAACTCCTCGT 600
Db 541 GTTGTCTTCTGAAAACTCAGGGTAATAATATTTTGGCACGCTGTGCACTCAGAACTCCTCGT 600
Qy 601 TTCTCTACAGATCTCTCGCATGTGTGGCATGAGACCGGAGGGAGGCACTTTGGAAATTTACTG 660
Db 601 TTCTCTACAGATCTCTCGCATGTGTGGCATGAGACCGGAGGGAGGCACTTTGGAAATTTACTG 660
Qy 661 GGTTCAGTGTGTTTATGCTCACAGCAAGGAATTAATCACAGCTTTGGTACATAGATTTTTCG 720
Db 661 GGTTCAGTGTGTTTATGCTCACAGCAAGGAATTAATCACAGCTTTGGTACATAGATTTTTCG 720
Qy 721 GTTCTTATTTTTCGCTTTCTTCTGTCTATCTGGTGGAAAAAGATGCCAATAAAGAGTTT 780
Db 721 GTTCTTATTTTTCGCTTTCTTCTGTCTATCTGGTGGAAAAAGATGCCAATAAAGAGTTT 780
Qy 781 TCTACATATGAGATGCTCTCTGGTGGGACCAATTACATTTGCAAACTATTGGCTATGGA 840
Db 781 TCTACATATGAGATGCTCTCTGGTGGGACCAATTACATTTGCAAACTATTGGCTATGGA 840
Qy 841 GACAAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTTGCACCTCCTTGGC 900
Db 841 GACAAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTTGCACCTCCTTGGC 900
Qy 901 ATTTCTTTCTTTGCACTTCTCTGCCGGCAATTTTGGCTCAGGTTTTCATTAAAGATACAA 960
Db 901 ATTTCTTTCTTTGCACTTCTCTGCCGGCAATTTTGGCTCAGGTTTTCATTAAAGATACAA 960
Qy 961 GAAACACCGCCGACAGAAACATTTTGGAAAAAGAACCCAGCTGCGCAACCTCATTCAG 1020
Db 961 GAAACACCGCCGACAGAAACATTTTGGAAAAAGAACCCAGCTGCGCAACCTCATTCAG 1020
Qy 1021 TGTGTTTGGCTGATTTAGCAGCTCATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db 1021 TGTGTTTGGCTGATTTAGCAGCTCATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Qy 1081 CACTTGAAGGCTTGCACACCTGCGAGCCCTACCAA----- 1115
Db 1081 CACTTGAAGGCTTGCACACCTGCGAGCCCTACCAAAGAAAGAACAGGGAAGCATCAAGC 1140
Qy 1116 ---TCAGAGCTTAAGTTTAAAGAGCGAGTGCSCATGGCTAGCCCGAGGGGCCAGAGTATT 1173
Db 1141 AGTCAGAGCTTAAGTTTAAAGAGCGAGTGCSCATGGCTAGCCCGAGGGGCCAGAGTATT 1200
Qy 1174 AAGAGCCGACAGCCCTCAGTAGTGCACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1233
Db 1201 AAGAGCCGACAGCCCTCAGTAGTGCACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1260
Qy 1234 GGCAGTCCCAACAAAGTGCAGAAAGCTGGAGCTTCAACGACCGAAACCCGCTTCCGGCCC 1293
Db 1261 GGCAGTCCCAACAAAGTGCAGAAAGCTGGAGCTTCAACGACCGAAACCCGCTTCCGGCCC 1320
Qy 1294 TGGCTGCGGCTCAAAAGTTCTCAGCCAAAACAGTATAGATGCTGACACAGCCCTTGGC 1353
Db 1321 TGGCTGCGGCTCAAAAGTTCTCAGCCAAAACAGTATAGATGCTGACACAGCCCTTGGC 1380
Qy 1354 ACTGATGATGTATATGATGAAAAAGATGCGCAGTGTGATGATCATCAGTGAAGACCTCAC 1413
Db 1381 ACTGATGATGTATATGATGAAAAAGATGCGCAGTGTGATGATCATCAGTGAAGACCTCAC 1440
Qy 1414 CCACCACTTAAACCTGTCAATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG 1473
Db 1441 CCACCACTTAAACCTGTCAATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG 1500
Qy 1474 AAGTTTAAAGAAACGTTACGTCATATGATGAAAAAGATGCTGAAACATATTCTGCT 1533
Db 1501 AAGTTTAAAGAAACGTTACGTCATATGATGAAAAAGATGCTGAAACATATTCTGCT 1560
Qy 1534 GGTCTATCTGGACATGCTGCTGTAGAAATTAAGAGCCCTTCAACACGCTTGTGATCAAAATCTT 1593
Db 1561 GGTCTATCTGGACATGCTGCTGTAGAAATTAAGAGCCCTTCAACACGCTTGTGATCAAAATCTT 1620
Qy 1594 GGAAAAAGGCAATCACATCAGATGAAGAGAGCGAGAGAAATAACAGCAGAACATGAG 1653

Db	1621	GGAAAGGGCAATCACATCAGATAAGAAGAGCCGAGAGAAATAACACGACAGAAATCATGAG	1680
Qy	1654	ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1713
Db	1681	ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1740
Qy	1714	ATAGAGTCCAAGCTGCAGCTGCCTACTAGACATCTATCAACAGGTCCCTTCGGAAGGCTCT	1773
Db	1741	ATAGAGTCCAAGCTGCAGCTGCCTACTAGACATCTATCAACAGGTCCCTTCGGAAGGCTCT	1800
Qy	1774	GCCTCAGCCCTCGCTTTGGTTTCATTTCCAGATCCACCTTTTGAATGTGAACAGACATCT	1833
Db	1801	GCCTCAGCCCTCGCTTTGGCTTCAITTCAGATCCACCTTTTGAATGTGAACAGACATCT	1860
Qy	1834	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGTTCGCGCAAAACAGTGGCTGC	1893
Db	1861	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGTTCGCGCAAAACAGTGGCTGC	1920
Qy	1894	TTATCCAGATCAACTAGTGCACATCTCGAGAGCCCTGCAGTTCATTTCTGACGCCAAT	1953
Db	1921	TTATCCAGATCAACTAGTGCACATCTCGAGAGCCCTGCAGTTCATTTCTGACGCCAAT	1980
Qy	1954	GAGTTTCAGTGCACAGACTTTCTACGGCTTTAGCCCTACTATGCACAGTCAAGCAACAG	2013
Db	1981	GAGTTTCAGTGCACAGACTTTCTACGGCTTTAGCCCTACTATGCACAGTCAAGCAACAG	2040
Qy	2014	GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTCGAAACCAA	2073
Db	2041	GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTCGAAACCAA	2100
Qy	2074	ATAAATACGGCACCCAAAGCCAGCAGCCCCAACAACTTTACAGATCCCACTCCTCTCCCA	2133
Db	2101	ATAAATACGGCACCCAAAGCCAGCAGCCCCAACAACTTTACAGATCCCACTCCTCTCCCA	2160
Qy	2134	GCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTAACCCCTCAGGCTTACAGGAA	2193
Db	2161	GCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTAACCCCTCAGGCTTACAGGAA	2220
Qy	2194	AGCATTTCTGACGTCACCACTGCTGTTGTCCTTCCAAAGGAAATGTTACAGTTGCACAG	2253
Db	2221	AGCATTTCTGACGTCACCACTGCTGTTGTCCTTCCAAAGGAAATGTTACAGTTGCACAG	2280
Qy	2254	TCAAATCTCAACAGGACGTTCTATGAGGAAAGCTTTGACATGGGAGAGAGAACTCTG	2313
Db	2281	TCAAATCTCAACAGGACGTTCTATGAGGAAAGCTTTGACATGGGAGAGAGAACTCTG	2340
Qy	2314	TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAACTTTTGTCTGTGCAAAACCTG	2373
Db	2341	TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAACTTTTGTCTGTGCAAAACCTG	2400
Qy	2374	ATCAGGTGCACCGAGGAATGAATATACAACTTTTCAGGGTAGTCAAGTGGCTCCAGA	2433
Db	2401	ATCAGGTGCACCGAGGAATGAATATACAACTTTTCAGGGTAGTCAAGTGGCTCCAGA	2460
Qy	2434	GGCAGCCAAATTTTATACCCAAATGGAGGGAATCCAAATTTTATACTGATGAAGAG	2493
Db	2461	GGCAGCCAAATTTTATACCCAAATGGAGGGAATCCAAATTTTATACTGATGAAGAG	2520
Qy	2494	GTGGGTCCGAGAGACAGACACACTTTTGTATCCGACCGCAGCCCTGCCAGGAA	2553
Db	2521	GTGGGTCCGAGAGACAGACACACTTTTGTATCCGACCGCAGCCCTGCCAGGAA	2580
Qy	2554	GCTGCTTTGTCATCAGACTCTCTAAAGGACTGGAAGGTCCAGATCATCTCAGAGCATTTGT	2613
Db	2581	GCTGCTTTGTCATCAGACTCTCTAAAGGACTGGAAGGTCCAGATCATCTCAGAGCATTTGT	2640
Qy	2614	AAGCGAGGAAAGTACAGATGCCCTCAGTTGCCTCATGTCCAACTCAAAATAA	2667
Db	2641	AAGCGAGGAAAGTACAGATGCCCTCAGTTGCCTCATGTCCAACTCAAAATAA	2694

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US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeglia, Timothy James
; APPLICANT: ICAGEN, INC.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCNQ5-1
; US-09-810-796-2

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Query Match	98.6%	Score 2630;	DB 9;	Length 2694;
Best Local Similarity	99.0%;	Pred. No. 0;		
Matches 2667;	Conservative 0;	Mismatches 0;	Indels 27;	Gaps 1;
QY	1	ATGAAGAGATGTGGAGTCGGGCGGGG	CAGGGTGTCTGTAAC	TCGGCAGCCGCGCAGGGGC 60
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QY	61	GACGGCCTGTCTACTGCTGGGCA	CCCGCGCGGCACACGCTTGGTGGCGGCGCGGTGGCCCTG 120	
DB	61	GACGGCCTGTCTACTGCTGGGCA	CCCGCGCGGCACACGCTTGGTGGCGGCGCGGTGGCCCTG 120	
QY	121	AGGGAGAGCCCGCGGGGCAACAG	CAGGGGCGCCGGATGAGCCTGTCTGGGGAAAGCCGCTCTCT 180	
DB	121	AGGGAGAGCCCGCGGGGCAACAG	CAGGGGCGCCGGATGAGCCTGTCTGGGGAAAGCCGCTCTCT 180	
QY	181	TACACGAGTAGCCAGAGCTGCCG	CGCGCAACGTCACGTCACGGCGGGTGCAGAACTACCTG 240	
DB	181	TACACGAGTAGCCAGAGCTGCCG	CGCGCAACGTCACGTCACGGCGGGTGCAGAACTACCTG 240	
QY	241	TACACGCTGCTGGAGAGACCCCG	CGGCTGGCGGTTCACTACCAACGCTTTTCGTTTTTCTC 300	
DB	241	TACACGCTGCTGGAGAGACCCCG	CGGCTGGCGGTTCACTACCAACGCTTTTCGTTTTTCTC 300	
QY	301	CTTGTCTTTGGTGTCTTGATTTT	GTACAGTGTTCCTACCATCCCTGAGCACACAAAATTG 360	
DB	301	CTTGTCTTTGGTGTCTTGATTTT	GTACAGTGTTCCTACCATCCCTGAGCACACAAAATTG 360	
QY	361	GGCTCAAGTGTGCTTGCATCTCG	AGGTTTCGTGATGATGTCGTTTGGTTCGAGTTC 420	
DB	361	GGCTCAAGTGTGCTTGCATCTCG	AGGTTTCGTGATGATGTCGTTTGGTTCGAGTTC 420	
QY	421	ATCAITTCGAATCTGTCTCGGGT	TGCTGTTCGATATAGAGATGCGCAAGAGACTG 480	
DB	421	ATCAITTCGAATCTGTCTCGGGT	TGCTGTTCGATATAGAGATGCGCAAGAGACTG 480	
QY	481	AGGTTTGTCTGAAGCCCTTCTGCT	TATAGATACCATGTTCTTATCGCTTCAATAGCA 540	
DB	481	AGGTTTGTCTGAAGCCCTTCTGCT	TATAGATACCATGTTCTTATCGCTTCAATAGCA 540	
QY	541	GTGTGTTCTCGAAAAACTCAGGG	TAAATATTTTGGCCACGTCGTGCACTCAGAAAGTCTCCGT 600	
DB	541	GTGTGTTCTCGAAAAACTCAGGG	TAAATATTTTGGCCACGTCGTGCACTCAGAAAGTCTCCGT 600	
QY	601	TTCCCTACAGATCTCCGCATGTG	CGCATGGACCGGAGGGAGGCACTTGGAAATTAAGT 660	
DB	601	TTCCCTACAGATCTCCGCATGTG	CGCATGGACCGGAGGGAGGCACTTGGAAATTAAGT 660	

Qy	661	GGTT	CAGTGGTTT	TATGCTCAGCAAGGAATTAATCA	CAGCTTGGTACATAGGATTTTG	720
Db	661	GGTT	CAGTGGTTT	TATGCTCAGCAAGGAATTAATCA	CAGCTTGGTACATAGGATTTTG	720
Qy	721	GTTCTT	ATTTTTTTT	TCGTCTTCTTGCTCTATCTGCTGGAAAAGGATGCCAATAAAGAGCTTT	780	
Db	721	GTTCTT	ATTTTTTTT	TCGTCTTCTTGCTCTAICTGCTGGAAAAGGATGCCAATAAAGAGCTTT	780	
Qy	781	TCTACATATG	CAGATGCTCTCTGCTGGGGCAAAATTACATTATGACAACTATTGGCTATGGA	840		
Db	781	TCTACATATG	CAGATGCTCTCTGCTGGGGCAAAATTACATTATGACAACTATTGGCTATGGA	840		
Qy	841	GACAAA	ACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAAGCTTTTGCACTCCTTTGGC	900		
Db	841	GACAAA	ACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAAGCTTTTGCACTCCTTTGGC	900		
Qy	901	ATTTC	TTTTCTTTTGCACTTCTCTGCCCGCATCTTGGCTCAGGTTTTGATTAAAGATGACAA	960		
Db	901	ATTTC	TTTTCTTTTGCACTTCTCTGCCCGCATCTTGGCTCAGGTTTTGATTAAAGATGACAA	960		
Qy	961	GAACAA	CACCGCCAGAAACACTTTTGAAGAAAGAACCCAGCTGCCAACCTCATTTGAG	1020		
Db	961	GAACAA	CACCGCCAGAAACACTTTTGAAGAAAGAACCCAGCTGCCAACCTCATTTGAG	1020		
Qy	1021	TGTGTTTTGGG	TAGTTACGGAGCTGATGAGAAATCTGTTTCCATTGGCAACTGGAGCCA	1080		
Db	1021	TGTGTTTTGGG	TAGTTACGGAGCTGATGAGAAATCTGTTTCCATTGGCAACTGGAGCCA	1080		
Qy	1081	CAC	TTGAAGGCTTTGCAACCTGCAGCGCTTACCAA-----	1115		
Db	1081	CAC	TTGAAGGCTTTGCAACCTGCAGCGCTTACCAAAGGAAGCATCAAGC	1140		
Qy	1116	--	TCAGAA	GCTAAGTTTAAAGACGAGTGCATGCTAGCCGCCAGGGCCAGAGTATT	1173	
Db	1141	AGT	CAGAAGCTTAAGTTTTAAGAGCGAGTGCATGCTAGCCGCCAGGGCCAGAGTATT	1200		
Qy	1174	AAGAG	CGCAAGCCTCAGTAGGTGACAGAGAGTCCCAGACACCGACATCAGACCGAG	1233		
Db	1201	AAGAG	CGCAAGCCTCAGTAGGTGACAGAGAGTCCCAGACACCGACATCAGACCGAG	1260		
Qy	1234	GGCAG	TCCCACAAAGTGCGAAGAGCTGGAGCTTCAACGACCGAAACCCGCTTCCGGCCC	1293		
Db	1261	GGCAG	TCCCACAAAGTGCGAAGAGCTGGAGCTTCAACGACCGAAACCCGCTTCCGGCCC	1320		
Qy	1294	TCGCTGG	CCCTCAAAAGTTCTCAGCCAAAACCCAGTGATAGATGCTGACACAGCCCTTTGGC	1353		
Db	1321	TCGCTGG	CCCTCAAAAGTTCTCAGCCAAAACCCAGTGATAGATGCTGACACAGCCCTTTGGC	1380		
Qy	1354	ACTGAT	CACTATGATATGATAAAGGATGCCAGTGTGATCTATCAGTGGGAACCTTCAAC	1413		
Db	1381	ACTGAT	CACTATGATATGATAAAGGATGCCAGTGTGATCTATCAGTGGGAACCTTCAAC	1440		
Qy	1414	CCACC	ACTTAAAACTGTTCATTCGAGCTATCAGAAATTATGAAATTTCAATGTTGCAAAACCG	1473		
Db	1441	CCACC	ACTTAAAACTGTTCATTCGAGCTATCAGAAATTATGAAATTTCAATGTTGCAAAACCG	1500		
Qy	1474	AAGTTT	TAAGGAACGTTACGTCCATATGATGTAAAGATGTCATTGAAACAATATTTCTGCT	1533		
Db	1501	AAGTTT	TAAGGAACGTTACGTCCATATGATGTAAAGATGTCATTGAAACAATATTTCTGCT	1560		
Qy	1534	GGT	CATCTGGACATGTTGTGTAGAAATTAAGGCCTTCAAAACAGCTGTTGATCAAAATTCCTT	1593		
Db	1561	GGT	CATCTGGACATGTTGTGTAGAAATTAAGGCCTTCAAAACAGCTGTTGATCAAAATTCCTT	1620		
Qy	1594	GGAAA	GGGCAAAATCACATCAGATAAGAGCGCGAGAGAAAAATAACAGCAGAACATGAG	1653		
Db	1621	GGAAA	GGGCAAAATCACATCAGATAAGAGCGCGAGAGAAAAATAACAGCAGAACATGAG	1680		
Qy	1654	ACCAC	AGACATCTCAGTATGCTCGGTGGTGAAGTTGAAAAAAGGTACAGTCC	1713		
Db	1681	ACCAC	AGACATCTCAGTATGCTCGGTGGTGAAGTTGAAAAAAGGTACAGTCC	1740		

QY	1714	ATAGAGTCCAAAGCTGGAGCTGCCTACTAGACATCTATCAACAGGTCTCTTCGGAAGGCTCT	1773
DB	1741	ATAGAGTCCAAAGCTGGAGCTGCCTACTAGACATCTATCAACAGGTCTCTTCGGAAGGCTCT	1800
QY	1774	GCCTCAGCCCTCGCTTTGGCTTCATTCACAGATCCACCTTTTGAATGTGAACAGACATCT	1833
DB	1801	GCCTCAGCCCTCGCTTTGGCTTCATTCACAGATCCACCTTTTGAATGTGAACAGACATCT	1860
QY	1834	GACTATCAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCCGCACAAAAACAGTGGCTGC	1893
DB	1861	GACTATCAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCCGCACAAAAACAGTGGCTGC	1920
QY	1894	TTATTCAGATCAACTAGTGCACCATCTCAGAGGCCCTGCAGTTCACTTCGACGCCAAAT	1953
DB	1921	TTATTCAGATCAACTAGTGCACCATCTCAGAGGCCCTGCAGTTCACTTCGACGCCAAAT	1980
QY	1954	GAGTTTCAGTGCACAGACTTTCTACGCCCTTAGCCCTACTATGCACAGTCAAGGAACACAG	2013
DB	1981	GAGTTTCAGTGCACAGACTTTCTACGCCCTTAGCCCTACTATGCACAGTCAAGGAACACAG	2040
QY	2014	GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCACTTGCAAAACCAA	2073
DB	2041	GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCACTTGCAAAACCAA	2100
QY	2074	ATAAATACGGCACCCAAAGCCAGCAGCCCAACAACTTTACAGATCCACACTCTCTCTCCCA	2133
DB	2101	ATAAATACGGCACCCAAAGCCAGCAGCCCAACAACTTTACAGATCCACACTCTCTCTCCCA	2160
QY	2134	GCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGGAA	2193
DB	2161	GCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGGAA	2220
QY	2194	AGCATTTTTCGACGTCAACCATCGCTCTGTGTTCCTTCAAAGGAAAATGTTTCAGGTTGCACAG	2253
DB	2221	AGCATTTTTCGACGTCAACCATCGCTCTGTGTTCCTTCAAAGGAAAATGTTTCAGGTTGCACAG	2280
QY	2254	TCAAATCTCACAAGGACCGTTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAAATCTCTG	2313
DB	2281	TCAAATCTCACAAGGACCGTTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAAATCTCTG	2340
QY	2314	TTGTCTGTCTGTCTCCATGTGGCCGGAAGACTCTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2373
DB	2341	TTGTCTGTCTGTCTCCATGTGGCCGGAAGACTCTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2400
QY	2374	ATCAGGTTCGACCGAGGAACCTGAATATACAACCTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2433
DB	2401	ATCAGGTTCGACCGAGGAACCTGAATATACAACCTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2460
QY	2434	GGCAGCCAAGATTTTAAACCCCAAAATGAGGGGAATCCAAAATGTTTATACTGATGAAGAG	2493
DB	2461	GGCAGCCAAGATTTTAAACCCCAAAATGAGGGGAATCCAAAATGTTTATACTGATGAAGAG	2520
QY	2494	GTGGGTCCCGAAGACAGAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA	2553
DB	2521	GTGGGTCCCGAAGACAGAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA	2580
QY	2554	GCTGCCCTTTTGCATCAGACTCTCTAAGGACTCGAAGGTTCAGATCATCTCAGAGCATTTGT	2613
DB	2581	GCTGCCCTTTTGCATCAGACTCTCTAAGGACTCGAAGGTTCAGATCATCTCAGAGCATTTGT	2640
QY	2614	AAGCCAGGAGAAAGTACAGATGCCCTCAGCTTCGCTCATGTGCAAACTGAATAA	2667
DB	2641	AAGCCAGGAGAAAGTACAGATGCCCTCAGCTTCGCTCATGTGCAAACTGAATAA	2694

RESULT 8
US-10-948-493-1.
; Sequence 1, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T

```

; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KNO5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-948-493-1

Query Match 98.6%; Score 2630; DB 19; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 1 ATGAAGGATGTGAGTTCGGGCGGGGCGAGGCTGCTGCTGAACCTGGCAGCCGCGGAGGGC 60
DB 1 ATGAAGGATGTGAGTTCGGGCGGGGCGAGGCTGCTGCTGAACCTGGCAGCCGCGGAGGGC 60
QY 61 GACGGCTGCTACTGCTGGGCAACCGCGCGGCACGCTTGGTGGCGGGCGGTGGCGCTG 120
DB 61 GACGGCTGCTACTGCTGGGCAACCGCGCGGCACGCTTGGTGGCGGGCGGTGGCGCTG 120
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DB 121 AGGGAGAGCGCGGGGCAAGCAGAGGGGCGCGGATGAGCCTGCTGGGGAACCGCTCTCT 180
QY 181 TACACAGTAGCAGAGCTGCGGGGCAACGTCAGTAGTCCGCGGGTGCAGAACTACCTG 240
DB 181 TACACAGTAGCAGAGCTGCGGGGCAACGTCAGTAGTCCGCGGGTGCAGAACTACCTG 240
QY 241 TACACAGTAGCAGAGCTGCGGGGCAACGTCAGTAGTCCGCGGGTGCAGAACTACCTG 300
DB 241 TACACAGTAGCAGAGCTGCGGGGCAACGTCAGTAGTCCGCGGGTGCAGAACTACCTG 300
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DB 301 CTGTGCTTTGGTTGCTTGAATTTGTCAGTGTGTTTCTACCATCCCTGAGCACACAAATG 360
QY 361 GCCTCAAGTTGCTCTTGAATCTCGAGTTCGTAAGTATGTCGCTTTGGTTGGAGTTC 420
DB 361 GCCTCAAGTTGCTCTTGAATCTCGAGTTCGTAAGTATGTCGCTTTGGTTGGAGTTC 420
QY 421 ATCAATTCGAATCTGGTCTGGGTTGCTGTCGATATAGAGGATGGCAAGGAAGACTG 480
DB 421 ATCAATTCGAATCTGGTCTGGGTTGCTGTCGATATAGAGGATGGCAAGGAAGACTG 480
QY 481 AGGTTGCTCGAAAGCCCTTCTGTGTATAGATACCAATTTGTTTATCGCTTCAATAGCA 540
DB 481 AGGTTGCTCGAAAGCCCTTCTGTGTATAGATACCAATTTGTTTATCGCTTCAATAGCA 540
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DB 541 GTTGTGTTCTGCAAAACTCAGGTAATATTTTGGCCAGCTCTGCACTCAGAGTCTCCGT 600
QY 601 TTCTCAGATCTCCGATGTTGGCAATGGAACCGGAGGGAGGCACCTTGGAAATTTACTG 660
DB 601 TTCTCAGATCTCCGATGTTGGCAATGGAACCGGAGGGAGGCACCTTGGAAATTTACTG 660
QY 661 GGTTCAGTGTGTTATGCTCAGCAAGGAATTAATCAGAGCTTGGTACATAGATTTTGG 720
DB 661 GGTTCAGTGTGTTATGCTCAGCAAGGAATTAATCAGAGCTTGGTACATAGATTTTGG 720
QY 721 GTTCTTATTTTGGTCTTCTGCTATCTGCTGGAAGGATGCCAATAAGAGTTT 780
DB 721 GTTCTTATTTTGGTCTTCTGCTATCTGCTGGAAGGATGCCAATAAGAGTTT 780

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781 TCTACATATGCAGATGCTCTCTGGTGGGCGCAAAATTAATTAAGCAACTATTGGCTATGGA 840
781 TCTACATATGCAGATGCTCTCTGGTGGGCGCAAAATTAATTAAGCAACTATTGGCTATGGA 840
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841 GACAAAACCTCCCTTAACCTTGGCTGGGAAAGATTGCTTTCTGCAAGGCTTTGCACTCTTGGC 900
901 ATTTCTTTCTTTGGCACTTCTGCGCGCATTTCTGGCTCAGGTTTGGCAATTAAGATACAA 960
901 ATTTCTTTCTTTGGCACTTCTGCGCGCATTTCTGGCTCAGGTTTGGCAATTAAGATACAA 960
961 GAACACACCGCCAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAACCTCAATTAG 1020
961 GAACACACCGCCAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAACCTCAATTAG 1020
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1021 TGTGTTTGGCGTAGTTACGCACTGATGAGAAATCTGTTTCCATTGCAACCTGGAGGCCA 1080
1081 CACTTGAAGGCTTGCACACCTGCGCCCTACCA----- 1115
1081 CACTTGAAGGCTTGCACACCTGCGCCCTACCAAGAAAGAACGAGGAGCATCAAGC 1140
1116 --TCAGAAGCTAAGTTTAAAGGAGCGAGTGGCGATGGCTAGCCCGAGGGGCGAGTATT 1173
1141 AGTCAGAGCTAAGTTTAAAGGAGCGAGTGGCGATGGCTAGCCCGAGGGGCGAGTATT 1200
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1201 AAGAGCGGCAACGCTCAGTAGTGACAGGAGTCCCAAGCACCCAGACATCACAGCCGAG 1260
1234 GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAAACCGAACCCGCTTCCGGGCC 1293
1261 GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAAACCGAACCCGCTTCCGGGCC 1320
1294 TCGTGGCGCTCAAAAGTTCTCAGCCAAACCAAGTAGTAGATGCTGACACAGCCCTTGGC 1353
1321 TCGTGGCGCTCAAAAGTTCTCAGCCAAACCAAGTAGTAGATGCTGACACAGCCCTTGGC 1380
1354 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
1381 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1414 CCACCACTTAAACCTGTCATTTCAGCTATCAGAAATTAAGAAATTCATGTTGCAAAACGG 1473
1441 CCACCACTTAAACCTGTCATTTCAGCTATCAGAAATTAAGAAATTCATGTTGCAAAACGG 1500
1474 AAGTTTAAAGGAAACGTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1533
1501 AAGTTTAAAGGAAACGTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1534 GGTCACTCGACATGTTGTTGTTAGAAATTAAGAAACCTTCAAAACAGCTGTTGATCAAAATCTT 1593
1561 GGTCACTCGACATGTTGTTGTTAGAAATTAAGAAACCTTCAAAACAGCTGTTGATCAAAATCTT 1620
1594 GGAAGAGGCGCAAAATCAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1653
1621 GGAAGAGGCGCAAAATCAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1654 ACCACAGAGCATCTCAGTATGCTCGGTGGGTGATGATGATGATGATGATGATGATGATGATGAT 1713
1681 ACCACAGAGCATCTCAGTATGCTCGGTGGGTGATGATGATGATGATGATGATGATGATGATGAT 1740
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1774 GCTCAGGCCCTCGCTTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCT 1833
1801 GCTCAGGCCCTCGCTTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
1834 GACTATCAAGGCCCTGTGGATAGCAAAAGATCTTTGGGTTCGCGCAAAACAGTGGCTGC 1893

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QY 1 ATGAAGGATGTGGAGTCGGGCGGGCAGGGTGTCTGTGAACCTCGGCAGCCGCGCAGGGGC 60
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1 ATGAAGGATGTGGAGTCGGGCGGGCAGGGTGTCTGTGAACCTCGGCAGCCGCGCAGGGGC 60
QY 61 GACGGCTGTCTACTGTCTGGGACACCGCGGGGCCACGCTTGGTGGCGGGCGGGTGGCCCTG 120
DB |||||
61 GACGGCTGTCTACTGTCTGGGACACCGCGGGGCCACGCTTGGTGGCGGGCGGGTGGCCCTG 120
QY 121 AGGGAGAGCGCGCGGGCAAGCAGAGGGGGCGCGATGAGCTGTGGGGAAGCGCTCTCT 180
DB |||||
121 AGGGAGAGCGCGGGCAAGCAGAGGGGGCGCGATGAGCTGTGGGGAAGCGCTCTCT 180
QY 181 TACACGAGTAGCAGAGCTGCGGGCGCAACGCTCAAGTACCGGGGTGCAGAACTACCTG 240
DB |||||
181 TACACGAGTAGCAGAGCTGCGGGCGCAACGCTCAAGTACCGGGGTGCAGAACTACCTG 240
QY 241 TACAAGCTGTGGAGAGACCGCGGGCTGGGGTTCATCTACACGCTTTCGTTTTC 300
DB |||||
241 TACAAGCTGTGGAGAGACCGCGGGCTGGGGTTCATCTACACGCTTTCGTTTTC 300
QY 301 CTGTGCTTTGGTGTGATTTGTTCAGTGTTCCTACCATCCCTGAGCACACAAATG 360
DB |||||
301 CTGTGCTTTGGTGTGATTTGTTCAGTGTTCCTACCATCCCTGAGCACACAAATG 360
QY 361 GCCTCAAGTTGCCCTTTGATCCTGGAGTTCTGATGATTTGCTCTTTGGTGTGAGTTT 420
DB |||||
361 GCCTCAAGTTGCCCTTTGATCCTGGAGTTCTGATGATTTGCTCTTTGGTGTGAGTTT 420
QY 421 ATCATTCGAATCTGFTCTGGGGTTCGTTGTCGATAGAGGATGCGAAGAGACTG 480
DB |||||
421 ATCATTCGAATCTGFTCTGGGGTTCGTTGTCGATAGAGGATGCGAAGAGACTG 480
QY 481 AGSTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCCGCTTCAATAGCA 540
DB |||||
481 AGSTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCCGCTTCAATAGCA 540
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601 TTCTCAGATCCTCGGATGTGGCGATGGACCGAGGGGAGGACATTGGAAATTTACTG 660
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661 GGTTCAGTGTATTGCTCACAGCAAGAAATTAATCACAGCTTGGTACATAGATTTTGG 720
QY 721 GTTCTTATTTTTCGFTCTTCTTGTCTATCTGGTGGAAAGGATGCGCAATAAAGATTT 780
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721 GTTCTTATTTTTCGFTCTTCTTGTCTATCTGGTGGAAAGGATGCGCAATAAAGATTT 780
QY 781 TCTACATATGAGATGCTCTCTGGTGGGCGACAAATTAATGACAACTATTGGCTATGGA 840
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781 TCTACATATGAGATGCTCTCTGGTGGGCGACAAATTAATGACAACTATTGGCTATGGA 840
QY 841 GACAAACCTCCCTAACTTGGCTGGGAGATTTCTTCTGAGGCTTTCGACTCTCTTGGC 900
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841 GACAAACCTCCCTAACTTGGCTGGGAGATTTCTTCTGAGGCTTTCGACTCTCTTGGC 900
QY 901 ATTTCTTTCTTTCGACTTCTCGGGCAATCTTGGCTCAGGTTTTCGATTTAAAGTACAA 960
DB |||||
901 ATTTCTTTCTTTCGACTTCTCGGGCAATCTTGGCTCAGGTTTTCGATTTAAAGTACAA 960
QY 961 GAACAAACCGCGCAGAAACACTTTGAGAAAGAGAAACCGAGCTGCGCAACCTCATTCAG 1020
DB |||||
961 GAACAAACCGCGCAGAAACACTTTGAGAAAGAGAAACCGAGCTGCGCAACCTCATTCAG 1020
QY 1021 TGTGTTTGGGTAGTTTACCGAGCTGATGAAATCTGTTTCCATTGCAACCTGGAGCCA 1080
DB |||||
1021 TGTGTTTGGGTAGTTTACCGAGCTGATGAAATCTGTTTCCATTGCAACCTGGAGCCA 1080

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DB |||||
1081 CACTTGAAGCCCTTGACACACCTTGAGCCCTTACCAAAGAAAGAAAGGGGAGCATCAAGC 1140
QY 1116 ---TCAGAGCTAAGCTTTTAAGAGCGAGTGGCATGGCTAGCCCGAGGGGCCAGATATT 1173
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1141 AGTCAGAGCTAAGCTTTTAAGAGCGAGTGGCATGGCTAGCCCGAGGGGCCAGATATT 1200
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1201 AAGAGCCGACAAAGCCTCAGTAGTGCAGAGAGGTCCCAAGCAACCGACATCAAGCCGAG 1260
QY 1234 GGCAGTCCCAACAAAGTGCAGAAAGTGGAGCTTCAACGACCGAACCCGCTTCGCGCCC 1293
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1261 GGCAGTCCCAACAAAGTGCAGAAAGTGGAGCTTCAACGACCGAACCCGCTTCGCGCCC 1320
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1381 ACTGATGATGTATATGATGAAAAGATGCCAGTGTGATGTATCAGTGGAAAGACCTCACC 1440
QY 1414 CCACCACTTAAACCTGATTCAGAGCTATCAGAAATTAAGAAATTTTCAATGTGCAAAACGG 1473
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1441 CCACCACTTAAACCTGATTCAGAGCTATCAGAAATTAAGAAATTTTCAATGTGCAAAACGG 1500
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DB |||||
1501 AAGTTTAAGGAAACATTAAGTCCATATGATGTAAAAGATGTCTATGAAACAAATTTCTGCT 1560
QY 1534 GGTCACTCGGACATGTGTGTAGAAATTAAGACCTTCAACACAGTGTTCATCAAAATTCCT 1593
DB |||||
1561 GGTCACTCGGACATGTGTGTAGAAATTAAGACCTTCAACACAGTGTTCATCAAAATTCCT 1620
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1621 GGAAAGGGCAATCACATCAGATAGAGAGCGGAGAGAAATTAACAGCAGAACATGAG 1680
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1741 ATAGAAATCCAGCTGACTGCTACTAGACATCTATCAACAGGTCTCTCGGAAAGCTCT 1800
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QY 1834 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGCGCAACCAAGTGGCTGC 1893
DB |||||
1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGCGCAACCAAGTGGCTGC 1920
QY 1894 TTATCCAGATCAACTAGTGCCAAATCTCGAGAGCGCTGCACTTCATTCGACGCCAAAT 1953
DB |||||
1921 TTATCCAGATCAACTAGTGCCAAATCTCGAGAGCGCTGCACTTCATTCGACGCCAAAT 1980
QY 1954 GAGTTTCAGTGGCCAGACTTTCTACGCGTTAGCCCTTACTATGACAGTCAAGCAACAG 2013
DB |||||
1981 GAGTTTCAGTGGCCAGACTTTCTACGCGTTAGCCCTTACTATGACAGTCAAGCAACAG 2040
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2041 GTGCCAAATTAAGTCGATGGCTCAGCAGTGGCGAGCCCAACACCACTTCGAACCAA 2100
QY 2074 ATAAATACGGCAACCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2133
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2101 ATAAATACGGCAACCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2160
QY 2134 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCTTAACCTTCAGGCTTACAGGAA 2193

ID	Sequence	Score	DB	Length	Query Match
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2194	AGCATTTCTGACGTACACACCTGCTTGTGCTCCAGGAAATAGTTTCAGGTTGCACAG	2253			
2221	AGCATTTCTGACGTACACACCTGCTTGTGCTCCAGGAAATAGTTTCAGGTTGCACAG	2280			
2254	TCAAAATCTCAACCAAGACCGTCTTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2313			
2281	TCAAAATCTCAACCAAGACCGTCTTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2340			
2314	TTGCTGTCTGTCCCATGGTGCCGAAGGACTTTGGGCAAAATCTTTGCTCTGCAAAACCTG	2373			
2341	TTGCTGTCTGTCCCATGGTGCCGAAGGACTTTGGGCAAAATCTTTGCTCTGCAAAACCTG	2400			
2374	ATCAGGTGCGACCGAGGAACTGAATATACAACCTTTCAAGGAGTGAGTCAAGTGGCTCCAGA	2433			
2401	ATCAGGTGCGACCGAGGAACTGAATATACAACCTTTCAAGGAGTGAGTCAAGTGGCTCCAGA	2460			
2434	GGCAGCCAAAGATTTTATACCCCAATGAGGGAATCCAAATTTGTTTAACTGATGAAGAG	2493			
2461	GGCAGCCAAAGATTTTATACCCCAATGAGGGAATCCAAATTTGTTTAACTGATGAAGAG	2520			
2494	GTGGGTCCCAAGAGACAGACAGACACTTTTGTATGCCCGCACCGCAGCTGCCAGGGAA	2553			
2521	GTGGGTCCCAAGAGACAGACAGACACTTTTGTATGCCCGCACCGCAGCTGCCAGGGAA	2580			
2554	GCTCCCTTTGTCATCAGACTCTCTAAGGACTTGAAGGAGTCAAGTCAAGTCAAGTCAAGT	2613			
2581	GCTCCCTTTGTCATCAGACTCTCTAAGGACTTGAAGGAGTCAAGTCAAGTCAAGTCAAGT	2640			
2614	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAA	2667			
2641	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAA	2694			

RESULT 11
 US-09-813-148-1
 ; Sequence 1, Application US/09813148
 ; Patent No. US2002007680A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STEINMEYER, Klaus
 ; APPLICANT: LERCHE, Christian
 ; APPLICANT: SCHERER, Constanze
 ; APPLICANT: SEEROHM, Guiscard
 ; APPLICANT: BUSCH, Andreas E.
 ; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNO5, A NEW TARGET FOR DISEASES OF THE NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
 ; FILE REFERENCE: 38005-119
 ; CURRENT APPLICATION NUMBER: US/09/813,148
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: DE 100 13 732.6
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/194,041
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3074
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-813-148-1

ID	Sequence	Score	DB	Length	Query Match
2161	GCATCAAGCATCTGCCAGGCCAGAACTCTGCACCCCTAACCCCTGCAGGCTTACAGAA	2220			
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2254	TCAAAATCTCAACCAAGACCGTCTTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2313			
2281	TCAAAATCTCAACCAAGACCGTCTTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2340			
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2374	ATCAGGTGCGACCGAGGAACTGAATATACAACCTTTCAAGGAGTGAGTCAAGTGGCTCCAGA	2433			
2401	ATCAGGTGCGACCGAGGAACTGAATATACAACCTTTCAAGGAGTGAGTCAAGTGGCTCCAGA	2460			
2434	GGCAGCCAAAGATTTTATACCCCAATGAGGGAATCCAAATTTGTTTAACTGATGAAGAG	2493			
2461	GGCAGCCAAAGATTTTATACCCCAATGAGGGAATCCAAATTTGTTTAACTGATGAAGAG	2520			
2494	GTGGGTCCCAAGAGACAGACAGACACTTTTGTATGCCCGCACCGCAGCTGCCAGGGAA	2553			
2521	GTGGGTCCCAAGAGACAGACAGACACTTTTGTATGCCCGCACCGCAGCTGCCAGGGAA	2580			
2554	GCTCCCTTTGTCATCAGACTCTCTAAGGACTTGAAGGAGTCAAGTCAAGTCAAGTCAAGT	2613			
2581	GCTCCCTTTGTCATCAGACTCTCTAAGGACTTGAAGGAGTCAAGTCAAGTCAAGTCAAGT	2640			
2614	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAA	2667			
2641	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAA	2694			

Query Match 98.1%; Score 2617.2; DB 9; Length 3074;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;

ID	Sequence	Score	DB	Length	Query Match
2161	GCATCAAGCATCTGCCAGGCCAGAACTCTGCACCCCTAACCCCTGCAGGCTTACAGAA	2220			
2194	AGCATTTCTGACGTACACACCTGCTTGTGCTCCAGGAAATAGTTTCAGGTTGCACAG	2253			
2221	AGCATTTCTGACGTACACACCTGCTTGTGCTCCAGGAAATAGTTTCAGGTTGCACAG	2280			
2254	TCAAAATCTCAACCAAGACCGTCTTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2313			
2281	TCAAAATCTCAACCAAGACCGTCTTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2340			
2314	TTGCTGTCTGTCCCATGGTGCCGAAGGACTTTGGGCAAAATCTTTGCTCTGCAAAACCTG	2373			
2341	TTGCTGTCTGTCCCATGGTGCCGAAGGACTTTGGGCAAAATCTTTGCTCTGCAAAACCTG	2400			
2374	ATCAGGTGCGACCGAGGAACTGAATATACAACCTTTCAAGGAGTGAGTCAAGTGGCTCCAGA	2433			
2401	ATCAGGTGCGACCGAGGAACTGAAT				

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1834	GACTATCAAGCCCTGTGTAGTGAAGATCTTTGGGTTCGCGACAAAACAGTGGCTGC	1893
241	GACTATCAAGCCCTGTGTAGTGAAGATCTTTGGGTTCGCGACAAAACAGTGGCTGC	300
1894	TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCCTGCAAGTTCATCTGACGCCAAAT	1953
301	TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCCTGCAAGTTCATCTGACGCCAAAT	360
1954	GAGTTCAGTCCAGACTTTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCT	2013
361	GAGTTCAGTCCAGACTTTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCT	420
2014	GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCCAACACCAATTCGAAACAA	2073
421	GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCCAACACCAATTCGAAACAA	480
2074	ATAAATACGCCACCCAGCAGCAGCCCAACCAATTCACAGATC	2118
481	ATAAATACGCCACCCAGCAGCAGCCCAACCAATTCACAGATC	524

RESULT 13

US-10-353-690-55

; Sequence 55, Application US/10353690

; Publication No. US20030215840A1

; GENERAL INFORMATION:

; APPLICANT: Logan, Thomas Joseph

; APPLICANT: Chun, Miyoung

; APPLICANT: Galvin, Katherine M.

; APPLICANT: Healy, Aileen

; APPLICANT: Acton, Susan L.

; APPLICANT: Donoghue, Mary

; APPLICANT: Stagliano, Nancy

; APPLICANT: Perodin, Jacqueline

; APPLICANT: Rodrigue-Way, Amelie

; TITLE OF INVENTION: Methods and compositions for treating

; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,

; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,

; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,

; TITLE OF INVENTION: 14245, 58488, 1870, 25856, 32394, 3484, 345, 9252, 9135,

; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2448, 64624, 84237, 8912, 2868,

; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,

; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,

; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules

; FILE REFERENCE: MP102-018P18NOWNIM

; CURRENT APPLICATION NUMBER: US/10/353,690

; PENDING FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: 60/353,224

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/364,529

; PRIOR FILING DATE: 2002-03-15

; PRIOR APPLICATION NUMBER: 60/373,861

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: 60/376,287

; PRIOR FILING DATE: 2002-04-29

; PRIOR APPLICATION NUMBER: 60/388,080

; PRIOR FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: 60/390,971

; PRIOR FILING DATE: 2002-06-24

; PRIOR APPLICATION NUMBER: 60/394,130

; PRIOR FILING DATE: 2002-07-03

; PRIOR APPLICATION NUMBER: 60/394,797

; PRIOR FILING DATE: 2002-07-10

; PRIOR APPLICATION NUMBER: 60/404,904

; PRIOR FILING DATE: 2002-08-21

; PRIOR APPLICATION NUMBER: 60/405,450

; PRIOR FILING DATE: 2002-08-23

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 126

; SOFTWARE: FastSeq for Windows Version 4.0

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Db 1280 CGGCGGGCCGTTACCGGAGGAGCACCTCCGTTACCGCGCGGTGGCCACCTGGCCAC 1339
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QY 1195 GGTGACAGAGGTGCCCAAGCACCAGACATCACAGCCGAGG---GAGTCCCAACCAAGTG 1251
Db 1460 ACAATGCCACCTCCCAAGCAGGAGCAGGTGGGTGAGGCCACAGCCCAAGGTG 1519
QY 1252 CAGAGAGCTGAGCTTCAACGACCGAACCCGTTCCGCGCTTGGTGGCCCTCAAAAGT 1311
Db 1520 CAAAAGAGCTGAGCTTCAATGACCGCACCCGCTTCCGGGCTCTCTGAGACTC----- 1573
QY 1312 TCTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGGCAGCTGATGATATGAT 1371
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QY 1492 CGTCATATGATGTAAGATGCTCAATGAACTATTTCTGCTGCTGCTGCTGACATGTTG 1551
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QY 1552 TGTAGAAATTAAGCCTTCAAAACAGCTGTTGATCAAAATTTCTTGGAAAGGGC---AAATC 1608
Db 1802 GSCCGGATCAAGAGCTCGCAACTCGGTGGACCAAAATTTGTTGGTTCGGGGCCCGGGAC 1861
QY 1609 ACATCAGATAGAAGAGCGGAGAGAAATAACAGCAGAACATGAGACACAGACGATCTC 1668
Db 1862 AGGAAGGCCCGGAGAGGCGACAAAGGGCGCTCCGACCGGAGGTGGTGGATGAAATC 1921
QY 1669 AGTATGCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1728
Db 1922 AGCATGATGGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981
QY 1729 GACTGCTACTAGACATCTATCAACAGGTCTCTTCCGAAAGGCTCTGCTCAGCCCTCGCT 1788
Db 1982 GACCTGCTGTTGGGCTTCTATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2035
QY 1789 TTGGCTTCAATCCAGATCCCACTTTGAAATGTAAGACAGATCTGATCAATCAAGCCCT 1848
Db 2036 CTGGGCGCGGTGCAAGTGGCGCTGTTTCAACCCCGACATCACCTCGGACTTACCAGCCCT 2095
QY 1849 GTGGATAGCAAGATCTTTCCGGTTCCGACAAA 1882
Db 2096 GTGGACCGAGGAGATCTCTCGTCTCCGACAGA 2129

RESULT 14

US-10-850-928-1

; Sequence 1, Application US/10850928

; Publication No. US20050037460A1

; GENERAL INFORMATION:

; APPLICANT: JENTSCH, Thomas J.

; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE

; FILE OF INVENTION: POTASSIUM CHANNELS

; FILE REFERENCE: 2815-127PUS2

; CURRENT APPLICATION NUMBER: US/10/850,928

; CURRENT FILING DATE: 2004-05-20

; PRIOR APPLICATION NUMBER: 09/492,361

; PRIOR FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2335

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: gene

; LOCATION: (1)..(2335)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (83)..(2170)

US-10-850-928-1

Query Match 18.4%; Score 492; DB 19; Length 2335;

Best Local Similarity 59.3%; Pred. No. 1.4e-140;

Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;

QY 217 TACCGCGGGTGACAACTACCTGTACAACTGCTGAGAGACCCCGCGGCTGGGGTTC 276
Db 320 TACCGCGGCTGACAACTGGGTCTACAACTGCTGAGCGGCCCGCGGCTGGGGCTTC 379
QY 277 ATCTACCAAGCTTTCGTTTTCCTCTGTTTGGTTGCTTGAATTTGTAGTGTTCCT 336
Db 380 GTCTACCAAGCTTTCATATTTTGGTCTTTCAGTCTGCTGCTGCTGCTGCTGCTG 439
QY 337 ACCATCCCTGAGCACACAAATTTGGCTTCAAGTTGCCCTTTCGATCTTGGAGTTTGTGATG 396
Db 440 ACTATCCAGGAGCACAGGAATTTGCCAAACGAGTGTCTCTCATCTTGGAAATTCGTGATG 499
QY 397 ATTGCTGCTTGTGTTTGGTTCAGTTCATCATTCGAACTCTGCTGCGGGTTCGTTGTTGCTCA 456
Db 500 ATGCTGGTTTTCGGCTTGGAGTACATCTGCGGGTCTGCTGCGCGGATGCTGCTGCCGC 559
QY 457 TATAGAGATGGCAAGAGACTGAGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACC 516
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QY 517 ATTGTTCTTATGCTTCAATAGCAGTGTCTTCTGCAAAATCTCAGGGTAAATTTTGGCC 576
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QY 697 ACAGTTGGTACATAGGATTTTGGTCTTATTTTTCGTTCTTCTGCTGCTGCTGCTGCTG 756
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 1460 ACAATGCCACCTCCCGAAGCAGCAGAGGTGGGTGAGGCGCACAGCCCGCCACAGGTG 1519
 1252 CAGAGAGCTGAGCTTCAACAGCAGAAACCGGCTTCCGGCCCTCGCTGCGCTCAAAAGT 1311
 1520 CAAGAAGCTGAGCTTCAATGACCGCAGCCGCTTCCGGGATCTCTGAGACTC----- 1573
 1312 TCTCAGCCAAAACCAAGTATAGATGCTGACACAGCCCTTGGCACTGATGATATATGAT 1371
 1574 -----AAACCCCGCACCTCTGCTGAGGATGCC---CCTCAGAGGAAGTACAGAG 1621
 1372 GAAAGAGTGCAGGTGATGATATCATGAGTGAAGACCTCACCCACCACTTAAAACTGTC 1431
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 1432 ATTCGAGCTATCAGAAATATGAAATTTCAATTTGCAAAACGGAAGTTTAAAGAAAGTTA 1491
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 1802 GCGCGGATCAAGAGCTTGCMAACTCGGGTGGACCAATTTGTGGTTCGGGGGCGCGGGAC 1861
 1609 ACATCAGATGAAGAGCGGAGAGAAATAACAGCAGAACATGAGACACACAGCATCTC 1668
 1862 AGGAAGCCCGGAGAAAGGCGCAAGAGGGCCCTCCGACGCGGAGGTGGTGAATGAATC 1921
 1669 AGTATGCTCGGTGGGTGCTGAGTTGAAACAGGTACAGTCCATAGAGTCCAAAGCTG 1728
 1922 AGCATGATGGAGCGCGGTGCTGAGGTGAGAGCAGAGTGCATCTCATCGAGCAGAGCTG 1981
 1729 GACTGCTCTAGACATCTATCAACAGAGTCTTTGGAAAGGCTCTGCTCAGCCCTCGCT 1788
 1982 GACTGCTGTTGGGCTTCTATTCGCGCTGCTGC-----GCTCTGGCAGCTCGGCCAGC 2035
 1789 TTGGCTTCTTCAGATCCACCTTTTGAATGTGAACAGACATCTCACTATCAAGCCCT 1848
 2036 CTGGGCGCGGTGCAAGTGGCGCTGTTTCGACCCCGCATCACTCCGACTACACAGCCCT 2095
 1849 GTGGATAGCAAAAGATCTTTGGGGTTCCGACAAA 1882
 2096 GTGACCAAGGAGATCTCGTCTCCGACAGA 2129

RESULT 15

US-10-096-578-88
 ; Sequence 88, Application US/10096578
 ; Publication No. US20030165874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leppert, Mark F.
 ; APPLICANT: Charlier, Carole
 ; TITLE OF INVENTION: KNO2 AND KNO3 - POTASSIUM CHANNEL GENES WHICH ARE
 ; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
 ; FILE REFERENCE: 2323-160
 ; CURRENT APPLICATION NUMBER: US/10/096,578
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: US 09/177,650
 ; PRIOR FILING DATE: 1998-10-23
 ; PRIOR APPLICATION NUMBER: US 60/063,147
 ; PRIOR FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 88
 ; LENGTH: 2273
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(2271)
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(2273)
 ; OTHER INFORMATION: n may be any nucleotide except at position
 ; OTHER INFORMATION: 272 at which n may be t, c or g.
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(757)
 ; OTHER INFORMATION: Xaa may be: S or R at 18, 19 and 69; V, A, E or G
 ; OTHER INFORMATION: at 31; D or E at 33; S, P, T or A at 39; I, T, N or
 ; OTHER INFORMATION: S at 52; F, L, I, M or V at 53; S, P, T or A at 64;
 ; OTHER INFORMATION: P at 68; L, S or W at 91; R at 365; V at 509 and 516.
 ; OTHER INFORMATION: 272 at which n may be t, c or g.
 ; US-10-096-578-88

Query Match 18.3%; Score 489.2; DB 16; Length 2273;
 Best Local Similarity 57.0%; Pred. No. 1e-139;
 Matches 1020; Conservative 2; Mismatches 667; Indels 99; Gaps 4;
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 DB 127 GCGGGCTCCGAGGCCCGCCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 186
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 DB 187 GGANCCGGGAAGCCCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 246
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 QY 304 GTCCTTGGTCTGCTTGAATTTGTCAGTGTCTTACCATCTTCCATCTTCCAGAGTACGAGAGCTCT 363
 DB 307 GTTTTCTCCTGCTTGTCTTCTGTTTTCACCATCAAGAGAGTACGAGAGAGCTCT 366
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 DB 367 GAGGGGGCGCTTACATCTTGAATCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCTG 426
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 DB 487 TTTGCGCAGAGCCGCTTCTGTGATGATATCATGTTGCTGTTGCTTCCATTCCTGCTG 546

[illegible]

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:10:16 ; Search time 8429.33 Seconds
(without alignments)
12043.352 Million cell updates/sec

Title: US-09-810-796-3

Perfect score: 2667

Sequence: 1 atgaagatgtggagtcggg.....ctcatgtcaactgaataa 2667

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2142.2	80.3	2729	9 AY407015	Mus muscu
3	1859.2	69.7	2014	9 AY407014	Pan trogl
4	1351.4	50.7	2276	3 AK033079	Mus muscu
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17	536.4	20.1	547	4 BI034993	BE158938
18	530.8	19.9	570	4 BI033850	BE158938
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ALIGNMENTS

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LOCUS
DEFINITION
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genomic survey sequence.
ACCESSION
AY407013
VERSION
AY407013.1
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 2733)
AUTHORS
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 2733)
AUTHORS
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="KCNQ5"
/locus_tag="HGM2749"

Query Match 99.5%; Score 2653.6; DB 9; Length 2733;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2656; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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|||||

Db 67 ATGAAGGATGTGAGTCCGGCCGGGCGAGGGTGTCTGTAACCTGGGAGCCGCGCAGGGGC 126
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Qy 1081 CACTTGAAGGCTTGGACACCTGAGCCCTTACCAATCAGAGCTTAAGTTTGAAGGAGCGA 1140
Db 1147 CACTTGAAGGCTTGGACACCTGAGCCCTTACCAATCAGAGCTTAAGTTTGAAGGAGCGA 1206

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DB	1150	CATCTGAAGCCCTTGACACCTTCAGCCCTACCAATCAGAAGCTGAGCTTTAAGGAGCGA	1209
QY	1141	GTGCGATGCTTAGCCCCAGGGGCGAGATTAAGAGCCGACAGCCCTCAGTAGGTGAC	1200
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DB	1863	CAGATCCCGCCTTTTGAATGTGAACAGACACCTCTGACTATCAAAGTCTGTGGATAGCAAA	1922
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[illegible]

AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source
1. 732
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Matches 699; Conservative 0; Mismatches 3; Indels 31; Gaps 3;
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QY 1113 -----CAATCAGAAGCTAAGTTTAAAGGAGCGAGTGGCGATGGTACGCCACAGGGG 1163
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QY 1284 CTTCCGGCCCTCGCTCGGCTCAAAAGTCTCAAGTTCAGCCAAACCCAGTGATGATGATG 1343
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QY 1344 AGCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1403
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QY 1404 AGACCTCAGCCCACTTAAAGTCTCAATTCAGCTATCAGAAATTTATGAAATTTTCATGT 1463
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QY 1524 ATATTCTGCTGCTATCGACATGTTGTTAGAAATTAAGGCTTCAACACAGTGTGA 1583
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QY 1704 GGTACAGTCCATA 1716
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RESULT 8
CD429754/c
LOCUS CD429754.1 742 bp mRNA linear EST 12-JAN-2004
DEFINITION 550493327J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629754
VERSION CD629754.1 GI:40278020
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 742)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source
1. 742
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/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

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Query Match 23.4%; Score 625.2; DB 6; Length 742;
Best Local Similarity 94.7%; Pred. No. 1.4e-167;
Matches 701; Conservative 0; Mismatches 8; Indels 31; Gaps 4;
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QY 1076 AGCCACACTTGAAGGCTTGCACACTGCGAGCCCTACCAAGAAAGAACCAAGGGGAAGCA 624
Db 683 AGCCACACTTGAAGGCTTGCACACTGCGAGCCCTACCAAGAAAGAACCAAGGGGAAGCA 1166
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Db 623 TCAGAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGGCCAGGGGCA 564
QY 1167 GAGTATTAAAGCCGACCAAGCTCAGTAGTGACAGGAGTCCCAAGCAGCAGCATCAC 1226
Db 563 GAGTATTAAAGCCGACCAAGCTCAGTAGTGACAGGAGTCCCAAGCAGCAGCATCAC 504
QY 1227 AGCCAGGGCAGTCCCAAGAGTGCAGAGAGCTGGAGCTTCAAGCAGCAGCAGCTT 1286
Db 503 AGCCAGGGCAGTCCCAAGAGTGCAGAGAGCTGGAGCTTCAAGCAGCAGCAGCTT 444
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QY 1347 CTTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1406
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Dd	143	AATTCTTTGAAAAAGGCCAATCATCATCAGATAAGAGAGCCGAGAGAAAATAAACAGCAGA	84
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Dd	83	ACATGAGACACACAGACGATCTCAGTAGTCCTCGGTCGGGTTGGTCAAGGTTGAAAAACAGG	24
Qy	1706	TACAGTCCATAGAGTCCAAG	1725
Dd	23	TACAGTCCATAGAAATCCTAG	4

RESULT	9
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LOCUS	CD629758 678 bp linear
DEFINITION	FLP Homo sapiens cDNA, mRNA sequence.
	55049351J1 EST 12-JAN-2004

VERSION CD629758.1 GI:40278024
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 678)
 REFERENCE Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
 AUTHORS Circular rapid amplification of cDNA ends for high-throughput
 TITLE extension cloning of partial genes
 JOURNAL Genomics 84 (1), 205-210 (2004)

CONTACT: FU GK
Incyte Genomics, Inc.
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Tel: 6508454102
Email: gfu@incyte.com.

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FEATURES
source
Email: Srean@cc.mcgill.ca
Location/Qualifiers
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/mol_type="mRNA"
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Query Match 22.3%; Score 595; DB 6; Length 678;
Best Local Similarity 99.0%; Pred. No. 6.3e-159;
Matches 609; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy	1469	AACGGAAGTTTAAAGAAAAGTGTACGTC	CATATGATGCTAAAGAGTGTCAATTGAACA	TAATT	1522
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Db	198	CTGCTGGTCATCTGGGACATGTTGTGT	PAGAAATTAAGAGCCTTCAACACGCTGT	TGATCAAA	139
Qy	1589	TTCTTGGAAAGGGCAAAATC	ATCAGATAGNAGAGCCGAGAGAAATAA	CAGCAGAAC	1648
Db	138	TTCTTGGAAAGGGCAAAATC	ATCAGATAGNAGAGCCGAGAGAAATAA	CAGCAGAAC	79
Qy	1649	ATGAGACCA	CAGACGATCTCAGTATGCTCGGTGGT	CGGTGAGGTTGAAAAACAGGTAC	1708
Db	78	ATGAGACCA	CAGACGATCTCAGTATGCTCGGTGGT	CGGTGAGGTTGAAAAACAGGTAC	20
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RESULT 10	717 bp	linear	EST 12-JAN-2004
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LOCUS	55049191J1	FLP Homo sapiens CDNA, mRNA sequence.	
DEFINITION			

ACCESSION	CD629766
VERSION	CD629766.1
KEYWORDS	GI:40278032
EST.	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 717)
AUTHORS	Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE	Circular rapid amplification of cDNA ends for high-throughput
	extension cloning of partial genes
JOURNAL	Genomics 84 (1), 205-210 (2004)

```

COMMENT
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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	Best Local Similarity	94.6%;	Pred. No. 4.1e-158;	Indels 31;	Gaps 5;
	Matches 678;	Conservative 0;	Mismatches 8;		
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Qy	1124	TAAAGTT-TTAAAGGACGAGTGCAGATGGCTAGGCCCGAGGGCCACAGAGTATTAAAGAGCC-G	1181		
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/notes="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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ORIGIN

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Matches 632	Conservative 0	Mismatches 106	Indels 0	Gaps 0

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DB 67 AGAGCCTGCGAGTTCAATTCGAGCGCAATGAGTTGAGTGCAGAGCTTTCTACGCGCTT 126

QY 1984 AGCCCTACTATGTCAGTCAAGCACAGAGTGCATTAATGATCAAGGATGGCTCAGCA 2043
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RESULT 13
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DEFINITION 55049359J1 FLP Homo sapiens cDNA, mRNA sequence.
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VERSION CD629760.1 GI:40278026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 714)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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ORIGIN

Query Match	21.3%	Score 567.6	DB 6	Length 714
Best Local Similarity	98.3%	Pred. No. 4.8e-151	Indels 1	Gaps 1
Matches 584	Conservative 0	Mismatches 9	Indels 1	Gaps 1

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DB 614 CAACAGTCAGAGCTAAGTTTAAAGGAGCGAGTGCATGGCTAGCCAGGCGCCAGA 555

QY 1169 GTATTAGAGCGGACAAAGCCTCAGTAGTGACAGAGGTTCCCAAGCACCCGACATCAG 1228
DB 554 GTATTAGAGCGGACAAAGCCTCAGTAGTGACAGAGGTTCCCAAGCACCCGACATCAG 495

QY 1229 CCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAA-CGACCGAACCGCTTC 1287
DB 494 CCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAAGCGACCGAACCGCTTC 435

QY 1288 CGGCGCTCGTGCCTCAAAAGTTCTCAGCAAAACCCAGTATAGTGTGACACAGCC 1347
DB 434 CGGCGCTCGTGCCTCAAAAGTTCTCAGCAAAACCCAGTATAGTGTGACACAGCC 375

QY 1348 CTTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
DB 374 CTTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 315

QY 1408 CTCACCCACCACTTAAACCTGCTATTCGAGCTATCAGAATTTATGAAATTTTCATGTTGCA 1467
DB 314 CTCACCCACCACTTAAACCTGCTATTCGAGCTATCAGAATTTATGAAATTTTCATGTTGCA 255

QY 1468 AAACGGAAGTTTAAAGGAAACGTTTACGTCATATGATGATGATGATGATGATGATGATGAT 1527
DB 254 AAACGGAAGTTTAAAGGAAACGTTTACGTCATATGATGATGATGATGATGATGATGATGAT 195

QY 1528 TCTCTGTCATCTGGACATGTTGTGATGATTTAAAGCCTTCAACACGCTGTTGATCAAA 1587
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Tue Apr 12 17:15:12 2005

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Db     181  TTGACATGGGAGGAGAACTCTGTGTCTGTCTGCCATGCTGCCGAGGACTTGGGCA 240
Qy      2351 AATCTTTGCTGTGCAAACTGATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAG 2410
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Qy      2411 GGAGTGAGTCAAGTGGCTCCAGAGGCGCCAAAGATTTTACCCCAATGGAGGAAATCCA 2470
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Qy      2471 AATTGTTTATTAAGTGAAGAGGTGGTCCGGAAGAGACAGACAGACACTTTTGATG 2530
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Db     421  CCGCACCGCAGCTGCCAGGGAAGCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGT 480
Qy      2591 CACGATCATCTCAGAGCATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCTC 2650
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Qy      2651 ATGTCAAACTGAAATAA 2667
Db     541  ATGTCAAACTGAAATAA 557
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Search completed: April 11, 2005, 21:32:05
Job time : 8438.33 secs

STIC-Biotech/ChemLib

150642

From: Bunner, Bridget
Sent: Wednesday, April 06, 2005 2:08 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/810,796:
1. the amino acid sequence of SEQ ID NO: 5 - 888777

CRF

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:33:11 ; Search time 44 Seconds
(without alignments)
1506.554 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVESGRVLLNSAARG.....SICKAGESTDALSLPHVCLK 888

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4547	100.0	923	4	US-09-825-147-2
2	4527.5	99.6	897	4	US-09-590-304-2
3	4527.5	99.6	932	4	US-09-813-148-2
4	4300.5	94.6	854	4	US-09-590-304-7
5	1985	43.7	695	4	US-09-590-304-6
6	1985	43.7	695	4	US-09-492-361-2
7	1985	43.7	696	4	US-09-813-148-6
8	1980	43.5	676	4	US-09-949-016-7694
9	1792	39.4	844	4	US-09-813-148-4
10	1792	39.4	844	4	US-09-590-304-4
11	1792	39.4	844	4	US-09-492-361-34
12	1790.5	39.4	822	4	US-09-105-058C-23
13	1788.5	39.3	930	4	US-09-177-650-96
14	1787.5	39.3	871	4	US-09-105-058C-20
15	1783	39.2	872	4	US-09-177-650-2
16	1759	38.7	757	4	US-09-177-650-89
17	1587.5	34.9	854	4	US-09-105-058C-27
18	1587.5	34.9	872	4	US-09-177-650-7
19	1587.5	34.9	872	4	US-09-813-148-5
20	1587.5	34.9	872	4	US-09-590-304-5
21	1587.5	34.9	872	4	US-09-492-361-35
22	1535.5	33.8	870	4	US-09-177-650-91
23	1207.5	26.6	300	4	US-09-105-058C-4
24	1207.5	26.6	300	4	US-09-105-058C-6
25	1188	26.1	807	4	US-09-177-650-3
26	1102	24.2	676	3	US-09-135-021-2
27	1102	24.2	676	3	US-09-135-020-2

ALIGNMENTS

RESULT 1

US-09-825-147-2

; Sequence 2, Application US/09825147

; Patent No. 6767736

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Kieke, James Alvin

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael C.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and

; FILE REFERENCE: Polynucleotides Encoding the Same

; CURRENT APPLICATION NUMBER: US/09/825,147

; CURRENT FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: US 60/194,255

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 923

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-825-147-2

Query Match 100.0%; Score 4547; DB 4; Length 923;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKDVESGRVLLNSAARGDGLLLTGTRATLGGGGGGLRESRRGQGRMSLLGKPLS	60
Db	36	MKDVESGRVLLNSAARGDGLLLTGTRATLGGGGGGLRESRRGQGRMSLLGKPLS	95
Qy	61	YTSQSCRRNVKRVQNYLVNLERPRGNWAFIVHAFVLLVFGCLLSVFSTIPEHTKL	120
Db	96	YTSQSCRRNVKRVQNYLVNLERPRGNWAFIVHAFVLLVFGCLLSVFSTIPEHTKL	155
Qy	121	ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRVGMQGRLLRPARKPFCVIDITVLIASIA	180
Db	156	ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRVGMQGRLLRPARKPFCVIDITVLIASIA	215
Qy	181	VSAKTOGNIFATSALRSFLQLRMVRDRGGTWKLLGSVVYAHSKELITAWYIGFL	240
Db	216	VSAKTOGNIFATSALRSFLQLRMVRDRGGTWKLLGSVVYAHSKELITAWYIGFL	275
Qy	241	VLIFSSFLVYLVKDNKEFTVADALWGWGITLTTIGYGDKPTLTLWGLRLLSAGFALLG	300
Db	276	VLIFSSFLVYLVKDNKEFTVADALWGWGITLTTIGYGDKPTLTLWGLRLLSAGFALLG	335

QY	301	ISFFALPAGILGSGFALKVQEOHROKHFEKRRNPAANLIQCVWRSVAADEKSVSIATWKP	360
Db	336	ISFFALPAGILGSGFALKVQEOHROKHFEKRRNPAANLIQCVWRSVAADEKSVSIATWKP	395
QY	361	HLKALHTCSPNOKLSFKERVRMASPRGQSIKSRQASVGGRRSPSPTDITAEAGSPTKVQKS	420
Db	396	HLKALHTCSPNOKLSFKERVRMASPRGQSIKSRQASVGGRRSPSPTDITAEAGSPTKVQKS	455
QY	421	WSFNDRTRFRPSRLKSSQPKPVIDADTALGTDVDEKCCQCDVSVDITPPLKTVIRA	480
Db	456	WSFNDRTRFRPSRLKSSQPKPVIDADTALGTDVDEKCCQCDVSVDITPPLKTVIRA	515
QY	481	IRIMKFHVAKKFKETLRPYDKVIOYQYAGHLDMLCRIKSLQTRVDQILGKGQITSDK	540
Db	516	IRIMKFHVAKKFKETLRPYDKVIOYQYAGHLDMLCRIKSLQTRVDQILGKGQITSDK	575
QY	541	KSREKITAHEHTDDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLRKGSASALALASF	600
Db	576	KSREKITAHEHTDDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLRKGSASALALASF	635
QY	601	QIPPFCEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFTLTNEFSAQTFYA	660
Db	636	QIPPFCEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFTLTNEFSAQTFYA	695
QY	661	LSPTMHSQATQVPIQSQDGSAAVATNTIANQINTAPKPAAPTTLQIPPPPLPAIKHLPRPE	720
Db	696	LSPTMHSQATQVPIQSQDGSAAVATNTIANQINTAPKPAAPTTLQIPPPPLPAIKHLPRPE	755
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QY	781	DLGKSLSVQNLIRSTEELNIQLSGESSGSGSQDFYPKWRESKLFITDEEVGPEETED	840
Db	816	DLGKSLSVQNLIRSTEELNIQLSGESSGSGSQDFYPKWRESKLFITDEEVGPEETED	875
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Db	876	TFDAAPQAPAREAFASDSLRGTGRSSQSIKCKAGESTDALSPLHVKLK	923
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; Sequence 2, Application US/09590304			
; Patent No. 6649371			
; GENERAL INFORMATION:			
; APPLICANT: JENTSCH, Thomas			
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN			
; FILE REFERENCE: 2815-0136P			
; CURRENT APPLICATION NUMBER: US/09/590,304			
; CURRENT FILING DATE: 2000-06-09			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: Patentin version 3.0			
; SEQ ID NO 2			
; LENGTH: 897			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-590-304-2			
Query Match 99.6%; Score 4527.5; DB 4; Length 897;			
Best Local Similarity 98.9%; Pred. No. 0;			
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;			
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Db	1	MKDVSQGRVLNLSAARGDGLLLGTRAAATLGGGGGLRESRGKQAGARMSLLGKPLS	60
QY	61	YTSQSCRNKVRQYVQNLVNLPRPGWAFIYHAFVLLVFGCLLSVSTIPEHTKL	120
Db	61	YTSQSCRNKVRQYVQNLVNLPRPGWAFIYHAFVLLVFGCLLSVSTIPEHTKL	120
QY	121	ASSCLLILEFVMIVVFGLEFIIRWSAGCCCRYGQGLRFPKPFVVIDIVILASTA	180

Db	121	ASSCLLILEFVMIVVFGLEFIIRWSAGCCCRYGQGLRFPKPFVVIDIVILASTA	180
QY	181	VVSATQGNIPATSAIRSLRFLQILRMVMDRRGGTGWLLGSAVVAHAKSKELITANYIGFL	240
Db	181	VVSATQGNIPATSAIRSLRFLQILRMVMDRRGGTGWLLGSAVVAHAKSKELITANYIGFL	240
QY	241	VLISSFLVYLVEKQANKEFSTYADALMWGTTTLTIGYDKTPTLTWLGRLLSAGFALLG	300
Db	241	VLISSFLVYLVEKQANKEFSTYADALMWGTTTLTIGYDKTPTLTWLGRLLSAGFALLG	300
QY	301	ISFFALPAGILGSGFALKVQEOHROKHFEKRRNPAANLIQCVWRSVAADEKSVSIATWKP	360
Db	301	ISFFALPAGILGSGFALKVQEOHROKHFEKRRNPAANLIQCVWRSVAADEKSVSIATWKP	360
QY	361	HLKALHTCSPNOKLSFKERVRMASPRGQSIKSRQASVGGRRSPSPTDITAE	411
Db	361	HLKALHTCSPNOKLSFKERVRMASPRGQSIKSRQASVGGRRSPSPTDITAE	420
QY	412	GSPTKVQKSWSNDRTRFRPSRLKSSQPKPVIDADTALGTDVDEKCCQCDVSVDIT	471
Db	421	GSPTKVQKSWSNDRTRFRPSRLKSSQPKPVIDADTALGTDVDEKCCQCDVSVDIT	480
QY	472	PPLKTVIRAIRIMKFHVAKKFKETLRPYDKVIOYQYAGHLDMLCRIKSLQTRVDQIL	531
Db	481	PPLKTVIRAIRIMKFHVAKKFKETLRPYDKVIOYQYAGHLDMLCRIKSLQTRVDQIL	540
QY	532	KGQITSDKSKREKITAHEHTDDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLRKGS	591
Db	541	KGQITSDKSKREKITAHEHTDDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLRKGS	600
QY	592	ASALALASFQIPPFCEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFTLT	651
Db	601	ASALALASFQIPPFCEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFTLT	660
QY	652	EFSAQTFYALSPTMHSQATQVPIQSQDGSAAVATNTIANQINTAPKPAAPTTLQIPPP	711
Db	661	EFSAQTFYALSPTMHSQATQVPIQSQDGSAAVATNTIANQINTAPKPAAPTTLQIPPP	720
QY	712	AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVQASNLTKDRSMRKSPDMG	771
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QY	832	VGPEETETDTFDAAPQAPAREAFASDSLRGTGRSSQSIKCKAGESTDALSPLHVKLK	888
Db	841	VGPEETETDTFDAAPQAPAREAFASDSLRGTGRSSQSIKCKAGESTDALSPLHVKLK	897

RESULT 3

US-09-813-148-2

; Sequence 2, Application US/09813148

; Patent No. 6617131

; GENERAL INFORMATION:

; APPLICANT: STEINMEYER, Klaus

; APPLICANT: LERCHE, Christian

; APPLICANT: SCHERER, Constanze

; APPLICANT: SEBOHM, Guiscard

; APPLICANT: BUSCH, Andreas E.

; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN

; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM

; FILE REFERENCE: 38005-119

; CURRENT APPLICATION NUMBER: US/09/813,148

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: DE 100 13 732.6

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/194,041

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-148-2

Query Match 99.6%; Score 4527.5; DB 4; Length 932;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

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DB 36 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRGKQGARMSSLLGKPLS 95
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DB 216 VVSAKTQGNIFATSALRSRFLQILRMVRMDRRGGTWKLLGSVVAHSEKELITAWIGFL 275
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DB 336 ISFFALPAGILSGGFALKVQEOHROKHFEKRRNPAANLIQCWRSYAADEKSVSIATWKP 395
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DB 396 HLKALHTCSPTKEQGEASSSQKLSFKERVMA SPRQSISKRSQASVGDRRSPSTITAE 455
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DB 456 GSPTKVQKSWSFNDRTRFRPSRLKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 515
QY 472 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDVKDVIQYSAGHLDMLCRIKSLQTRVDQIL 531
DB 516 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDVKDVIQYSAGHLDMLCRIKSLQTRVDQIL 575
QY 532 GKQITSDKKSREKITAHEHTTDDLSMLGRVVKVQVQVQIESKLDCLLDIYQOVLKRG 591
DB 576 GKQITSDKKSREKITAHEHTTDDLSMLGRVVKVQVQVQIESKLDCLLDIYQOVLKRG 635
QY 592 ASALALASFOIPPFCEQTSQSDYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILT 651
DB 636 ASALALASFOIPPFCEQTSQSDYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILT 695
QY 652 EFSAQTFYALSPTHSQATQVPIQSODGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 711
DB 696 EFSAQTFYALSPTHSQATQVPIQSODGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 755
QY 712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVQVQIESKLDCLLDIYQOVLKRG 771
DB 756 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVQVQIESKLDCLLDIYQOVLKRG 815
QY 772 LSVCPMPVKDLGKLSLVQNLIRSTEELNIQLSGSSSGSRGSDQFPYKWRKSLFTIDEE 831
DB 816 LSVCPMPVKDLGKLSLVQNLIRSTEELNIQLSGSSSGSRGSDQFPYKWRKSLFTIDEE 875
QY 832 VGPETETDTFDDAPOPAREAAAFASLSLRTGRSSQSICKAGESTDALSLPHVKLK 888
DB 876 VGPETETDTFDDAPOPAREAAAFASLSLRTGRSSQSICKAGESTDALSLPHVKLK 932
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RESULT 4
US-09-590-304-7

; Sequence 7, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTISCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-304-7

Query Match 94.6%; Score 4300.5; DB 4; Length 854;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 841; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

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DB 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRGKQGARMSSLLGKPLS 60
QY 61 YTSQSCRRNVKRRVQNYLYNVLEPRGWFATYHAFVFLVFGCLLSVFSSTIPBHTKL 120
DB 61 YTSQSCRRNVKRRVQNYLYNVLEPRGWFATYHAFVFLVFGCLLSVFSSTIPBHTKL 120
QY 121 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPCVDTIVLIASIA 180
DB 121 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPCVDTIVLIASIA 180
QY 181 VVSAKTQGNIFATSALRSRFLQILRMVRMDRRGGTWKLLGSVVAHSEKELITAWIGFL 240
DB 181 VVSAKTQGNIFATSALRSRFLQILRMVRMDRRGGTWKLLGSVVAHSEKELITAWIGFL 240
QY 241 VLIFFSFLVYLVEKDANKFSTYADALWNGTITLTITIGYDKTPTLWGLRLSAGFALLG 300
DB 241 VLIFFSFLVYLVEKDANKFSTYADALWNGTITLTITIGYDKTPTLWGLRLSAGFALLG 300
QY 301 ISFFALPAGILSGGFALKVQEOHROKHFEKRRNPAANLIQCWRSYAADEKSVSIATWKP 360
DB 301 ISFFALPAGILSGGFALKVQEOHROKHFEKRRNPAANLIQCWRSYAADEKSVSIATWKP 360
QY 361 HLKALHTCSPT-----NOKLSFKERVMA SPRQSISKRSQASVGDRRSPSTITAE 411
DB 361 HLKALHTCSPTKEQGEASSSQKLSFKERVMA SPRQSISKRSQASVGDRRSPSTITAE 420
QY 412 GSPTKVQKSWSFNDRTRFRPSRLKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 471
DB 421 GSPTKVQKSWSFNDRTRFRPSRLKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 480
QY 472 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDVKDVIQYSAGHLDMLCRIKSLQTRVDQIL 531
DB 481 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDVKDVIQYSAGHLDMLCRIKSLQTRVDQIL 540
QY 532 GKQITSDKKSREKITAHEHTTDDLSMLGRVVKVQVQVQIESKLDCLLDIYQOVLKRG 591
DB 541 GKQITSDKKSREKITAHEHTTDDLSMLGRVVKVQVQVQIESKLDCLLDIYQOVLKRG 600
QY 592 ASALALASFOIPPFCEQTSQSDYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILT 651
DB 601 ASALALASFOIPPFCEQTSQSDYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILT 660
QY 652 EFSAQTFYALSPTHSQATQVPIQSODGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 711
DB 661 EFSAQTFYALSPTHSQATQVPIQSODGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 720
QY 712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVQVQIESKLDCLLDIYQOVLKRG 771
DB 721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVQVQIESKLDCLLDIYQOVLKRG 780
QY 772 LSVCPMPVKDLGKLSLVQNLIRSTEELNIQLSGSSSGSRGSDQFPYKWRKSLFTIDEE 831
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Db 781 LSVCPMPKDLGKSLVQNLIRSTEELNQLSGSESSGSRGQDFYPKWRESKLFITDEE 840
Qy 832 VGPEETETDTF 842
Db 841 VGPEETETDTF 851

RESULT 5
US-09-304-6
; Sequence 6, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHAN
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-304-6

Query Match 43.7%; Score 1985; DB 4; Length 695;
Best Local Similarity 60.3%; Pred. No. 4.8e-171;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;
Qy 35 GGGGLRESRRGKQARMSLLGKPL-----SYTSSQCRNRNKKYRRVQNYL 80
Db 37 GGGGSPR-----RLGLGSPLPDGPAPLPGSGSGSACGQRSSAAHKRYRRLQNV 87
Qy 81 YNVLERPRGWAIFYHAFVFLVFCCLILSVFSTIPEHTKLASSCLLILFVMIIVFGLEF 140
Db 88 YNVLERPRGWAIFYHVFIFLLVFCCLVSLVSTIQEHOELANECCLLILFVMIIVFGLE 147
Qy 141 IIRWSAGCCCRYRGWQGRLEFARKPCVIDITVLIASTAVSAKTOGNIFFATSALRSR 200
Db 148 IVRWSAGCCCRYRGWQGRFFARKPCVIDIFVVASVAVIAAGTQGNIFATSALRSR 207
Qy 201 FLQLRMVRMDRGGTWKLLGSGVVAHAKELITAWYIGFLVLFSSFLVYLVEKDANKF 260
Db 208 FLQLRMVRMDRGGTWKLLGSGVVAHAKELITAWYIGFLVLFASFLVYLAEKDANSDF 267
Qy 261 STYADALWMTITLTTIGYDKTPTLWGLRLLSAGFALLIGISFFALPAGILSGFALKVQ 320
Db 268 SSVADSLWMTITLTTIGYDKTPTLWGLRLLSAGFALLIGISFFALPAGILSGFALKVQ 327
Qy 321 EHQKQHFERRNPAANL1QCWRSYAAD-EKSVSIATW----- 358
Db 328 EHQKQHFERRMFAANL1QAARLYSTDMRSAYLTATWYYDLSILPSPRELALLFEHVQ 387
Qy 359 -----KPHLKALHT-----CSPTNOKLSFKERVMSAPRG 388
Db 388 RARNGGLRPLEVRAPVDPGAPSPYPVATCHRPGSTSPCGESSRMGIKDIRMGSSOR 447
Qy 389 QSIKSRQ--ASVGDRRSPSTDTITAEQ--SPTKVQKSWSFNDRTRFRPSLRKLSQPKPV 445
Db 448 RTGFSKQOLAPPTMPTSPSSQGEATSPYKQKSWSFNDRTRFRASRL-----KPTS 502
Qy 446 ADTALGTDVVDEKGCQCDVSVEDLTPPLKTVIRAIRIMKHFVAKRKFETLRPYDVQDV 505
Db 503 AEDA-PSEEAEEKSYQCELTVDDIMPAVKTVIRSIIRLFLVAKRKFETLRPYDVQDV 561
Qy 506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAHEHTTDDLMLGRV 562
Db 562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDGKPSDAEVDIISMGRV 619
Qy 563 VKVEKQVQSIKSLDCLLDIYQOVLKSGSALALASFOIPPECEQTSYQSPVDSKDL 622
Db 620 VKVEKQVQSIKSLDCLLDIYQOVLKSGSALASFOIPPECEQTSYQSPVDSKDL 677

Qy 623 SGSAQNSCCLSRSTSANI 640
Db 678 SVSAQTLISRSVSTNM 694
RESULT 6
US-09-492-361-2
; Sequence 2, Application US/09492361
; Patent No. 6794161
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
; FILE REFERENCE: 2815-127P
; CURRENT APPLICATION NUMBER: US/09/492,361
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-492-361-2
Query Match 43.7%; Score 1985; DB 4; Length 695;
Best Local Similarity 60.3%; Pred. No. 4.8e-171;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;
Qy 35 GGGGLRESRRGKQARMSLLGKPL-----SYTSSQCRNRNKKYRRVQNYL 80
Db 37 GGGGSPR-----RLGLGSPLPDGPAPLPGSGSGSACGQRSSAAHKRYRRLQNV 87
Qy 81 YNVLERPRGWAIFYHAFVFLVFCCLILSVFSTIPEHTKLASSCLLILFVMIIVFGLEF 140
Db 88 YNVLERPRGWAIFYHVFIFLLVFCCLVSLVSTIQEHOELANECCLLILFVMIIVFGLE 147
Qy 141 IIRWSAGCCCRYRGWQGRLEFARKPCVIDITVLIASTAVSAKTOGNIFFATSALRSR 200
Db 148 IVRWSAGCCCRYRGWQGRFFARKPCVIDIFVVASVAVIAAGTQGNIFATSALRSR 207
Qy 201 FLQLRMVRMDRGGTWKLLGSGVVAHAKELITAWYIGFLVLFSSFLVYLVEKDANKF 260
Db 208 FLQLRMVRMDRGGTWKLLGSGVVAHAKELITAWYIGFLVLFASFLVYLAEKDANSDF 267
Qy 261 STYADALWMTITLTTIGYDKTPTLWGLRLLSAGFALLIGISFFALPAGILSGFALKVQ 320
Db 268 SSVADSLWMTITLTTIGYDKTPTLWGLRLLSAGFALLIGISFFALPAGILSGFALKVQ 327
Qy 321 EHQKQHFERRNPAANL1QCWRSYAAD-EKSVSIATW----- 358
Db 328 EHQKQHFERRMFAANL1QAARLYSTDMRSAYLTATWYYDLSILPSPRELALLFEHVQ 387
Qy 359 -----KPHLKALHT-----CSPTNOKLSFKERVMSAPRG 388
Db 388 RARNGGLRPLEVRAPVDPGAPSPYPVATCHRPGSTSPCGESSRMGIKDIRMGSSOR 447
Qy 389 QSIKSRQ--ASVGDRRSPSTDTITAEQ--SPTKVQKSWSFNDRTRFRPSLRKLSQPKPV 445
Db 448 RTGFSKQOLAPPTMPTSPSSQGEATSPYKQKSWSFNDRTRFRASRL-----KPTS 502
Qy 446 ADTALGTDVVDEKGCQCDVSVEDLTPPLKTVIRAIRIMKHFVAKRKFETLRPYDVQDV 505
Db 503 AEDA-PSEEAEEKSYQCELTVDDIMPAVKTVIRSIIRLFLVAKRKFETLRPYDVQDV 561
Qy 506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAHEHTTDDLMLGRV 562
Db 562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDGKPSDAEVDIISMGRV 619
Qy 563 VKVEKQVQSIKSLDCLLDIYQOVLKSGSALALASFOIPPECEQTSYQSPVDSKDL 622
Db 620 VKVEKQVQSIKSLDCLLDIYQOVLKSGSALASFOIPPECEQTSYQSPVDSKDL 677

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QY 623 SGSAQNSGCLSRSTSANI 640
Db 678 SVSAQTLS-ISRVSSTNM 694

RESULT 7
US-09-813-148-6
; Sequence 6, Application US/09813148
; Patent No. 6617131
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEBOHM, Guiseard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CNS
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-148-6

Query Match 43.7%; Score 1985; DB 4; Length 696;
Best Local Similarity 60.3%; Pred. No. 4.8e-171;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;

QY 35 GGGGLRESRRGQARMISLIGKPL-----SYTSSQSCRRNVKRRVQNYL 80
Db 37 GGGGSPR-----RLGLGSLPPGAPLPFGSGSGSACCQSSAAHKRYRRLQNWV 87

QY 81 YNVLEPRGWAFYHAFVFLVFGCLILSVFSTPEHTKLASSCLLILEFVMIWVFGLEF 140
Db 88 YNVLEPRGWAFYHVFIFLLVFSCLVLSVLSIQEHOELANECLLILEFVMIWVFGLEY 147

QY 141 IIRWSAGCCCRVGRWGQRLRFARKPCVIDITVLIAIVASAKTQGNIFATSALRSR 200
Db 148 IVRWSAGCCCRVGRWGQRFARKPCVIDITVVFASVAVIAAGTQGNIFATSALRSR 207

QY 201 FLOILRMVRDRGGTWKLGSGVVAHAKELITAWYIGFLVLIFSSFLVYLVEKDANKF 260
Db 208 FLOILRMVRDRGGTWKLGSGVVAHAKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

QY 261 STYADALWMTITLTTIGYGDKTPLTWGLRLLSAGFALLGISFPFALPAGILSGGFALKVQ 320
Db 268 SSVADSLWMTITLTTIGYGDKTPLTWGLRVLAAGFALLGISFPFALPAGILSGGFALKVQ 327

QY 321 EQRQKHFEKRRNPAANLIQCVRWSYAAD-EKSVSIATW----- 358
Db 328 EQRQKHFEKRRNPAANLIQAARWLYSTDMRAYLTATWYIYDYSILPSFRELALLFEHVQ 387

QY 359 -----KPHLKALHT----- 358
Db 388 RARNGGLRPLEVRAPVDPGAPSRYPVATCHRPGSTSFPCGESSRMGIKDRIMGSSQR 447

QY 389 QSIKSRQ--ASVGDRRSPSTDTIAEG-SPTKVOKSWSFNDRTRFRPSRLKSSQPKPVID 445
Db 448 RTGFSKQHLAPPTMPTSPSEQVEATSPTKVOKSWSFNDRTRFRASRLI-----KPTS 502

QY 446 ADTALGTDVYDEKGCQCVDSVEDLTPPLKTVIRAIRIMKPHVAKRKFKETLTPYDKOV 505
Db 503 AEDA-PSEEAEEKSYQCELTVDIMPVAKTVIRSIIRILKFLVAKRKFKETLTPYDKOV 561

QY 506 IEQYSAGHLDMLCRIKSLQTRVDQILGKQITSDKKSRE---KITAEHETDLDLMLGRV 562

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Db 562 IEQYSAGHLDMLCRIKSLQTRVDQIVGRG--PQDRKAREKDGKPSDAEVDLSMMGRV 619
QY 563 VKVEKQVQSIKSLDCLLDIYQQVLRKGSASALALASFOIPPECEQTSYQSPVDSKOL 622
Db 620 VKVEKQVQSIKSLDCLLDIYQVLRKGSASALALASFOIPPECEQTSYQSPVDSKOL 677

QY 623 SGSAQNSGCLSRSTSANI 640
Db 678 SVSAQTLS-ISRVSSTNM 694

RESULT 8
US-09-949-016-7694
; Sequence 7694, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7694
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7694

Query Match 43.5%; Score 1980; DB 4; Length 676;
Best Local Similarity 60.3%; Pred. No. 1.3e-170;
Matches 409; Conservative 75; Mismatches 102; Indels 92; Gaps 13;

QY 35 GGGGLRESRRGQARMISLIGKPL-----SYTSSQSCRRNVKRRVQNYL 80
Db 18 GGGGSPR-----RLGLGSLPPGAPLPFGSGSGSACCQSSAAHKRYRRLQNWG 68

QY 81 YNVLEPRGWAFYHAFVFLVFGCLILSVFSTPEHTKLASSCLLILEFVMIWVFGLEF 140
Db 69 YNVLEPRGWAFYHVFIFLLVFSCLVLSVLSIQEHOELANECLLILEFVMIWVFGLEY 128

QY 141 IIRWSAGCCCRVGRWGQRLRFARKPCVIDITVLIAIVASAKTQGNIFATSALRSR 200
Db 129 IVRWSAGCCCRVGRWGQRFARKPCVIDITVVFASVAVIAAGTQGNIFATSALRSR 188

QY 201 FLOILRMVRDRGGTWKLGSGVVAHAKELITAWYIGFLVLIFSSFLVYLVEKDANKF 260
Db 189 FLOILRMVRDRGGTWKLGSGVVAHAKELITAWYIGFLVLIFASFLVYLAEKDANSDF 248

QY 261 STYADALWMTITLTTIGYGDKTPLTWGLRLLSAGFALLGISFPFALPAGILSGGFALKVQ 320
Db 249 SSVADSLWMTITLTTIGYGDKTPLTWGLRVLAAGFALLGISFPFALPAGILSGGFALKVQ 308

QY 321 EQRQKHFEKRRNPAANLIQCVRWSYAAD-EKSVSIATW----- 358
Db 309 EQRQKHFEKRRNPAANLIQAARWLYSTDMRAYLTATWYIYDYSILPSFRELALLFEHVQ 368

QY 359 -----KPHLKALHT----- 358
Db 369 RARNGGLRPLEVRAPVDPGAPSRYPVATCHRPGSTSFPCGESSRMGIKDRIMGSSQR 428

QY 389 QSIKSRQ--ASVGDRRSPSTDTIAEG-SPTKVOKSWSFNDRTRFRPSRLKSSQPKPVID 445
Db 429 RTGFSKQHLAPPTMPTSPSEQVEATSPTKVOKSWSFNDRTRFRASRLI-----KPTS 483

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QY 317 LKVOEQHROKHFKEKRRNPAAANLIQCVRSAAD-----EKSVSIAATWK--PH 361
Db 318 LKVOEQHROKHFKEKRRNPAAAGLIQSAWRFYATNLSRDLHSTWQYVERTVTPMYRLIPP 377
QY 362 LKALHTC-----SPTNOKLSFKERVMSAPRGOSIKSROASVGD-- 400
Db 378 LKQLELLRNLSKSGLAFRKDPPEPSP-SQKVSLEKDRV-FSSPRGVAAGKSGSPQAQTV 435
QY 401 RRSPTDITAEAGSPTKQKSWSPNDTRFRPSLRKSSQPKVIDADTALGTDDVYDEKG 460
Db 436 RRSFSAQSLSDSPSKVPKSWSPGDRSRAQAFRIKGAASRQNSE-EASLPGEDIVDDKS 494
QY 461 CQCDVSVDLTPLKTVIRAIRIMKHFVAKRKETLRPYDVVDKQVVEQYSAGHLDMLCRI 520
Db 495 CPCEFTEDLTPLGLKVSIRAVCMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLCRI 554
QY 521 KSLQTRVDQILGQITSDKSKREKITAHEHTDDLSMLGRVVKVEKQVOSIESKLDCLL 580
Db 555 KSLQSRVDQIVGRGPAITD-KDRTKGAFAELPDSMMGRGKVEKQVLSMEKKLDLFLV 613
QY 581 DIYOQVLRKGSASALALASQIIPFFEC-----EQTSQYQSPVDSKDLGSAQNSGC 631
Db 614 NIYMQ--RMG-----IPPTETEAYFGAKEPEPAPPYHSPEDSRE--HVDRHGC 657
QY 632 LRSSTANISRGLOFILTNPNEFAQTFYALSPTMHSQATQVPIQS-----DGSAVA 683
Db 658 IVKIVRSSSTG-----QKNFSAPP--AAPP-----VQCPSTSMQPOSHPRQGHGTS 703
QY 684 ATNTIANQINTAPKPAAPTTLQI-----PP-----PLP 711
Db 704 PVGDHGLSVRIPPPPAHERLSAYGGNRSASMEFLRQEDTPGCRPEGTLRDSDTSISIP 763
QY 712 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVQVAQS 752
Db 764 SVDH-----BELERSFSGF--SISQ-----SKENLDALNS 791

RESULT 11
US-09-492-361-34
; Sequence 34, Application US/09492361
; Patent No. 6794161
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
; FILE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127P
; CURRENT APPLICATION NUMBER: US/09/492,361
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 34
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-492-361-34

Query Match 39.4%; Score 1792; DB 4; Length 844;
Best Local Similarity 49.5%; Pred. No. 2.1e-153;
Matches 406; Conservative 88; Mismatches 179; Indels 148; Gaps 24;

QY 17 AARGDGLLGTAAATLGGGGGLRESRRGKQARMSSLLGKPLSYTSSQSCRNVYRRV 76
Db 34 STRDGALLIAGSEAPK--RGSILSKPRAGGAGA-----GKP-----PKENAFYRKL 77
QY 77 QNLYNVLERPRGWAITYHAFVLLVFGCLLSVFTSTIPHTKLASSCLLILFVIMVIF 136
Db 78 QNLYNVLERPRGWAITYHAFVLLVFGCLLSVFTSTIPHTKLASSCLLILFVIMVIF 137
QY 137 GLFIFIRWSAGCCCRVGRQGRRLRFAKPFCDITDVLIASIAVVSAKTQGNIFATSAL 196
Db 138 GVEYFVRWIAAGCCCRVGRQGRRLRFAKPFCDITDVLIASIAVLAAGSQGNVATSAL 197

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QY 197 RSLRFLQILRMVEMDRGGTWTLLGSSVVAHSHKELITAWYIGLVLFSSFLVYLVKDA 256
Db 198 RSLRFLQILRMVEMDRGGTWTLLGSSVVAHSHKELITAWYIGLVLFSSFLVYLVKDA 257
QY 257 NKEFSTYADALMWGTTTLTTIGYGDKTPLTTLGRLLSAGFALLGIGIFFALPAGILSGGFA 316
Db 258 NDHFDIYADALMWGLTLTTIGYGDKYPTQWNGRLLAAFTLLIGVFFALPAGILSGGFA 317
QY 317 LKVOEQHROKHFKEKRRNPAAANLIQCVRSAAD-----EKSVSIAATWK--PH 361
Db 318 LKVOEQHROKHFKEKRRNPAAAGLIQSAWRFYATNLSRDLHSTWQYVERTVTPMYRLIPP 377
QY 362 LKALHTC-----SPTNOKLSFKERVMSAPRGOSIKSROASVGD-- 400
Db 378 LKQLELLRNLSKSGLAFRKDPPEPSP-SQKVSLEKDRV-FSSPRGVAAGKSGSPQAQTV 435
QY 401 RRSPTDITAEAGSPTKQKSWSPNDTRFRPSLRKSSQPKVIDADTALGTDDVYDEKG 460
Db 436 RRSFSAQSLSDSPSKVPKSWSPGDRSRAQAFRIKGAASRQNSE-EASLPGEDIVDDKS 494
QY 461 CQCDVSVDLTPLKTVIRAIRIMKHFVAKRKETLRPYDVVDKQVVEQYSAGHLDMLCRI 520
Db 495 CPCEFTEDLTPLGLKVSIRAVCMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLCRI 554
QY 521 KSLQTRVDQILGQITSDKSKREKITAHEHTDDLSMLGRVVKVEKQVOSIESKLDCLL 580
Db 555 KSLQSRVDQIVGRGPAITD-KDRTKGAFAELPDSMMGRGKVEKQVLSMEKKLDLFLV 613
QY 581 DIYOQVLRKGSASALALASQIIPFFEC-----EQTSQYQSPVDSKDLGSAQNSGC 631
Db 614 NIYMQ--RMG-----IPPTETEAYFGAKEPEPAPPYHSPEDSRE--HVDRHGC 657
QY 632 LRSSTANISRGLOFILTNPNEFAQTFYALSPTMHSQATQVPIQS-----DGSAVA 683
Db 658 IVKIVRSSSTG-----QKNFSAPP--AAPP-----VQCPSTSMQPOSHPRQGHGTS 703
QY 684 ATNTIANQINTAPKPAAPTTLQI-----PP-----PLP 711
Db 704 PVGDHGLSVRIPPPPAHERLSAYGGNRSASMEFLRQEDTPGCRPEGTLRDSDTSISIP 763
QY 712 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVQVAQS 752
Db 764 SVDH-----BELERSFSGF--SISQ-----SKENLDALNS 791

RESULT 12
US-09-105-058C-23
; Sequence 23, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grikoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 23
; LENGTH: 722
; TYPE: PRT
; ORGANISM: mouse
US-09-105-058C-23

Query Match 39.4%; Score 1790.5; DB 4; Length 722;
Best Local Similarity 55.0%; Pred. No. 2.4e-153;

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; Sequence 20, Application US/09105058C
; Patent No. 8403360
; GENERAL INFORMATION:
; APPLICANT: Blanz, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grikoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-105-058C-20

Query Match 39.3%; Score 1787.5; DB 4; Length 871;
Best Local Similarity 47.9%; Pred. No. 6.2e-153;
Matches 406; Conservative 89; Mismatches 178; Indels 175; Gaps 24;

QY 17 AARGDGLLLGTAAATLGGGGGLRESRRKQKQARMSLLGKPLSYTSSQSCRNVKRVV 76
DB 34 STRDGALLIAGSEAPK---RGSILSKPRAGAGA-----GKP-----PKNAFYRKL 77
QY 77 QNYLYNVLERPRGWAFTYHAFVLLVFGCLLSVFSTIPEHTKLASSCLLILFVWVVF 136
DB 78 QNFYLVNLERPRGWAFTYHAFVLLVFGCLLSVFSTIPEHTKLASSCLLILFVWVVF 137
QY 137 GLFPIIRWAGCCCRVGRGRLRFAKPFVCTIDTIVLIASAVSAKTQGNIFATSAL 196
DB 138 GVBYFVRIWAAGCCCRVGRGRLRFAKPFVCTIDTIVLIASAVSAKTQGNIFATSAL 197
QY 197 RSLRFLQILRMVDRGGGTWKLGSVVVAHSELITAWIGFLVILFSSFLVYLVEKDA 256
DB 198 RSLRFLQILRMVDRGGGTWKLGSVVVAHSELITAWIGFLVILFSSFLVYLVEKDA 257
QY 257 NKFSFTYADALWGTITLTIGYDKYPTWNGRLLAATFTLIGVSFFALPAGILSGGFA 316
DB 258 NDHFDYADALWGLITLTIGYDKYPTWNGRLLAATFTLIGVSFFALPAGILSGGFA 317
QY 317 LKQVQHQHROKHFKERNRPAANLIQCVRSAAD-----EKSVSIATWK----- 359
DB 318 LKQVQHQHROKHFKERNRPAANLIQCVRSAAD-----EKSVSIATWK----- 377
QY 360 -----PHLKALHT-----CSP--TNOKL 375
DB 378 TYGASRLIPLNQLLELLRNLSKSLGAFKDPPEPSPSKGSPCRGPGCLCCGGRSSQKV 437
QY 437 SPKERVMAASPRGQSIKRSQASVGD--RRSPSTDTITAGSPTKVQKSWSNDRTRFRPSL 433
DB 438 SLKDRV--FSSPRGVAAGKGSQAQTVRRSPASQDSLEDSPSKVPSKSPGDRSRAQAF 496
QY 434 RLKSSQPKPIDADTALGTDDVDEKCCQDVSVEDLTPLKTVIRAIRMKHFAKRF 493
DB 497 RIKGAASRQ--NSEASLPGEDIVDDKSCPCFEVTEDTPLGLKVSIRAVCMVRLVSKRF 554
QY 494 KETLRPDVDKVOYBOYAGHLDMLCRITKSLQTRVDQILGGOITSDKSKSEKITAHETT 553
DB 555 KESLRPDVMDVIEQYAGHLDMLSRKISLQSRVDQIVGRGPAITD--KDTKGPAAELP 613
QY 554 DLSMLGRVVKVQKQVQSIKESKLDCLDIYQQVLRKGSASALASQIIPPFEC----- 607
DB 614 EDPSSMGRGKVKQVLSMEKLDFLVNIYQ--RMG-----IPTTEAYFGA 660
QY 608 ---EQTSDYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOQFILTNPFSQAQTYALSPT 664

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Db 661 KEPEPAPPVHSPEDSRE---HVDRHGCIIVKIVSSSTG-----QKNFAPP--AAPP- 708
QY 665 MHSQATQVPIQS-----DGSAVAATNTIANQINTAPKPAAPTTLQI----- 706
Db 709 -----VQCPSTSQSHRPGHGTSVPGDHGSLVRIPPPAPHAERSLSAYGNGRASME 763
QY 707 -----PP-----PLPAIKHLPRPETHLPNPAQLOESISDVTTCVLVASK 744
Db 764 FLRQEDTPGCRPEPTGLRSDTISIPSDH-----BELERSFSGF--SISO-----SK 810
QY 745 ENVOVAQS 752
Db 811 ENLDALNS 818

RESULT 15
US-09-177-650-2
; Sequence 2, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 872
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-650-2

Query Match 39.2%; Score 1783; DB 4; Length 872;
Best Local Similarity 47.9%; Pred. No. 1.6e-152;
Matches 406; Conservative 88; Mismatches 180; Indels 174; Gaps 24;

QY 17 AARGDGLLLGTAAATLGGGGGLRESRRKQKQARMSLLGKPLSYTSSQSCRNVKRVV 76
Db 34 STRDGALLIAGSEAPK---RGSILSKPRAGAGA-----GKP-----PKNAFYRKL 77
QY 77 QNYLYNVLERPRGWAFTYHAFVLLVFGCLLSVFSTIPEHTKLASSCLLILFVWVVF 136
Db 78 QNFYLVNLERPRGWAFTYHAFVLLVFGCLLSVFSTIPEHTKLASSCLLILFVWVVF 137
QY 137 GLFPIIRWAGCCCRVGRGRLRFAKPFVCTIDTIVLIASAVSAKTQGNIFATSAL 196
Db 138 GVBYFVRIWAAGCCCRVGRGRLRFAKPFVCTIDTIVLIASAVSAKTQGNIFATSAL 197
QY 197 RSLRFLQILRMVDRGGGTWKLGSVVVAHSELITAWIGFLVILFSSFLVYLVEKDA 256
Db 198 RSLRFLQILRMVDRGGGTWKLGSVVVAHSELITAWIGFLVILFSSFLVYLVEKDA 257
QY 257 NKFSFTYADALWGTITLTIGYDKYPTWNGRLLAATFTLIGVSFFALPAGILSGGFA 316
Db 258 NDHFDYADALWGLITLTIGYDKYPTWNGRLLAATFTLIGVSFFALPAGILSGGFA 317
QY 317 LKQVQHQHROKHFKERNRPAANLIQCVRSAAD-----EKSVSIATWK----- 359
Db 318 LKQVQHQHROKHFKERNRPAANLIQCVRSAAD-----EKSVSIATWK----- 377
QY 360 -----PHLKALHT-----CSP--TNOKL 375
Db 378 TYGASRLIPLNQLLELLRNLSKSLGAFKDPPEPSPSKGSPCRGPGCLCCGGRSSQKV 437
QY 376 SFKERVMAASPRGQSIKRSQASVGD--RRSPSTDTITAGSPTKVQKSWSNDRTRFRPSL 433

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Db	438	SLKDRV-FSSPRGVAAGKGSPOAQTVRRSPSADQSLSDSPSKVPKSWSGDRSRARQAF	496
Qy	434	RLKSSQPKVIDADTALGTDDVDEKCCQCDVSVEDLTPPLKTVIRAIRIMKPHVAKRKF	493
Db	497	RIKGAASRQNSE-EASLPGEDIVDDKSCPCFVTEDLTPGLKVSIRAVCMFVLSKRKF	555
Qy	494	KETLRPYDVVDVIEOYSAGHLMCRKISLQTRVDOILGKGQITSOKKREKITAHEHTT	553
Db	556	KESLRPYDVNDVIEOYSAGHLMLSRIKSLQSRVDQIVGEGPAITD-KORTKGPAEALP	614
Qy	554	DDLMLGRVVVKVKQVQSIKSLDCLDIYQQVLRKGSASALASFOIPPFEC-----	607
Db	615	EDFSMMGRLGKVEKQVLSMEKLDLFLVWQ-RMG-----IPPTETAYFGA	661
Qy	608	---EQTSDYQSPVDSKDLGSAQNSGCLSRSTANISRGLOFILTNEFSAQTFYALSPT	664
Db	662	KEPEPAPPYHSPEDSRE---HVDRHGCIKIVRSSSTG-----QKNFSAPP--AAPP-	709
Qy	665	MHSQATQVPIQS-----DGSVAATNTIANQINTAPKPAAPTTLQI-----	706
Db	710	-----VQCPFSTWQPOSHPRQGHGTSFVGDHGSGLVRIPPPAAHERSLSAYGGNEASME	764
Qy	707	-----PP-----PLPAIKHLPRPETLHPNPAGLOESISDVTTCVLVASK	744
Db	765	FLRQEDTPGCRPPEGNLRDSDTSISIPSDH---BELERSFSGF--SISQ-----SK	811
Qy	745	ENVQVAQS	752
Db	812	ENLDALNS	819

Search completed: April 8, 2005, 16:43:40
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:23:30 ; Search time 180 Seconds
(without alignments)
1908.018 Million cell updates/sec

Title: US-09-810-796-5

Perfect score: 4547

Sequence: 1 MKOVESGRVLLNSAARG.....SICKAGESTALSLPHVKLK 888

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4547	100.0	888	AAU09021	Human vol
2	4547	100.0	923	AAU09021	Human ion
3	4527.5	99.6	897	AAU09020	Human vol
4	4527.5	99.6	897	AAU09020	Human vol
5	4527.5	99.6	897	AAU09020	Human vol
6	4524.5	99.5	897	AAU09025	Human vol
7	4524.5	99.5	897	AAU09025	Human vol
8	4523.5	99.5	897	AAU09023	Human vol
9	4521.5	99.4	897	AAU09022	Human vol
10	4513.5	99.3	932	AAU09022	Human vol
11	4269.5	93.9	846	AAU09022	Human vol
12	1985	43.7	695	AAU09022	Human vol
13	1985	43.7	695	AAU09022	Human vol
14	1985	43.7	695	AAU09022	Human vol
15	1803.5	39.7	852	AAU09022	Human vol
16	1792	39.4	844	AAU09022	Human vol
17	1792	39.4	844	AAU09022	Human vol
18	1792	39.4	844	AAU09022	Human vol
19	1792	39.4	844	AAU09022	Human vol
20	1790.5	39.4	722	AAU09022	Human vol
21	1788.5	39.3	930	AAU09022	Human vol
22	1787.5	39.3	871	AAU09022	Human vol
23	1785	39.3	854	AAU09022	Human vol
24	1785	39.3	912	AAU09022	Human vol
25	1783	39.2	872	AAU09022	Human vol

26	1783	39.2	872	7	AAE38588	Human pot
27	1783	39.2	872	8	ADH51121	Potassium
28	1783	39.2	872	8	ADM77997	KCNQ2-fl
29	1783	39.2	914	4	ABG10643	Novel hum
30	1775	39.0	872	8	ADSL17845	Human KCN
31	1762	38.8	842	8	ADSL17846	Human KCN
32	1759	38.7	757	2	AAU08345	Mouse par
33	1710.5	37.6	942	4	ABG10645	Novel hum
34	1611	35.4	615	8	ADH51120	Potassium
35	1611	35.4	615	8	ADM77996	KCNQ2-15b
36	1604	35.3	625	8	ADH51118	Potassium
37	1604	35.3	625	8	ADM77994	KCNQ2-15b
38	1602	35.2	643	8	ADH51116	Potassium
39	1602	35.2	643	8	ADM77992	KCNQ2-15b
40	1587.5	34.9	854	2	AAU01534	Human KCN
41	1587.5	34.9	854	2	AAU01534	Human KCN
42	1587.5	34.9	872	2	AAU08344	Human KCN
43	1587.5	34.9	872	5	AAE16620	Human pot
44	1587.5	34.9	872	7	ADB78616	Human pot
45	1587.5	34.9	872	7	ADE55396	Human Pro

ALIGNMENTS

RESULT 1

AAU09021
ID AAU09021 standard; protein; 888 AA.

XX AC AAU09021;

XX DT 18-DEC-2001 (first entry)

XX DE Human voltage gated potassium channel hKCNQ5-2.

XX KW Human; voltage-gated potassium channel; hKCNQ5-2; nootropic;

XX KW cerebroprotective; neurotropic; analgesic; vision disorder;

XX KW central nervous system disorder; epilepsy; migraine; hearing disorder;

XX KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;

XX KW pain; gene therapy; splice variant.

XX OS Homo sapiens.

XX PN WO200170759-A1.

XX PD 27-SEP-2001.

XX PF 20-MAR-2001; 2001WO-US009328.

XX PR 21-MAR-2000; 2000US-0190954P.

XX PA (ICAG-) ICAGEN INC.

XX PI Jegla TJ;

XX DR WPI; 2001-611467/70.

XX DR N-ESDB; AAS14653.

XX PT Polypeptides and polynucleotides of potassium channel KCNQ5 for

XX PT identifying a compound modulating ion flux in eukaryotic cell or cell

XX PT membrane expressing the protein, comprises KCNQ approximately alpha-subunits.

XX FS Claim 17; Page 64; 78pp; English.

XX CC The invention relates to an isolated polypeptide comprising an alpha-

XX CC subunit of a KCNQ potassium channel, with a subsequence having 65%

XX CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence

XX CC and forms a KCNQ potassium channel having the characteristic of voltage-

XX CC gating with at least an additional KCNQ alpha-subunit. Also included in

XX CC the scope of the invention are the nucleic acids encoding hKCNQ5

XX CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression

XX CC vectors encoding them, antibodies against them, the use of 3-dimensional

XX CC computer modelling to identify molecules that bind to a KCNQ containing

CC potassium channel and modulate ion flux through the channel. The KCNQ polypeptide is useful for identifying a compound that increases or decreases ion flux through a potassium channel expressed in an eukaryotic host cell or cell membrane. The compound (and the KCNQ nucleic acid when used in gene therapy) is useful as a pharmaceutical agent for treating diseases involving abnormal ion flux, such as disorders of the central nervous system, such as epilepsy, migraines, hearing and vision problems, psychotic disorders, seizures, learning and memory disorders, stroke and pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a human tissue and the use of a nucleotide sequence of KCNQ5 to search computer databases to find variants of the sequence which are associated with disease states, is useful for screening mutations of KCNQ5. The present sequence is encoded by a splice variant of KCNQ5 and is hKCNQ5-2

xx
SQ Sequence 888 AA;

Query Match 100.0%; Score 4547; DB 4; Length 888;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDVESGRVLLNSAARGDGLLLGTRATLGGGGGLRSGRGQGRMSLLGKPLS 60
DB 1 MKDVESGRVLLNSAARGDGLLLGTRATLGGGGGLRSGRGQGRMSLLGKPLS 60

QY 61 YTSQSCRRNVKRVQNYLVNLERPGWAFIYHAFVLLVFGCLLSVFSIPEHTKL 120
DB 61 YTSQSCRRNVKRVQNYLVNLERPGWAFIYHAFVLLVFGCLLSVFSIPEHTKL 120

QY 121 ASSCLLILFVWVVGLEFIIRWSAGCCCRVQWGRFARFPCFVIDTIVLIASIA 180
DB 121 ASSCLLILFVWVVGLEFIIRWSAGCCCRVQWGRFARFPCFVIDTIVLIASIA 180

QY 181 VVSATQGNIFATSALRSLRFLQILRMVMDRGTWKLGSVVYVAHSELITAWYIGEL 240
DB 181 VVSATQGNIFATSALRSLRFLQILRMVMDRGTWKLGSVVYVAHSELITAWYIGEL 240

QY 241 VLIFSFVLVYVEKDANKEFTYADALWGWGITLTITIGYGDKTPLTWGLRLLSAGFALLG 300
DB 241 VLIFSFVLVYVEKDANKEFTYADALWGWGITLTITIGYGDKTPLTWGLRLLSAGFALLG 300

QY 301 ISFPALPAGILGSGFALKVQBOHQKFEKRNPAANLIQCVWRSYAADKSVSIAATWKP 360
DB 301 ISFPALPAGILGSGFALKVQBOHQKFEKRNPAANLIQCVWRSYAADKSVSIAATWKP 360

QY 361 HLKALHTCPTNOKLSFKERVMSRPGOSIKSROASVDRRSPSTDITAGSPKVKQS 420
DB 361 HLKALHTCPTNOKLSFKERVMSRPGOSIKSROASVDRRSPSTDITAGSPKVKQS 420

QY 421 WSNFDRTRFRPSLRKSSQPKFVIDADTALGTDVYDEKGCQCVSVEDLTPPLKTIVIRA 480
DB 421 WSNFDRTRFRPSLRKSSQPKFVIDADTALGTDVYDEKGCQCVSVEDLTPPLKTIVIRA 480

QY 481 IRIMKPHVAKRKFETLRPYDKVIEQYSAGHLDMLCRIKSLQTRVDQIILGKQITSDK 540
DB 481 IRIMKPHVAKRKFETLRPYDKVIEQYSAGHLDMLCRIKSLQTRVDQIILGKQITSDK 540

QY 541 KSREKITABETHTDLSMLGRVVKVQVQSIKSLDCLLDIYQVLRKGSASALALASF 600
DB 541 KSREKITABETHTDLSMLGRVVKVQVQSIKSLDCLLDIYQVLRKGSASALALASF 600

QY 601 QIPPECEQTSYQSPVDSKILGSAQNSGCLSRSTSANISRGLOFILTPEFSAQTYYA 660
DB 601 QIPPECEQTSYQSPVDSKILGSAQNSGCLSRSTSANISRGLOFILTPEFSAQTYYA 660

QY 661 LSPTMHSQATQVPIQSODGSAVAANTIANQINTAPKPAAPTLOIPPLPAIKHLRPE 720
DB 661 LSPTMHSQATQVPIQSODGSAVAANTIANQINTAPKPAAPTLOIPPLPAIKHLRPE 720

QY 721 TLHPNPAGIQESISDVTTCVASKENQVQAQSNLTKDRSMRKSFDWGGETLLSVCPMPVK 780
DB 721 TLHPNPAGIQESISDVTTCVASKENQVQAQSNLTKDRSMRKSFDWGGETLLSVCPMPVK 780

QY 781 DLGKLSLVQNILRSTELNIQLSGSESSGRSQDPYFKWRSEKLFITDEEVGPETETD 840

DB 781 DLGKLSLVQNILRSTELNIQLSGSESSGRSQDPYFKWRSEKLFITDEEVGPETETD 840

QY 841 TFDAAPQAPAREAAAFASDLSIRGSRSSOSICKAGESTALSPLHVKLK 888
DB 841 TFDAAPQAPAREAAAFASDLSIRGSRSSOSICKAGESTALSPLHVKLK 888

RESULT 2
AAB47678
ID AAB47678 standard; protein; 923 AA.
XX AAB47678;
XX AAB47678;
XX 21-JAN-2002 (first entry)
XX Human ion-channel forming protein.
DE DE
DE Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe.
XX Homo sapiens.
OS WO200175108-A1.
PN 11-OCT-2001.
XX 03-APR-2001; 2001WO-US010875.
PF 03-APR-2000; 2000US-0194255P.
PR (LEXI-) LEXICON GENETICS INC.
XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;
XX WPI; 2001-656987/75.
DR N-PSDB; AAH43633, AAH43634.
XX New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosing or treating diseases, in drug screening, and in
PT clinical trial monitoring.
XX Claim 2; Page 35-37; 4lpp; English.
PS This sequence represent a novel ion-channel forming protein. This protein
XX shares structural similarity with mammalian ion channel proteins,
XX particularly voltage-gated potassium channel proteins. The protein is
XX expressed in many human cell lines including fetal brain, brain,
XX thymus, prostate, heart and skeletal muscle. The novel protein can be used
XX in the diagnosis or treatment of diseases, in drug screening, and in
XX clinical trial monitoring. The oligonucleotides may be used as
XX hybridization probes for screening libraries, and assessing gene
XX expression patterns (particularly using a micro array or high throughput
XX drug discovery, to screen collections of genetic material from patients
XX who have a particular medical condition, to identify mutations associated
XX with a particular disease, as a diagnostic or prognostic assay, and to
XX screen for drugs which can be used to treat symptomatic or phenotypic
XX manifestations of perturbing the normal function of novel human protein.
XX The polypeptides are further used in generating antibodies

SQ Sequence 923 AA;

Query Match 100.0%; Score 4547; DB 4; Length 923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDVESGRVLLNSAARGDGLLLGTRATLGGGGGLRSGRGQGRMSLLGKPLS 60
DB 36 MKDVESGRVLLNSAARGDGLLLGTRATLGGGGGLRSGRGQGRMSLLGKPLS 95

Qy	61	YTSSQSCRNVKRRVQNYLNVLRPRGMAFIYHAFVFLVFGCLILSVFSTIPEHTKL	120
Db	96	YTSSQSCRNVKRRVQNYLNVLRPRGMAFIYHAFVFLVFGCLILSVFSTIPEHTKL	155
Qy	121	ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVWGQRLRFARKPCFVIDIVILASIA	180
Db	156	ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVWGQRLRFARKPCFVIDIVILASIA	215
Qy	181	VVSAKTOGNIPTATSLRSLRFLQILRMVMDRRGGTWKLLGSVVYAHSKELITAWYIGFL	240
Db	216	VVSAKTOGNIPTATSLRSLRFLQILRMVMDRRGGTWKLLGSVVYAHSKELITAWYIGFL	275
Qy	241	VLISSFLVYLVEKDANKFETADALWNGIITLITTYGDKTPTLWGLRLLSAGFALLG	300
Db	276	VLISSFLVYLVEKDANKFETADALWNGIITLITTYGDKTPTLWGLRLLSAGFALLG	335
Qy	301	ISPFALPAGILGSGFALKVQHQKHPEKRRNPAANLIQCWRSYAADEKSVSIATWKP	360
Db	336	ISPFALPAGILGSGFALKVQHQKHPEKRRNPAANLIQCWRSYAADEKSVSIATWKP	395
Qy	361	HLKALHTCSPNQKLSFKERVMSAPRQSIKSRQASVGDRRSPSTDIATBSGSPKVKQS	420
Db	396	HLKALHTCSPNQKLSFKERVMSAPRQSIKSRQASVGDRRSPSTDIATBSGSPKVKQS	455
Qy	421	WSFNDRTRFRPSIRLKSQPKPVIDADTALGTDDVYDEKGCQCDVSEDLTPPLKTVIRA	480
Db	456	WSFNDRTRFRPSIRLKSQPKPVIDADTALGTDDVYDEKGCQCDVSEDLTPPLKTVIRA	515
Qy	481	IRIMKHFVAKRKFETLRPYDKDVIQYSAGHLMCLCRIKSLQTRVDQIILKGQITSDK	540
Db	516	IRIMKHFVAKRKFETLRPYDKDVIQYSAGHLMCLCRIKSLQTRVDQIILKGQITSDK	575
Qy	541	KSREKITAETHETDDLSMLGRVWVKEQVQVIESKLDCLDIYQOVLKRGKSASALALASF	600
Db	576	KSREKITAETHETDDLSMLGRVWVKEQVQVIESKLDCLDIYQOVLKRGKSASALALASF	635
Qy	601	QIPPFCEQTSIDYQSPVDSKDLGSAQNSGCLSRSTGANISRGLOFILTNPFSQAOTFYA	660
Db	636	QIPPFCEQTSIDYQSPVDSKDLGSAQNSGCLSRSTGANISRGLOFILTNPFSQAOTFYA	695
Qy	661	LSPTMHSQATQVPIQSQSGSAVAANTIANQINTAPKPAAPTTLQIIPPLPAIKHLRPE	720
Db	696	LSPTMHSQATQVPIQSQSGSAVAANTIANQINTAPKPAAPTTLQIIPPLPAIKHLRPE	755
Qy	721	TLHPNPAGLQBSISDVTTCLVASKENVQVQASNLTKDRSMRKSFDMGGETLLSVCMPVPK	780
Db	756	TLHPNPAGLQBSISDVTTCLVASKENVQVQASNLTKDRSMRKSFDMGGETLLSVCMPVPK	815
Qy	781	DLGKSLSVQNLIRSTEELNIQLSGSSGSGSGSQDFPKWRKSLFITDEEVGPEETETD	840
Db	816	DLGKSLSVQNLIRSTEELNIQLSGSSGSGSGSQDFPKWRKSLFITDEEVGPEETETD	875
Qy	841	TFDAAPQAPAREAAAFASDSLRTRGRSSQSIKAGESTDALSHPVKLK	888
Db	876	TFDAAPQAPAREAAAFASDSLRTRGRSSQSIKAGESTDALSHPVKLK	923
RESULT 3			
ID	AAU09020	standard; protein; 897 AA.	
XX	AAU09020;		
AC	AAU09020;		
XX	18-DEC-2001	(first entry)	
DT	18-DEC-2001	(first entry)	
XX	Human voltage gated potassium channel hKCNQ5-1.		
DE	Human; voltage-gated potassium channel; hKCNQ5-1; nootropic;		
KW	cerebroprotective; neurotropic; analgesic; vision disorder;		
KW	central nervous system disorder; epilepsy; migraine; hearing disorder;		
KW	psychotic disorder; seizure; learning disorder; memory disorder; stroke;		
KW	pain; gene therapy; splice variant.		
XX			

OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
PH	Region	343..640	
FT		/label= Conserved region	
FT		/note= "This sequence is specifically claimed in claim	
FT		13"	
XX	WO200170759-A1.		
PN	27-SEP-2001.		
XX	20-MAR-2001; 2001WO-US009328.		
XX	21-MAR-2000; 2000US-0190954P.		
XX	(ICAG-) ICAGEN INC.		
XX	Jegla TJ;		
DR	WPI; 2001-611467/70.		
DR	N-PSDB; AAS14652.		
XX	Polypeptides and polynucleotides of potassium channel KCNQ5 for		
PT	identifying a compound modulating ion flux in eukaryotic cell or cell		
PT	membrane expressing the protein, comprises KCNQ approximately- subunits.		
XX	Claim 17; Page 64; 78pp; English.		
PS	The invention relates to an isolated polypeptide comprising an alpha-		
XX	subunit of a KCNQ potassium channel, with a subsequence having 65%		
CC	sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence		
CC	and forms a KCNQ potassium channel having the characteristic of voltage-		
CC	gating with at least an additional KCNQ alpha-subunit. Also included in-		
CC	the scope of the invention are the nucleic acids encoding hKCNQ5		
CC	(including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression		
CC	vectors encoding them, antibodies against them, the use of 3-dimensional		
CC	computer modelling to identify molecules that bind to a KCNQ containing		
CC	potassium channel and modulate ion flux through the channel. The KCNQ		
CC	polypeptide is useful for identifying a compound that increases or		
CC	decreases ion flux through a potassium channel expressed in an eukaryotic		
CC	host cell or cell membrane. The compound (and the KCNQ nucleic acid when		
CC	used in gene therapy) is useful as a pharmaceutical agent for treating		
CC	diseases involving abnormal ion flux, such as disorders of the central		
CC	nervous system, such as epilepsy, migraines, hearing and vision problems,		
CC	psychotic disorders, seizures, learning and memory disorders, stroke and		
CC	pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a		
CC	human tissue and the use of a nucleotide sequence of KCNQ5 to search		
CC	computer databases to find variants of the sequence which are associated		
CC	with disease states, is useful for screening mutations of KCNQ5. The		
CC	present sequence is encoded by a splice variant of hKCNQ5 and is hKCNQ5-1		
XX	Sequence 897 AA;		
SQ	Query Match	99.6%; Score 4527.5; DB 4; Length 897;	
	Best Local Similarity	98.9%; Pred. No. 0;	
	Matches	887; Conservative	1; Mismatches
		0; Indels	9; Gaps
Qy	1	MKDVESGRVLLNSAAARGDGLLLIGTAAATLGGGGGLRESRRGQAGMSLLGKPLS	60
Db	1	MKDVESGRVLLNSAAARGDGLLLIGTAAATLGGGGGLRESRRGQAGMSLLGKPLS	60
Qy	61	YTSSQSCRNVKRRVQNYLNVLRPRGMAFIYHAFVFLVFGCLILSVFSTIPEHTKL	120
Db	61	YTSSQSCRNVKRRVQNYLNVLRPRGMAFIYHAFVFLVFGCLILSVFSTIPEHTKL	120
Qy	121	ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVWGQRLRFARKPCFVIDIVILASIA	180
Db	121	ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVWGQRLRFARKPCFVIDIVILASIA	180
Qy	181	VVSAKTOGNIPTATSLRSLRFLQILRMVMDRRGGTWKLLGSVVYAHSKELITAWYIGFL	240
Db	181	VVSAKTOGNIPTATSLRSLRFLQILRMVMDRRGGTWKLLGSVVYAHSKELITAWYIGFL	240

QY	241	VLIFSFLVYLVEKDANKPSTYADALWVGITITLTITIGYDKTPTLTWLGRLISAGFALLG	300
Db	241	VLIFSFLVYLVEKDANKPSTYADALWVGITITLTITIGYDKTPTLTWLGRLISAGFALLG	300
QY	301	ISFFPALPAGILGSGFALKVQSHQKHQKPEKRRPAAANLTCQWRSVAADEKSVSTATWKP	360
Db	301	ISFFPALPAGILGSGFALKVQSHQKHQKPEKRRPAAANLTCQWRSVAADEKSVSTATWKP	360
QY	361	HLKALHTCSPT-----NOKLSFKERVMA SPRGQSIKRSQASVGDRRSPSDDITAE	411
Db	361	HLKALHTCSPTKKEOGEASSQKLSFKERVMA SPRGQSIKRSQASVGDRRSPSDDITAE	420
QY	412	GSPTKVQKSWSPFNDRTRRPSRLRLKSSQPKVEDDADTALGTTDDVDYDEKQCQCDVSVEDT	471
Db	421	GSPTKVQKSWSPFNDRTRRPSRLRLKSSQPKVEDDADTALGTTDDVDYDEKQCQCDVSVEDT	480
QY	472	PLPKTVIRAIRIMKFHVAKRPFKETLPYDVQKVDIEQYSAGHLDMLCRIKSLQTRVDQIL	531
Db	481	PLPKTVIRAIRIMKFHVAKRPFKETLPYDVQKVDIEQYSAGHLDMLCRIKSLQTRVDQIL	540
QY	532	GRGQITSDKKSEKITAHEHTDDLSMLGRVVKVEKQVQSIKSLDCLLDITQOVLKRS	591
Db	541	GRGQITSDKKSEKITAHEHTDDLSMLGRVVKVEKQVQSIKSLDCLLDITQOVLKRS	600
QY	592	ASALALASFOIPPFCEQTSYQSPVDSKOTLGSQAQNSGCLSRSTSANISRGLOFLTNP	651
Db	601	ASALALASFOIPPFCEQTSYQSPVDSKDLTGSQAQNSGCLSRSTSANISRGLOFLTNP	660
QY	652	EPFAQTFYALSTMHSQATQVPIQSODGSAVAANTTANQINTAPKPAAPTLLQIPEPPLP	711
Db	661	EPFAQTFYALSTMHSQATQVPIQSODGSAVAANTTANQINTAPKPAAPTLLQIPEPPLP	720
QY	712	AIKHLPRPETLHPNAGLOESIDVYTTCLVASKENVQVAOSNLTKDRSMKSKFDMGGETL	771
Db	721	AIKHLPRPETLHPNAGLOESIDVYTTCLVASKENVQVAOSNLTKDRSMKSKFDMGGETL	780
QY	772	LSVCPMVPKDILGKLSLVQNLIRSTELNITQLSGSESSGRSQDIFYPKWRESKLFITDEE	831
Db	781	LSVCPMVPKDILGKLSLVQNLIRSTELNITQLSGSESSGRSQDIFYPKWRESKLFITDEE	840
QY	832	VGPEETETDFAAPOPAEEAFAADSILRTGRSRSSQSIKAGBSTDALSIPHVKLK	888
Db	841	VGPEETETDFAAPOPAEEAFAADSILRTGRSRSSQSIKAGBSTDALSIPHVKLK	897

RESULT 4	
AAAB47046	
ID	AAAB47046 standard; protein; 897 AA.
XX	
AC	AAAB47046;
XX	
XX	20-APR-2001 (first entry)
XX	
XX	Human KCNQ5 potassium channel subunit.
XX	
KW	Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
KW	central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
KW	CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
KW	compulsive behaviour; dementia; depression; Huntington's disease; mania;
KW	memory impairment; memory dysfunction; spinal cord damage; phobia;
KW	Pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
Binding-site	93
FT	/label= Site 1
FT	120..138
FT	/label= Site 2
FT	166..185
FT	/label= Site 3
FT	188..213
FT	Binding-site

FT	Binding-site	/label= Site 4
FT	Region	230..252
FT	Region	/label= Site 5
FT	Region	265..284
FT	Binding-site	/label= P-loop
FT	Binding-site	291..314
FT	Domain	/label= Site 6
FT	Domain	495..544
FT	Domain	/label= A-domain
PN	WO200077035-A2.	
XX	21-DEC-2000.	
XX	29-MAY-2000; 2000WO-DK000289.	
XX	11-JUN-1999; 99DK-00000828.	
XX	(NEUR-) NEUROSEARCH AS.	
XX	Jentech TJ;	
XX	WPI; 2001-080678/09.	
DR	N-PSDB; AAC85414.	
XX	Novel genes encoding KCNQ5 potas	
PT	treating Alzheimer's disease, an	
PT	depression, Huntington's disease	
XX	Claim 8; Page 48-50; 50pp; Engli	
XX	This sequence shows the human KC	
CC	heteromeric channels with other	
CC	KCNQ3 and KCNQ4. The KCNQ5 gene	
CC	chromosome 6 (qg14). Chemicals w	
CC	are useful for diagnosis, treatm	
CC	diseases related to diseases of	
CC	system (CNS), including affectiv	
CC	anxiety, ataxia, CNS damage caus	
CC	illness, cognitive deficits, com	
CC	Huntington's disease, mania, mem	
CC	dysfunction, motion disorders, m	
CC	diseases, Parkinson's disease an	
CC	phobias, pick's disease, psychos	
CC	stroke, tremor, seizures, convul	
XX	Sequence 897 AA;	
SO		

Query Match	99.6%	Score 4527.5	DB 4	Length 897
Best Local Similarity	98.9%	pred. No. 0		
Matches 887	Conservative 1	Mismatches 0	Indels 9	Gaps 1
QY	1	MKDVESGRGVLLNSAARGDGLLLIGTRAAATLGGGGGGLRESRRGQAGARMSSLLGKPLS	60	
DB	1	MKDVESGRGVLLNSAARGDGLLLIGTRAAATLGGGGGGLRESRRGQAGARMSSLLGKPLS	60	
QY	61	YTSOSCRNNKYRRVQNYLVNLERPRGNWAFIYHAFVLLVFCGLILSVFSTPIPEHTKL	120	
DB	61	YTSOSCRNNKYRRVQNYLVNLERPRGNWAFIYHAFVLLVFCGLILSVFSTPIPEHTKL	120	
QY	121	ASSCLLILEFVMIYVFGLEFIIRIWSAGCCCRYRGWGQRLRPARKPCVIDTIVLLASIA	180	
DB	121	ASSCLLILEFVMIYVFGLEFIIRIWSAGCCCRYRGWGQRLRPARKPCVIDTIVLLASIA	180	
QY	181	VVSATQGNIFATSALRSLSRFLQILRWMDRRGSTWKLGSVVVAHSKELITAWYIGFL	240	
DB	181	VVSATQGNIFATSALRSLSRFLQILRWMDRRGSTWKLGSVVVAHSKELITAWYIGFL	240	
QY	241	VLIFFSFLVYLVEKDANKEFSTYADALWWGTTITLTIGYGDKTPLTWLGRLLSAGFALLG	300	
DB	241	VLIFFSFLVYLVEKDANKEFSTYADALWWGTTITLTIGYGDKTPLTWLGRLLSAGFALLG	300	
QY	301	ISFFPALPAGILGSGFALKVQEOHROKHEKRNPNANLQCWRSYAADEKSVSIATWKP	360	

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Db 301 ISFFALPAGILGSGFALKVQEQHQRKHFEKERNPAANLIQCVMWSYAADKSVSIATWKP 360
Qy 361 HLKALHTCSPT-----NQLSFKERVMSAPRGOSIKSROASVGDRRSPSTDITAE 411
Db 361 HLKALHTCSPTKQGEASSQKLSFKERVMSAPRGOSIKSROASVGDRRSPSTDITAE 420
Qy 412 GSPTKVKQSWFNDRTRFRPSRLRLKSSQPKVIDADTALGTDVDDYDEKGCQCVSVDLT 471
Db 421 GSPTKVKQSWFNDRTRFRPSRLRLKSSQPKVIDADTALGTDVDDYDEKGCQCVSVDLT 480
Qy 472 PPLKTVIRAIRIMKPHVAKRFKFTLRPYDKVIEQYSAGHLMCLCRIKSLQTRVDIOL 531
Db 481 PPLKTVIRAIRIMKPHVAKRFKFTLRPYDKVIEQYSAGHLMCLCRIKSLQTRVDIOL 540
Qy 532 KGQITSDKKSREKITAEHETDLSMLGRVVKVEKQVQSTESKLDCLLDIYQOVLKGS 591
Db 541 KGQITSDKKSREKITAEHETDLSMLGRVVKVEKQVQSTESKLDCLLDIYQOVLKGS 600
Qy 592 ASALALASFOIPPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTPN 651
Db 601 ASALALASFOIPPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTPN 660
Qy 652 EFSAQTFVALSPMHSQATQVPIQSOGSAVAANTIANQINTAPKAAPTLQIPPLP 711
Db 661 EFSAQTFVALSPMHSQATQVPIQSOGSAVAANTIANQINTAPKAAPTLQIPPLP 720
Qy 712 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVQVQSNLTKDRSMRKSFDWGGETL 771
Db 721 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVQVQSNLTKDRSMRKSFDWGGETL 780
Qy 772 LSVCPMPVKDLGKSLSVONLIRSTEELNIQLSGSESSGSRGSDQFYPKWRRESKLFIIDEE 831
Db 781 LSVCPMPVKDLGKSLSVONLIRSTEELNIQLSGSESSGSRGSDQFYPKWRRESKLFIIDEE 840
Qy 832 VGPEETDTDFDAAPQAPAREAFASDSLRTGRSSQSICKAGESTDALSIPHVKLK 888
Db 841 VGPEETDTDFDAAPQAPAREAFASDSLRTGRSSQSICKAGESTDALSIPHVKLK 897

RESULT 5
AAE16599 standard; protein; 897 AA.
XX AC AAE16599;
XX DT 09-APR-2002 (first entry)
XX DE Human potassium channel polypeptide, KCNQ5.
XX KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;
KW multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW learning deficiency; cognitive disorder; motor disease; neuron disease;
KW neuropsychological disorder; neuropsychological disorder; asthma;
KW neuron cell death; brain tumour; gene therapy; antisenese therapy;
KW synaptic transmission; electrical excitability.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 191..209
XX FT /note="Pore region"
XX FT Region 265..285
XX FT /note="S4 voltage sensor region"
XX WO200192526-A1.
XX FN
XX PD 06-DEC-2001.
XX PF 24-MAY-2001; 2001WO-US017314.
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XX 26-MAY-2000; 2000US-0207389P.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX Dworetzky SI, Ramanathan CS, Trojnacki JT, Boissard CG;
XX Gribkoff VK;
XX WPI; 2002-122069/16.
XX DR N-PSDB; AAD27192.
XX Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
XX it, for diagnosing, treating and identifying modulators useful in
XX treating neurological, neuropsychological and neuropsychological
XX diseases.
XX Claim 25; Fig 2; 128pp; English.
XX The invention relates to potassium channel polypeptides referred to as
XX KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
XX polypeptides are useful for identifying compounds that modulate their
XX biological activity. The compounds identified and KCNQ5 polynucleotides
XX are useful for treating acute and chronic pain, migraine, acute stroke,
XX dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),
XX multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,
XX depression, bipolar disorders, sleep disorders, eating disorders,
XX addiction, myokymia, Alzheimer's disease, age-associated memory loss,
XX learning deficiencies, cognitive disorders and motor neuron diseases. The
XX nucleic acid molecules of the invention are further useful for treating
XX neuropsychological, neuropsychological disorders, asthma, neuron cell
XX death and brain tumors. They are also used in gene therapy and antisense
XX therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical
XX excitability in the brain and are useful for generating antibodies. They
XX are also useful to affinity purify biological effectors from biological
XX materials e.g. disease tissues or cells. The present sequence is human
XX KCNQ5 protein
XX SQ Sequence 897 AA;
Query Match 99.6%; Score 4527.5; DB 5; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
Qy 1 MKDVESGRGRVLLNSAAARGDGLLLLTGTRATIGGGGGGLRESRRGQGRMSLLGKPLS 60
Db 1 MKDVESGRGRVLLNSAAARGDGLLLLTGTRATIGGGGGGLRESRRGQGRMSLLGKPLS 60
Qy 61 YTSQSCRRNVKVRVQNVLYNVLERPRGNWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120
Db 61 YTSQSCRRNVKVRVQNVLYNVLERPRGNWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120
Qy 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRVGMQGRLFARFKPFCDITIVILASIA 180
Db 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRVGMQGRLFARFKPFCDITIVILASIA 180
Qy 181 VSAKTOGNIFATLSALRSFLQLRLNVRMDRGSTWKLIGSVVYAHSKELITAWYIGFL 240
Db 181 VSAKTOGNIFATLSALRSFLQLRLNVRMDRGSTWKLIGSVVYAHSKELITAWYIGFL 240
Qy 241 VLIFFSFLVYLVEKDANKFSTVADALWNGTITLTTIGYGDKTPLTWGLRLLSAGFALLG 300
Db 241 VLIFFSFLVYLVEKDANKFSTVADALWNGTITLTTIGYGDKTPLTWGLRLLSAGFALLG 300
Qy 301 ISFFALPAGILGSGFALKVQEQHQRKHFEKERNPAANLIQCVMWSYAADKSVSIATWKP 360
Db 301 ISFFALPAGILGSGFALKVQEQHQRKHFEKERNPAANLIQCVMWSYAADKSVSIATWKP 360
Qy 361 HLKALHTCSPT-----NQLSFKERVMSAPRGOSIKSROASVGDRRSPSTDITAE 411
Db 361 HLKALHTCSPTKQGEASSQKLSFKERVMSAPRGOSIKSROASVGDRRSPSTDITAE 420
Qy 412 GSPTKVKQSWFNDRTRFRPSRLRLKSSQPKVIDADTALGTDVDDYDEKGCQCVSVDLT 471
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661 EFSAQTFYALSPMTMHSQATQVPIQSQSGSAVAANTNTIANQINTAPKPAAPTTLQIPPLP 720
712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENQVQASNLTKDRSMKSFDMGGETL 771
721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENQVQASNLTKDRSMKSFDMGGETL 780
772 LSVCPMPVKDLGKLSLVQNLIRSTEELNIQLSGSESGSGSGSQDFPKWRESKLFITDEE 831
781 LSVCPMPVKDLGKLSLVQNLIRSTEELNIQLSGSESGSGSGSQDFPKWRESKLFITDEE 840
832 VGPSETTDFDAAPQAPAREAFASDSLRTRGRSSQSIKAGESTDALSLPHVKLK 888
841 VGPSETTDFDAAPQAPAREAFASDSLRTRGRSSQSIKAGESTDALSLPHVKLK 897

RESULT 8
AAU09024
ID AAU09024 standard; protein; 897 AA.
XX
AC AAU09024;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human voltage gated potassium channel hKCNQ5-1 variant #3.
XX
KW Human; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW cerebrotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; mutant; mutein.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT 343..640
FT /label= Conserved region
FT /note= "This sequence is specifically claimed in claim
FT 13"
FT Misc-difference 446
FT /note= "Wild-type Ser substituted by Gly"
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US009328.
XX
PR 21-MAR-2000; 2000US-0190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
XX
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximately a- subunits.
XX
PS Disclosure; Page; 78pp; English.

XX
XX The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic

CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy) is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a polymorphic variant of hKCNQ5-1. Note: The present
CC sequence does not appear in the specification but is based on hKCNQ5-1
CC sequence appearing as AAU09020
XX
SQ Sequence 897 AA;

Query Match 99.5%; Score 4523.5; DB 4; Length 897;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 886; Conservative 1; Mismatches 1; Indels 9; Gaps 1;
QY 1 MKDVESGRVLLNSAAARGDGLLLLTGTRAAATLGGGGGGLRESRRKGQARMSLGKPLS 60
DB 1 MKDVESGRVLLNSAAARGDGLLLLTGTRAAATLGGGGGGLRESRRKGQARMSLGKPLS 60
QY 61 YTSQSCRRNVKRRVQNYLVNLRPRGWAFIYHAFVFLVFGCLLSVFTSTIPEHTKL 120
DB 61 YTSQSCRRNVKRRVQNYLVNLRPRGWAFIYHAFVFLVFGCLLSVFTSTIPEHTKL 120
QY 121 ASSCLLLEFVMVVGLEFIIRWSAGCCRYRGQGRLEFARFPFCVIDIVLIATIA 180
DB 121 ASSCLLLEFVMVVGLEFIIRWSAGCCRYRGQGRLEFARFPFCVIDIVLIATIA 180
QY 181 VVSATQGNIFATLSALRSRFLQILRMVMDRRGGTWKLLGVSVAHSEKELITAWYIGEL 240
DB 181 VVSATQGNIFATLSALRSRFLQILRMVMDRRGGTWKLLGVSVAHSEKELITAWYIGEL 240
QY 241 VLFSSFLVLYVEKDANKFSTYADALWGGTTLTITIGYDKTPTLWGLLSAGFALLG 300
DB 241 VLFSSFLVLYVEKDANKFSTYADALWGGTTLTITIGYDKTPTLWGLLSAGFALLG 300
QY 301 ISFFALPAGILGSGFALKVQEQHROKHFEKRRNPANLIQCVWRSYAADKSVSIATWKP 360
DB 301 ISFFALPAGILGSGFALKVQEQHROKHFEKRRNPANLIQCVWRSYAADKSVSIATWKP 360
QY 361 HLKALHTCSPT-----NOKLSPKERVNRASPRGQSIKRSQASVGRDRSPSTDTAE 411
DB 361 HLKALHTCSPTKEQGEASSQKLSFKERVNRASPRGQSIKRSQASVGRDRSPSTDTAE 420
QY 412 GSPTKVQKWSFNDRTRFRPSRLKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 471
DB 421 GSPTKVQKWSFNDRTRFRPSRLKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 480
QY 472 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDKVDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
DB 481 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDKVDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540
QY 532 GKQITSDKKSREKITAETHETDLSMLGHVVKVQVQVQVQVQVQVQVQVQVQVQVQVQV 591
DB 541 GKQITSDKKSREKITAETHETDLSMLGHVVKVQVQVQVQVQVQVQVQVQVQVQVQV 600
QY 592 ASALALASFOIPPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTNP 651
DB 601 ASALALASFOIPPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTNP 660
QY 652 EFSAQTFYALSPMTMHSQATQVPIQSQSGSAVAANTNTIANQINTAPKPAAPTTLQIPPLP 711
DB 661 EFSAQTFYALSPMTMHSQATQVPIQSQSGSAVAANTNTIANQINTAPKPAAPTTLQIPPLP 720
QY 712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENQVQASNLTKDRSMKSFDMGGETL 771
DB 721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENQVQASNLTKDRSMKSFDMGGETL 780
QY 772 LSVCPMPVKDLGKLSLVQNLIRSTEELNIQLSGSESGSGSGSQDFPKWRESKLFITDEE 831

AAB86979
 ID AAB86979 standard; protein; 932 AA.
 XX AC AAB86979;
 XX DT 11-DEC-2001 (first entry)
 XX DE Human KCNQ5 protein.
 XX KW KCNQ5; potassium channel protein; human; neurological; cardiovascular;
 KW anticonvulsant; excitability modulator; membrane potential; neuron;
 KW voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
 KW screening; central nervous system disease; cardiovascular disease.
 XX OS Homo sapiens.
 XX FN DE10013732-A1.
 XX PD 27-SEP-2001.
 XX PF 21-MAR-2000; 2000DE-01013732.
 XX PR 21-MAR-2000; 2000DE-01013732.
 XX PA (AVET) AVENTIS PHARMA DEUT GNEH.
 XX PI Steinmeyer K, Lerche C, Scherer C, Seeborn G, Busch AE;
 XX DR WPI; 2001-571700/65.
 XX DR N-PSDB; AAH49499.
 XX PT New DNA sequence encoding potassium channel KCNQ5, useful in screening
 PT for specific modulators, potential agents for treating central nervous
 PT system and cardiovascular diseases.
 XX PS Claim 1b; Page 10-14; 20pp; German.
 XX CC This invention describes a novel DNA sequence (I) encoding: (i) a
 CC polypeptide (ii) with potassium channel KCNQ5 activity; (ii) a
 CC polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
 CC the invention have neurological, cardiovascular and anticonvulsant
 CC activity and act as modulators of the voltage-dependent KCNQ5 potassium
 CC channel, a key regulator of membrane potential and modulator of
 CC excitability of electrically activated cells such as neurons and
 CC cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
 CC are used to screen for compounds that modulate the activity of KCNQ5,
 CC potentially useful for treating central nervous system (e.g. epilepsy)
 CC and cardiovascular diseases. This sequence represents the human potassium
 CC channel KCNQ5 protein described in the invention
 XX SQ Sequence 932 AA;
 Query Watch 99.3%; Score 4513.5; DB 4; Length 932;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 885; Conservative 1; Mismatches 2; Indels 9; Gaps 1;
 QY 1 MKDVEGGRVLLNSAAAGDGLLLGTRAAATLGGGGGLRESRRGKQGMRLGKPLS 60
 DB 36 MKDVEGGRVLLNSAAAGDGLLLGTRAAATLGGGGGLRESRRGKQGMRLGKPLS 95
 QY 61 YTSQSCRRNVKRRVQNYLVNLERPRGWAFIYHAFVFLVFGCLLSVFSFTPEHTKL 120
 DB 96 YTSQSCRRNVKRRVQNYLVNLERPRGWAFIYHAFVFLVFGCLLSVFSFTPEHTKL 155
 QY 121 ASSCLLILFVMIWFGLEFIIRWSAGCCCRVWGQRLRFARPPFCVIDIVILASIA 180
 DB 156 ASSCLLILFVMIWFGLEFIIRWSAGCCCRVWGQRLRFARPPFCVIDIVILASIA 215
 QY 181 VVSAKTQGNIFATSALESRLFLQILRMVRMDRRGGTWKLLGVSVAHSELITAWYIGFL 240
 DB 216 VVSAKTQGNIFATSALESRLFLQILRMVRMDRRGGTWKLLGVSVAHSELITAWYIGFL 275
 QY 241 VLIFSSFLVYLVEKDANKFSTYADALWNGTITLTIGYDKTPTLWLGRLLSAGFALLG 300

DB 276 VLIFSSFLVYLVEKDANKFSTYADALWNGTITLTIGYDKTPTLWLGRLLSAGFALLG 335
 QY 301 ISFPALPAGILSGFALKVQBOHROKHFEKRRNPANLIQVWRSYAADSKSVSIATWKP 360
 DB 336 ISFPALPAGILSGFALKVQBOHROKHFEKRRNPANLIQVWRSYAADSKSVSIATWKP 395
 QY 361 HLKALHTCSPT-----NOKLSFKERVRMASPRGQSIKRSQASVGRDRSPSTDTAE 411
 DB 396 HLKALHTCSPTKQGEASSQKLSFKERVRMASPRGQSIKRSQASVGRDRSPSTDTAE 455
 QY 412 GSPTKVQKWSFNDRTPRPSRLKSSQPFVIDADTALGTDVDDVDEKGCOCDSVSDLT 471
 DB 456 GSPTKVQKWSFNDRTPRPSRLKSSQPFVIDADTALGTDVDDVDEKGCOCDSVSDLT 515
 QY 472 PPLKTVIRAIRIMKPHVAKRKFTLPRYDVQVIEQVSAGHLDMLCRIKSLQTRVQIL 531
 DB 516 PPLKTVIRAIRIMKPHVAKRKFTLPRYDVQVIEQVSAGHLDMLCRIKSLQTRVQIL 575
 QY 532 GKGQITSDKSKREKITAETHETDLSMLGRVVKVEKQVQSIKSLDCLLDIYQVLRKGS 591
 DB 576 GKGQITSDKSKREKITAETHETDLSMLGRVVKVEKQVQSIKSLDCLLDIYQVLRKGS 635
 QY 592 ASALALASFOIPPECEQTSYQSPVDSKDLSSAONSGCLSRSTSANISRLQFILTPN 651
 DB 636 ASALALASFOIPPECEQTSYQSPVDSKDLSSAONSGCLSRSTSANISRLQFILTPN 695
 QY 652 EFSAQTFVALSPTMHSQATQVPIQSOGSAVAANTIANQINTAPKPAAPTTLQIPPLP 711
 DB 696 EFSAQTFVALSPTMHSQATQVPIQSOGSAVAANTIANQINTAPKPAAPTTLQIPPLP 755
 QY 712 AIKHLPRPETHLPNAGLOESISDVTTCLVASKENVQVQASNLTKDRSNRKSFDMGSTL 771
 DB 756 AIKHLPRPETHLPNAGLOESISDVTTCLVASKENVQVQASNLTKDRSNRKSFDMGSTL 815
 QY 772 LSVCPMPVKDLCKSLSVQNLIRSTELNITQLSGSSSGSRGSDQFYPKWRSKLPITDEE 831
 DB 816 LSVCPMPVKDLCKSLSVQNLIRSTELNITQLSGSSSGSRGSDQFYPKWRSKLPITDEE 875
 QY 832 VGPEETETDTFADAPQAPAREAFASDSLRGTGRSSQSI CKAGESTDALSLPHVKLK 888
 DB 876 VGPEETETDTFADAPQAPAREAFASDSLRGTGRSSQSI CKAGESTDALSLPHVKLK 932
 RESULT 11
 AAB24241
 ID AAB24241 standard; protein; 846 AA.
 XX AC AAB24241;
 XX DT 07-FEB-2001 (first entry)
 XX DE Human KCNQ5 (KCN6q) protein sequence SEQ ID NO:3.
 XX KW Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salla disease; ophthalmological; auditory; central nervous system;
 KW cardioactive; anticonvulsant; gastrointestinal; muscular active;
 KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder.
 XX OS Homo sapiens.
 XX FN WO200061606-A1.
 XX PD 19-OCT-2000.
 XX PF 10-APR-2000; 2000WO-US009587.
 XX PR 14-APR-1999; 99US-0129274P.
 XX PA (MERI) MERCK & CO INC.

Petrukhin K, Caskey CT, Li W, Metzker ML;
 WPI; 2000-647417/62.
 N-PSDB; AAC64370, AAC64371.
 Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying inhibitors and activators which can treat e.g. Stargardt-like macular dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
 Claim 8; Fig 2; 99pp; English.

The present sequence represents the human KCNQ5 (also called KCN6q) protein, which is a voltage-gated potassium channel protein. Human KCNQ5 has ophthalmological, auditory, central nervous system (CNS), cardiovascular, anticonvulsant, gastrointestinal and muscular active activities. Sequences and methods from the present invention are useful for identifying activators or inhibitors of KCNQ5 protein. These activators and inhibitors are useful for treating Stargardt-like macular dystrophy, cone-rod dystrophy, Salla disease, age-related macular degeneration, other forms of macular degeneration, deafness, epilepsy, and different forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders. Stargardt-like macular dystrophy and cone-rod dystrophies are located at chromosome 6q

Sequence 846 AA;

Query Match 93.9%; Score 4269.5; DB 3; Length 846;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 835; Conservative 1; Mismatches 1; Indels 9; Gaps 1;

Qy 52 MSLGKPLSYSSQSRNRYRQVLYNVLPRGMAFIYHAFVLLVFGCLILSVF 111
 Db 1 MSLGKPLSYSSQSRNRYRQVLYNVLPRGMAFIYHAFVLLVFGCLILSVF 60

Qy 112 STIPEHTKLASSCLLIEFVMIIVVFGLEFIIRWSAGCCCYRQWGLRPAKPFV 171
 Db 61 STIPEHTKLASSCLLIEFVMIIVVFGLEFIIRWSAGCCCYRQWGLRPAKPFV 120

Qy 172 TIVLIASIVASAKTQGNIFATSALRSRFLQILRMVMDRRGGTWKLLGSVVYAHSKEL 231
 Db 121 TIVLIASIVASAKTQGNIFATSALRSRFLQILRMVMDRRGGTWKLLGSVVYAHSKEL 180

Qy 232 ITAWYIGFLVLIPIPSFLVYVEKANKFEFSTYADALMWGTTITLTIGYDKTPTLWGLRL 291
 Db 181 ITAWYIGFLVLIPIPSFLVYVEKANKFEFSTYADALMWGTTITLTIGYDKTPTLWGLRL 240

Qy 292 LSAGFALLIGISFFALPAGILGSGFALKVQEOHROKHFEKRNPAANLIQCVWRSYAADK 351
 Db 241 LSAGFALLIGISFFALPAGILGSGFALKVQEOHROKHFEKRNPAANLIQCVWRSYAADK 300

Qy 352 SVSIATWPKPHLKALHTCSPT-----NQKLSFKERVNRMASPRGOSIKSRQASVGDRR 402
 Db 301 SVSIATWPKPHLKALHTCSPTKKEQGEASSQKLSFKERVNRMASPRGOSIKSRQASVGDRR 360

Qy 403 SPSTDTIATGSPTKVQKSWSNDRTRRPSRLKSSQPKVIDADTALGTDDVDYDKGCQ 462
 Db 361 SPSTDTIATGSPTKVQKSWSNDRTRRPSRLKSSQPKVIDADTALGTDDVDYDKGCQ 420

Qy 463 CDVSVEDLTPLKTVIRAIRIMKPHVAKRKPEKTLRPVDVKDVEQYSAGHLMCLCRKS 522
 Db 421 CDVSVEDLTPLKTVIRAIRIMKPHVAKRKPEKTLRPVDVKDVEQYSAGHLMCLCRKS 480

Qy 523 LQTRVDQILGKGQITSDKSKREKITAHEHTDDLSMLGRVVKVQKQVQSIIESKLDCLLDI 582
 Db 481 LQTRVDQILGKGQITSDKSKREKITAHEHTDDLSMLGRVVKVQKQVQSIIESKLDCLLDI 540

Qy 583 YQOVLKGSASALALAFQIPPFCEQTSYDQSPVDKDLGSGAQNSGCLSRSTANISR 642
 Db 541 YQOVLKGSASALALAFQIPPFCEQTSYDQSPVDKDLGSGAQNSGCLSRSTANISR 600

Qy 643 GLQFILPNEFSATQTFVALSPTMHSQATQVPIQSODGSAVAATNTIANQINTAPKPAAPT 702

Db 601 GLQFILPNEFSATQTFVALSPTMHSQATQVPIQSODGSAVAATNTIANQINTAPKPAAPT 660
 Qy 703 TLQIPPLPAIKHLPRPETLHPNPAQLOESISDVTTCLVASKENVQVAQSNLTIDKRSNRK 762
 Db 661 TLQIPPLPAIKHLPRPETLHPNPAQLOESISDVTTCLVASKENVQVAQSNLTIDKRSNRK 720
 Qy 763 SFDMGGSTLLSVCPMPVKDLGKLSVQNLIRSTELMIQLSGSSSSSGRSQDFFPKWRE 822
 Db 721 SFDMGGSTLLSVCPMPVKDLGKLSVQNLIRSTELMIQLSGSSSSSGRSQDFFPKWRE 780
 Qy 823 SKLFIITDEEVGPETETDTDAAPQAPAREAAFAASDLSRTGRSSQSICKAGESTDALS 882
 Db 781 SKLFIITDEEVGPETETDTDAAPQAPAREAAFAASDLSRTGRSSQSICKAGESTDALS 840
 Qy 883 PHVKLK 888
 Db 841 PHVKLK 846

RESULT 12
 AAB01476
 ID AAB01476 standard; protein; 695 AA.
 AC AAB01476;
 XX 08-NOV-2000 (first entry)
 DT XX
 DE XX
 DE XX
 KW KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;
 KW deafness; probes; treatment; therapy; transgenic animal; antibody;
 KW agonist; antagonist; tinnitus; hearing loss; neonatal deafness;
 KW presbycusis; affective disorder; Alzheimer's disease; anxiety; ataxia;
 KW cognitive deficits; compulsive behavior; dementia; depression;
 KW Huntington's disease; mania; memory impairment; motor disorders;
 KW neurodegenerative disease; Parkinson's disease; Pick's disease;
 KW psychosis; schizophrenia; spinal cord damage; stroke; tremor.
 XX Homo sapiens.
 OS
 PN XX
 XX WO200044786-A1.
 XX
 PD 03-AUG-2000.
 XX
 XX 19-JAN-2000; 2000WO-DK000024.
 XX
 XX 26-JAN-1999; 99DK-00000076.
 XX
 XX 19-MAY-1999; 99DK-00000593.
 XX
 XX (NEUR-) NEUROSEARCH AS.
 PA
 XX
 XX Jentsch TJ;
 PI
 XX WPI; 2000-548813/50.
 XX
 XX N-PSDB; AAA47618.
 DR
 XX
 XX Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's diseases.
 PT
 XX
 XX
 PS Claim 8; Page 48-51; 65pp; English.
 CC
 CC Mutations in 3 known genes of the KCNQ branch of the potassium channel gene family underlie inherited cardiac arrhythmia's, neonatal epilepsy and in some cases associated with deafness. KCNQ4 has been mapped to the DFN2 locus for autosomal dominant hearing loss, and a dominant negative KCNQ4 mutation that causes deafness in a DFN2 pedigree has been identified. KCNQ4 is the first potassium channel gene underlying non-syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4 protein and the protein itself may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate KCNQ4 expression. The nucleotides may also be used as DNA probes in diagnostic assays (e.g.

CC	polymerase chain reactions (PCR)) to detect and quantitate the presence
CC	of similar nucleic acid sequences in samples and to identify mutations
CC	within them, and hence which patients may be in need of restorative
CC	therapy. They may also be used to study the expression and function of
CC	KCNQ4 polypeptides and their role in metabolism, for example through the
CC	production of transgenic animals. The KCNQ4 polypeptides may be used as
CC	antigens in the production of antibodies and to identify modulators
CC	(agonists and antagonists) of KCNQ4 expression and activity. The anti-
CC	KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate
CC	KCNQ4 expression and activity. They may be used in this way to treat
CC	tinnitus, loss of hearing (especially progressive hearing loss, neonatal
CC	deafness and presbycusis (deafness of the elderly)) and disease or
CC	adverse conditions of the central nervous system (CNS) such as affective
CC	disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by
CC	trauma, stroke or neurodegenerative illnesses, cognitive deficits,
CC	compulsive behavior, dementia, depression, Huntington's disease, mania,
CC	memory impairment, memory disorders and dysfunctions, motion disorders,
CC	motor disorders, neurodegenerative diseases, Parkinson's disease,
CC	Parkinson-like motor disorders, phobias, pick's disease, psychosis,
CC	schizophrenia, spinal cord damage, stroke and/or tremor. Conversely,
CC	antisense nucleic acid molecules may be administered to down regulate
CC	KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing
CC	their expression
XX	Sequence 695 AA;
XX	Sequence 695 AA;
QY	Query Match 43.7%; Score 1985; DB 3; Length 695;
DB	Beat Local Similarity 60.3%; Pred. No. 1.1e-167; Indels 92; Gaps 13;
	Matches 409; Conservative 76; Mismatches 101;
QY	35 GGGGLRESRRGKQARMMLGKPL-----SYTSSQSCRRNVKRRVQNYL 80
DB	37 GGGGSPR-----RLGLGSLPLPGAPLPGSGSGSAGGQSSAAHKRYRLQNV 87
QY	81 YNVLEPRGWAIFYHAFVFLVFGCLILSVSTTPEHTKLASSCLLILEFMIVVFGLEF 140
DB	88 YNVLEPRGWAIFYHAFVFLVFGCLILSVSTTPEHTKLASSCLLILEFMIVVFGLEF 147
QY	141 IIRWSAGCCCRGQWGLRFAKPCFVIDTIVLIASIVVSAKTQGNIFATSALRSR 200
DB	148 IVRWSAGCCCRGQWGLRFAKPCFVIDTIVLIASIVVSAKTQGNIFATSALRSR 207
QY	201 FLQILRMVMDRGGTGWKLGSSVYVAHSHKELITAWYIGFLVIFSSFLVYLVEKDKNEP 260
DB	208 FLQILRMVMDRGGTGWKLGSSVYVAHSHKELITAWYIGFLVIFASFLVYLAERDANSDF 267
QY	261 STYADALWNGTITLTIGYDKTPTLWGLLSAGFALLGTFEPALPAGILGSGFALKVQ 320
DB	268 SSYADSLWNGTITLTIGYDKTPTLWGLLSAGFALLGTFEPALPAGILGSGFALKVQ 327
QY	321 EOHROKHFEKRNPAANLIQCVRSYAAD-EKSVSIATW----- 358
DB	328 EOHROKHFEKRNPAANLIQAARLYSTDMSPAYLATWYIYDLSILPSRELALLFEHVQ 387
QY	359 -----KPHLKALHT-----CSPTNOKLSFKERVMA SPRG 388
DB	388 RARNGGLRPLEVRAPVDPGAPSPYPVATCRPGSTFCPGESSRMGKDIRMGSSQR 447
QY	389 QSIKSRQ--ASVGDRRSPSTDLTAG-SPTKVQKSWSFNDRFRPRLKSSQPKPID 445
DB	448 RTGPSKQQLAAPTMTPTSPSEQVGEATSPTKVQKSWSFNDRFRASRL-----KPTS 502
QY	446 ADTALGTDDVDYKGCQCDVSVEDLTPPLKTVIRAIRMKFHVAKRKETLRPPVDKDV 505
DB	503 AEDA-PSEVABEKSQCELTVDVIMPAVKTVIRSIKILKFLVAKRKETLRPPVDKDV 561
QY	506 IEQYSAGHLDMLCRIKSLQTRVDQILGKQITSDKKSR-----KITAEHTTDDL SMLGRV 562
DB	562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PCDRKAREKDGKGFSDAEVDEISMGV 619
QY	563 VKVEKQVQSTESKLDLLIYQOVLKRGSAALASQIIPPECEQTSYQSPVDSKDL 622
DB	620 VKVEKQVQSTESKLDLLIYQOVLKRGSAALASQIIPPECEQTSYQSPVDSKDL 677

QY	623 SGSAGNSCGLSRSTSANI 640
DB	678 SVSAQTLS-ISRVSSTNM 694
RESULT 13	
AAEL16621	
ID	AAEL16621 standard; protein; 695 AA.
XX	AAEL16621;
AC	AAEL16621;
DT	09-APR-2002 (first entry)
XX	Human potassium channel polypeptide, KCNQ4.
DE	Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
XX	dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;
KW	multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW	anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW	addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW	learning deficiency; cognitive disorder; motor disease; neuron disease;
KW	neurophysiological disorder; neuropsychological disorder; asthma;
KW	neuron cell death; brain tumour; gene therapy; antisense therapy;
KW	synaptic transmission; electrical excitability; KCNQ4 protein;
KW	hearing loss.
XX	Homo sapiens.
OS	WO200192526-A1.
XX	06-DEC-2001.
PD	24-MAY-2001; 2001WO-US017314.
XX	26-MAY-2000; 2000US-0207389P.
PF	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	Dworetzky SI, Ramanathan CS, Trojnacki JT, Boissard CG;
PI	Gribkoff VK;
XX	WPI; 2002-122069/16.
DR	Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
XX	it, for diagnosing, treating and identifying modulators useful in
PT	treating neurological, neurophysiological and neuropsychological
PT	diseases.
XX	Disclosure; Fig 5; 128pp; English.
PS	The invention relates to potassium channel polypeptides referred to as
XX	KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
CC	polypeptides are useful for identifying compounds that modulate their
CC	biological activity. The compounds identified and KCNQ5 polynucleotides
CC	are useful for treating acute and chronic pain, migraine, acute stroke,
CC	dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),
CC	multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,
CC	depression, bipolar disorders, sleep disorders, eating disorders,
CC	addiction, myokymia, Alzheimer's disease, age-associated memory loss,
CC	learning deficiencies, cognitive disorders and motor neuron diseases. The
CC	nucleic acid molecules of the invention are further useful for treating
CC	neurophysiological, neuropsychological disorders, asthma, neuron cell
CC	death and brain tumours. They are also used in gene therapy and antisense
CC	therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical
CC	excitability in the brain and are useful for generating antibodies. They
CC	are also useful to affinity purify biological effectors from biological
CC	materials e.g. disease tissues or cells. The present sequence is human
CC	KCNQ4 protein. Mutations in this protein is associated with particular
CC	disease e.g. hearing loss
XX	Sequence 695 AA;
SQ	

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Query Match 43.7%; Score 1985; DB 5; Length 695;
Best Local Similarity 60.3%; Pred. No. 1.1e-167;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;

QY 35 GGGGLRESRRGKQARMSSLLGKPL-----SVTSQSCRRNVKRVQNYL 80
DB 37 GGGGSPR-----RLGLGSLPPGAPLPGPGSGSGACGQRSSAAHKRYRLQNVV 87
QY 81 YNVLEPRGWAFIYHAFVFLVFGCLLSVFTPIHTKLASSCLLILEFMVVFGLF 140
DB 88 YNVLEPRGWAFVYHVFIFLLVFSCLVSLSTQEHQELANECLLILEFMVVFGLF 147
QY 141 IIRWSAGCCCRVGMGRLEARKPCVDITVLIASIVSVSAKTGNIFFATSLRSLR 200
DB 148 IVRWSAGCCCRVGMGRLEARKPCVDITVLIASIVSVSAKTGNIFFATSLRSMR 207
QY 201 FLQILRMVDRRGTTWKLGLSVVYVYHASKELITAWYIGFLVLPSSFLVYLVEKDNKEF 260
DB 208 FLQILRMVDRRGTTWKLGLSVVYVYHASKELITAWYIGFLVLPSSFLVYLVEKDNKEF 267
QY 261 STYADALWNGTITLTITGYGDKTPTLWGLRLLSAGFALLGIFSPALPAGILGSGFALKVQ 320
DB 268 SSYADSLWNGTITLTITGYGDKTPTLWGLRLLSAGFALLGIFSPALPAGILGSGFALKVQ 327
QY 321 EQRQKHFEKRRNPAANLIQCVWSYAAD-EKSVSIATW----- 358
DB 328 EQRQKHFEKRRNPAANLIQAAWRLYSTDMRSAYLTATWYYSILPSFRELALLFEHVQ 387
QY 359 -----KPHLKALHT-----CSPYNQKLSFKERVMSAPRG 388
DB 388 RARNGGLRPLEVRRAVPDGPSPYPPVATCHRPGSTFCFGESSRMGIKDIRMSSQR 447
QY 389 QSTKSRQ--ASVGDRRSPSTDTIATAG-SPTKVQKSWSFNDRTFRPSLRKSKOPKPVID 445
DB 448 RTGPSKQOLAPPTMPTSPSSEOVGEATSPTKVQKSWSFNDRTFRASRL-----KPTS 502
QY 446 ADTALGCTDDVYDEKGCOCVSVEDLTPLKTVIRAIRIMKHFYAKRFKETLRPYDKV 505
DB 503 AEDA-PSEEAEEVABEAKSYOCYELTDDIMPAKTVIRISIRILKPLVAKRFKETLRPYDKV 561
QY 506 IEQVSAGHLMCLRIKSLQTRVDQILGKQITSDKKSRE---KITABHETTTDLSMLGRV 562
DB 562 IEQVSAGHLMCLRIKSLQTRVDQILGKQITSDKKSRE---KITABHETTTDLSMLGRV 619
QY 563 VKVEKQVQSIKSLDCLLDIYQVQLRKSASALAFQIPPECEQTSYQSGPVDKSL 622
DB 620 VKVEKQVQSIKSLDCLLDIYQVQLRKSASALAFQIPPECEQTSYQSGPVDKSL 677
QY 623 SGSNQNSGCLSRSTSANI 640
DB 678 SVSAQTLIS-ISRVSSTNM 694

RESULT 14
ADE31699
ID ADE31699 standard; protein; 695 AA.
XX AC ADE31699;
XX DT 29-JAN-2004 (first entry)
XX DE Human 32394 protein #SEQ ID 56.
XX KW Antiartherosclerotic; cardiant; vasotropic; antiinflammatory;
KW thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
KW cardiovascular; disorder; ischaemia; aortic bending;
KW vascular heart disease; endocarditis; atrial fibrillation; heart failure;
KW angina; cardiomyopathy; cardiac death.
XX OS Homo sapiens.
XX PN W02003065984-A2.
XX
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PD 14-AUG-2003.
XX 29-JAN-2003; 2003WO-US0002571.
XX 01-FEB-2002; 2002US-03533224P.
PR 15-MAR-2002; 2002US-0364529P.
PR 19-APR-2002; 2002US-0373861P.
PR 29-APR-2002; 2002US-0376287P.
PR 12-JUN-2002; 2002US-0388080P.
PR 24-JUN-2002; 2002US-0390971P.
PR 03-JUL-2002; 2002US-0394130P.
PR 10-JUL-2002; 2002US-0394797P.
PR 21-AUG-2002; 2002US-0404904P.
PR 23-AUG-2002; 2002US-0405450P.
PR 04-SEP-2002; 2002US-0408070P.
PR 06-NOV-2002; 2002US-0424300P.
PR 05-DEC-2002; 2002US-0431042P.
PR 05-DEC-2002; 2002US-0431079P.
XX (MILL-) MILLENNIUM PHARM INC.
PA Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;
PI Stagliano N, Perodin J, Rodrigue-Way A;
XX WPI; 2003-731468/69.
DR N-PSDB; ADE31698.
XX
XX Identifying a compound capable of treating a cardiovascular disorder
XX (e.g. atherosclerosis) comprises assaying the ability of the compound to
XX modulate the expression or activity of e.g. 1682, 6169 or 6193
XX polypeptide or nucleic acid.
XX Disclosure; SEQ ID NO 56; 328pp; English.
XX
XX The invention relates to a method for identifying a compound capable of
XX treating a cardiovascular disorder. The present invention identifies the
XX differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
XX 33276, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
XX 32707, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484,
XX 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
XX 2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,
XX 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
XX 6585 genes in cardiovascular disease states. The methods are useful in
XX diagnosing, preventing and treating cardiovascular disorders, such as
XX atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
XX stenosis, arterial inflammation, vascular wall remodeling, coronary
XX microembolism, tachycardia, bradycardia, pressure overload, aortic
XX bending, coronary artery ligation, vascular heart disease, valvular
XX disease, including but not limited to, valvular degeneration caused by
XX calcification, rheumatic heart disease, endocarditis, or complications of
XX artificial valves; atrial fibrillation, long-QT syndrome, congestive
XX heart failure, sinus node dysfunction, angina, heart failure,
XX hypertension, atrial fibrillation, atrial flutter, pericardial disease,
XX including but not limited to, pericardial effusion and pericarditis;
XX cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
XX cardiomyopathy, myocardial infarction, coronary artery disease, coronary
XX artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
XX cardiovascular developmental disorders. The methods may also be used for
XX identifying compounds that modulate cardiovascular disorders. Sequences
XX given in ADE31644-ADE31769 represent the genes and proteins that may be
XX regulated by a compound of the invention.
XX Sequence 695 AA;
XX
XX Query Match 43.7%; Score 1985; DB 7; Length 695;
XX Best Local Similarity 60.3%; Pred. No. 1.1e-167;
XX Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;
QY 35 GGGGLRESRRGKQARMSSLLGKPL-----SVTSQSCRRNVKRVQNYL 80
DB 37 GGGGSPR-----RLGLGSLPPGAPLPGPGSGSGACGQRSSAAHKRYRLQNVV 87
QY 81 YNVLEPRGWAFIYHAFVFLVFGCLLSVFTPIHTKLASSCLLILEFMVVFGLF 140
DB 88 YNVLEPRGWAFVYHVFIFLLVFSCLVSLSTQEHQELANECLLILEFMVVFGLF 147
QY 141 IIRWSAGCCCRVGMGRLEARKPCVDITVLIASIVSVSAKTGNIFFATSLRSLR 200
DB 148 IVRWSAGCCCRVGMGRLEARKPCVDITVLIASIVSVSAKTGNIFFATSLRSMR 207
QY 201 FLQILRMVDRRGTTWKLGLSVVYVYHASKELITAWYIGFLVLPSSFLVYLVEKDNKEF 260
DB 208 FLQILRMVDRRGTTWKLGLSVVYVYHASKELITAWYIGFLVLPSSFLVYLVEKDNKEF 267
QY 261 STYADALWNGTITLTITGYGDKTPTLWGLRLLSAGFALLGIFSPALPAGILGSGFALKVQ 320
DB 268 SSYADSLWNGTITLTITGYGDKTPTLWGLRLLSAGFALLGIFSPALPAGILGSGFALKVQ 327
QY 321 EQRQKHFEKRRNPAANLIQCVWSYAAD-EKSVSIATW----- 358
DB 328 EQRQKHFEKRRNPAANLIQAAWRLYSTDMRSAYLTATWYYSILPSFRELALLFEHVQ 387
QY 359 -----KPHLKALHT-----CSPYNQKLSFKERVMSAPRG 388
DB 388 RARNGGLRPLEVRRAVPDGPSPYPPVATCHRPGSTFCFGESSRMGIKDIRMSSQR 447
QY 389 QSTKSRQ--ASVGDRRSPSTDTIATAG-SPTKVQKSWSFNDRTFRPSLRKSKOPKPVID 445
DB 448 RTGPSKQOLAPPTMPTSPSSEOVGEATSPTKVQKSWSFNDRTFRASRL-----KPTS 502
QY 446 ADTALGCTDDVYDEKGCOCVSVEDLTPLKTVIRAIRIMKHFYAKRFKETLRPYDKV 505
DB 503 AEDA-PSEEAEEVABEAKSYOCYELTDDIMPAKTVIRISIRILKPLVAKRFKETLRPYDKV 561
QY 506 IEQVSAGHLMCLRIKSLQTRVDQILGKQITSDKKSRE---KITABHETTTDLSMLGRV 562
DB 562 IEQVSAGHLMCLRIKSLQTRVDQILGKQITSDKKSRE---KITABHETTTDLSMLGRV 619
QY 563 VKVEKQVQSIKSLDCLLDIYQVQLRKSASALAFQIPPECEQTSYQSGPVDKSL 622
DB 620 VKVEKQVQSIKSLDCLLDIYQVQLRKSASALAFQIPPECEQTSYQSGPVDKSL 677
QY 623 SGSNQNSGCLSRSTSANI 640
DB 678 SVSAQTLIS-ISRVSSTNM 694
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Db      701  -----WQOSHQRHGTSPVGDHGLVRIPP-----PAH-ERSLSAYSG 737
Qy      739  CLVASKENVOVAQSNLTK--DRSMKSFDMGGETLLSVCMPVPKDLCKSLSVQNLIRSTE 796
Db      738  GNRASTEFLRLEGTACKRPSALRDS-----DTSISIPVDHEELERSFGFSISQSKE 792
Qy      797  ELN 799
Db      793  NLN 795

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Search completed: April 8, 2005, 16:38:40
 Job time : 185 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2005, 16:35:41 ; Search time 151 Seconds
(without alignments)
1952.408 Million cell updates/sec

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Perfect score: 4547
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues
Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4547	100.0	888	9	US-09-810-796-5
2	4547	100.0	923	9	US-09-825-147-2
3	4547	100.0	923	16	US-10-803-268-2
4	4527.5	99.6	897	9	US-09-866-020-2
5	4527.5	99.6	897	9	US-09-810-796-4
6	4527.5	99.6	897	16	US-10-661-629-2
7	4527.5	99.6	897	17	US-10-948-493-2
8	4527.5	99.6	932	9	US-09-813-148-2
9	4300.5	94.6	854	16	US-10-661-629-7
10	1985	43.7	695	9	US-09-866-020-31
11	1985	43.7	695	9	US-09-810-796-15
12	1985	43.7	695	15	US-10-353-690-56
13	1985	43.7	695	16	US-10-661-629-6

14	1985	43.7	695	17	US-10-850-928-2	Sequence 2, Appli
15	1985	43.7	695	17	US-10-948-493-31	Sequence 31, Appl
16	1985	43.7	696	9	US-09-813-148-6	Sequence 6, Appli
17	1803.5	39.7	852	16	US-10-820-307-9	Sequence 9, Appli
18	1792	39.4	844	9	US-09-866-020-30	Sequence 30, Appl
19	1792	39.4	844	9	US-09-813-148-4	Sequence 4, Appli
20	1792	39.4	844	9	US-09-810-796-14	Sequence 14, Appl
21	1792	39.4	844	15	US-10-295-027-282	Sequence 282, App
22	1792	39.4	844	16	US-10-661-629-4	Sequence 4, Appli
23	1792	39.4	844	17	US-10-850-928-34	Sequence 34, Appl
24	1792	39.4	844	17	US-10-948-493-29	Sequence 29, Appl
25	1792	39.4	844	17	US-10-948-518-152	Sequence 152, App
26	1790.5	39.4	722	13	US-10-128-870-23	Sequence 23, Appl
27	1790.5	39.4	722	14	US-10-131-685-23	Sequence 23, Appl
28	1788.5	39.3	930	14	US-10-096-578-96	Sequence 96, Appl
29	1787.5	39.3	871	13	US-10-128-870-20	Sequence 20, Appl
30	1787.5	39.3	871	14	US-10-131-685-20	Sequence 20, Appl
31	1783	39.2	872	14	US-10-345-680-17	Sequence 17, Appl
32	1783	39.2	872	14	US-10-096-578-2	Sequence 2, Appli
33	1775	39.0	872	16	US-10-820-307-2	Sequence 3, Appli
34	1762	38.8	842	16	US-10-820-307-3	Sequence 3, Appli
35	1759	38.7	757	14	US-10-096-578-89	Sequence 89, Appl
36	1587.5	34.9	825	16	US-10-820-307-5	Sequence 5, Appli
37	1587.5	34.9	854	13	US-10-128-870-27	Sequence 27, Appl
38	1587.5	34.9	854	14	US-10-131-685-27	Sequence 27, Appl
39	1587.5	34.9	872	9	US-09-813-148-5	Sequence 5, Appli
40	1587.5	34.9	872	14	US-10-096-578-7	Sequence 7, Appli
41	1587.5	34.9	872	16	US-10-661-629-5	Sequence 5, Appli
42	1587.5	34.9	872	17	US-10-850-928-35	Sequence 35, Appl
43	1587.5	34.9	872	17	US-10-948-493-30	Sequence 30, Appl
44	1546	34.0	835	16	US-10-820-307-7	Sequence 7, Appli
45	1535.5	33.8	870	14	US-10-096-578-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-09-810-796-5
; Sequence 5, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeggla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNO5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNO5-2
US-09-810-796-5

Query Match	100.0%;	Score	4547;	DB	9;	Length	888;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	888;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MKDVEGRGVLLNSAARGDGLLLGTRATATCGGGGGLRSGRRGQAGMSLLGKPLS	60				
Qy	61	YTSQSCRRNKVRRYQVNLVNLPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL	120				
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Db 361 HLKALHTCSTNOKLSFKERVRWASPRGOSIKRSQASVGDRRSPSTDITAEKSPTKVQKS 420
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Db 421 WSNFDRTRFRPSPRLKSSQPKVIDADTALGTDDVYDEKGCQCDVSVEDLTPLKTVIRA 480
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; Sequence 2, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1: Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 923
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-825-147-2

Query Match 100.0%; Score 4547; DB 9; Length 923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDVESGRVRLNLSAARGDGLILLGTPRAATLGGGGGLRESRRKQCGARSLLGKPLS 60
Db 36 MKDVESGRVRLNLSAARGDGLILLGTPRAATLGGGGGLRESRRKQCGARSLLGKPLS 95
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QY 121 ASSCLLILEFVMIVFGLFIIIRWSAGCCCRVGMQGRRLRFARKPFCVIDITVLIASIA 180
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QY 181 VWSAKTQGNIFATSALESRLRFLQILRMVRMDRGCTWKLGSVYVAHSEKELITAWYIGFL 240
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Db 396 HLKALHTCSTNOKLSFKERVRWASPRGOSIKRSQASVGDRRSPSTDITAEKSPTKVQKS 455
QY 421 WSNFDRTRFRPSPRLKSSQPKVIDADTALGTDDVYDEKGCQCDVSVEDLTPLKTVIRA 480
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QY 481 IRIMKPHVAKRKFKETLRPYDKVDIEQYSAGHLDMLCRIKSLQTRVDQILKGQITSDK 540
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; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 923
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-803-268-2

Query Match 100.0%; Score 4547; DB 16; Length 923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 36 MKDVESGRVLLNSAAAGDGLLLGTRAAATLGGGGGLRESRRGKQGARMILLGKPLS 95
QY 61 YTSQSCRRNVKRRVQNYLVNLERPRGWAFFIYHAFVLLVFGCLLSVFSTIPEHTKL 120
DB 96 YTSQSCRRNVKRRVQNYLVNLERPRGWAFFIYHAFVLLVFGCLLSVFSTIPEHTKL 155
QY 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRVGMQGRIRFARKPCFVIDTIVLIASIA 180
DB 156 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRVGMQGRIRFARKPCFVIDTIVLIASIA 215
QY 181 VSAKTOGNIPTATLSALRSRFLQILRMVMDRRGGTWKLLGSGVVYAHSKELITAWYIGFL 240
DB 216 VSAKTOGNIPTATLSALRSRFLQILRMVMDRRGGTWKLLGSGVVYAHSKELITAWYIGFL 275
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QY 301 ISFFALPAGILGSGFALKVQEQHROKHFEKRRNPAAANLIQCVWRSYAADEKSVSIATWKP 360
DB 336 ISFFALPAGILGSGFALKVQEQHROKHFEKRRNPAAANLIQCVWRSYAADEKSVSIATWKP 395
QY 361 HLKALHTCSPNQKLSFKERVMA SPRGQSIKSRQASVGDRRSPSTDTITAEQSPTKVQKS 420
DB 396 HLKALHTCSPNQKLSFKERVMA SPRGQSIKSRQASVGDRRSPSTDTITAEQSPTKVQKS 455
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DB 456 WSNDRTRFRPSRLKSSQPKVIDADTALGTDVYDEKQCQDVSEDLTPPLKTVIRA 515
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QY 541 KSREKITAETHETDLSMLGRVVKVQVQIESKLDCLLDIYQOVLKRGKSASALASAF 600
DB 576 KSREKITAETHETDLSMLGRVVKVQVQIESKLDCLLDIYQOVLKRGKSASALASAF 635
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US-09-866-020-2
; Sequence 2, Application US/09866020
; Publication No. US2002004000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-020-2

Query Match 99.6%; Score 4527.5; DB 9; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

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DB 1 MKDVESGRVLLNSAAAGDGLLLGTRAAATLGGGGGLRESRRGKQGARMILLGKPLS 60
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DB 61 YTSQSCRRNVKRRVQNYLVNLERPRGWAFFIYHAFVLLVFGCLLSVFSTIPEHTKL 120
QY 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRVGMQGRIRFARKPCFVIDTIVLIASIA 180
DB 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRVGMQGRIRFARKPCFVIDTIVLIASIA 180
QY 181 VSAKTOGNIPTATLSALRSRFLQILRMVMDRRGGTWKLLGSGVVYAHSKELITAWYIGFL 240
DB 181 VSAKTOGNIPTATLSALRSRFLQILRMVMDRRGGTWKLLGSGVVYAHSKELITAWYIGFL 240
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DB 241 VLIFFSSFLVYLVEKDANKFSTYADALWVGTTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
QY 301 ISFFALPAGILGSGFALKVQEQHROKHFEKRRNPAAANLIQCVWRSYAADEKSVSIATWKP 360
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Query Match 99.6%; Score 4527.5; DB 16; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

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Db 1 MKDVESGRVLLNSAARGDGLLLGTRAAATLGGGGGLRESRRGKQAGMSLLGKPLS 60

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Qy 121 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPCFVIDTIVILASIA 180
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Qy 181 VVSATQGNIFATSALESRLFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
Db 181 VVSATQGNIFATSALESRLFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy 241 VLIPSSFLVYLVKEDANKFSTYADALWVGTTITLTIGYGDKTPLTWLGRLLSAGFALLG 300
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Qy 301 ISFPALPAGILGSFALKVQEOHROKHFEKERNPAANLIQCVWRSYAADKSUSIATWKP 360
Db 301 ISFPALPAGILGSFALKVQEOHROKHFEKERNPAANLIQCVWRSYAADKSUSIATWKP 360

Qy 361 HLKALHTCSPPT-----NQLSFKEVRVMASSPGQSIKSRQASVGDRRSPSTDITAE 411
Db 361 HLKALHTCSPPT-----NQLSFKEVRVMASSPGQSIKSRQASVGDRRSPSTDITAE 420

Qy 412 GSPTKVQKWSFNDRTRFRPSRLKSSQPKVPIDADTALGTDDVYDEKGCQCVSVDLT 471
Db 421 GSPTKVQKWSFNDRTRFRPSRLKSSQPKVPIDADTALGTDDVYDEKGCQCVSVDLT 480

Qy 472 PPLKTVIRAIRIMKPHVAKRKFTLRYDVQDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
Db 481 PPLKTVIRAIRIMKPHVAKRKFTLRYDVQDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy 532 GKQITSDKKSREKITAETHETDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKRG 591
Db 541 GKQITSDKKSREKITAETHETDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKRG 600

Qy 592 ASALASFOIPPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTNP 651
Db 601 ASALASFOIPPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTNP 660

Qy 652 EFSAQTFYALSPTHSQATQVPIQSQSGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 711
Db 661 EFSAQTFYALSPTHSQATQVPIQSQSGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 720

Qy 712 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVOVQASNLTKDRSMRKSFDMGGETL 771
Db 721 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVOVQASNLTKDRSMRKSFDMGGETL 780

Qy 772 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGESSGSGSQDFYKPKWRESKLFITDEE 831
Db 781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGESSGSGSQDFYKPKWRESKLFITDEE 840

Qy 832 VGPETETDTFDDAAPQAPARAAAFASDSLRTRGRSSQSIKAGESTDALSPLHVKLK 888
Db 841 VGPETETDTFDDAAPQAPARAAAFASDSLRTRGRSSQSIKAGESTDALSPLHVKLK 897

RESULT 7

US-10-948-493-2
; Sequence 2, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S

APPLICANT: TROJNACKI, JOANNE T
APPLICANT: BOISSARD, CHRISTOPHER G
APPLICANT: GRIBKOFF, VALENTIN K
TITLE OF INVENTION: HUMAN KINQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: D0023 DIV
CURRENT APPLICATION NUMBER: US/10/948,493
CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: 60/207,389
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 897
TYPE: PRT
ORGANISM: Homo sapiens
US-10-948-493-2

Query Match 99.6%; Score 4527.5; DB 17; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

Qy 1 MKDVESGRVLLNSAARGDGLLLGTRAAATLGGGGGLRESRRGKQAGMSLLGKPLS 60
Db 1 MKDVESGRVLLNSAARGDGLLLGTRAAATLGGGGGLRESRRGKQAGMSLLGKPLS 60

Qy 61 YTSQSCRRNVKRRVQNYLVNLERPRGNAFIYHAFVLLVFGCLLSVFSPTIPEHTKL 120
Db 61 YTSQSCRRNVKRRVQNYLVNLERPRGNAFIYHAFVLLVFGCLLSVFSPTIPEHTKL 120

Qy 121 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPCFVIDTIVILASIA 180
Db 121 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPCFVIDTIVILASIA 180

Qy 181 VVSATQGNIFATSALESRLFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
Db 181 VVSATQGNIFATSALESRLFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy 241 VLIPSSFLVYLVKEDANKFSTYADALWVGTTITLTIGYGDKTPLTWLGRLLSAGFALLG 300
Db 241 VLIPSSFLVYLVKEDANKFSTYADALWVGTTITLTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy 301 ISFPALPAGILGSFALKVQEOHROKHFEKERNPAANLIQCVWRSYAADKSUSIATWKP 360
Db 301 ISFPALPAGILGSFALKVQEOHROKHFEKERNPAANLIQCVWRSYAADKSUSIATWKP 360

Qy 361 HLKALHTCSPPT-----NQLSFKEVRVMASSPGQSIKSRQASVGDRRSPSTDITAE 411
Db 361 HLKALHTCSPPT-----NQLSFKEVRVMASSPGQSIKSRQASVGDRRSPSTDITAE 420

Qy 412 GSPTKVQKWSFNDRTRFRPSRLKSSQPKVPIDADTALGTDDVYDEKGCQCVSVDLT 471
Db 421 GSPTKVQKWSFNDRTRFRPSRLKSSQPKVPIDADTALGTDDVYDEKGCQCVSVDLT 480

Qy 472 PPLKTVIRAIRIMKPHVAKRKFTLRYDVQDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
Db 481 PPLKTVIRAIRIMKPHVAKRKFTLRYDVQDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy 532 GKQITSDKKSREKITAETHETDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKRG 591
Db 541 GKQITSDKKSREKITAETHETDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKRG 600

Qy 592 ASALASFOIPPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTNP 651
Db 601 ASALASFOIPPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTNP 660

Qy 652 EFSAQTFYALSPTHSQATQVPIQSQSGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 711
Db 661 EFSAQTFYALSPTHSQATQVPIQSQSGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 720

Qy 712 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVOVQASNLTKDRSMRKSFDMGGETL 771
Db 721 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVOVQASNLTKDRSMRKSFDMGGETL 780

QY 772 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSGSGSQDFYPKWRKSLFITDEE 831
Db 781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSGSGSQDFYPKWRKSLFITDEE 840
QY 832 VGPETETDTFDDAPOPAREAAAFASDLRTGRSSQSICKAGESTDALSPLHVKLK 888
Db 841 VGPETETDTFDDAPOPAREAAAFASDLRTGRSSQSICKAGESTDALSPLHVKLK 897

RESULT 8
US-09-813-148-2
; Sequence 2, Application US/09813148
; Patent No. US20020076809A1
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SERBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813.148
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-148-2

Query Match 99.6%; Score 4527.5; DB 9; Length 932;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

QY 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRGKGARMSLLGKPLS 60
Db 36 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRGKGARMSLLGKPLS 95
QY 61 YTSQSCRRNVKRYRQVNYLVNLERPRGWAFIYHAFVFLVFGCLILSVFSTIPEHTKL 120
Db 96 YTSQSCRRNVKRYRQVNYLVNLERPRGWAFIYHAFVFLVFGCLILSVFSTIPEHTKL 155
QY 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRYRGWQGLRFPKPCFVIDTIVILASIA 180
Db 156 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRYRGWQGLRFPKPCFVIDTIVILASIA 215
QY 181 VVSATQGNIFATSALESRLRFLQILRMVMDRGGTWMKLLGSVVYAHSKELITAWYIGFL 240
Db 216 VVSATQGNIFATSALESRLRFLQILRMVMDRGGTWMKLLGSVVYAHSKELITAWYIGFL 275
QY 241 VLIFFSFLVYLVEKDANKFSTYADALWNGTITLTITIGYDKTPTLTWGLRLLSAGFALLG 300
Db 276 VLIFFSFLVYLVEKDANKFSTYADALWNGTITLTITIGYDKTPTLTWGLRLLSAGFALLG 335
QY 301 ISFFALPAGILGSGFALKVQEOHQHFKFRKRNPAANLIQCVRYSYAADKSVSTATWKP 360
Db 336 ISFFALPAGILGSGFALKVQEOHQHFKFRKRNPAANLIQCVRYSYAADKSVSTATWKP 395
QY 361 HLKALHTCSPT-----NOKLSFKERVASPRGQSIKSRQASVGDRRSPSDITAE 411
Db 396 HLKALHTCSPTKEQGEASSQKLSFKERVASPRGQSIKSRQASVGDRRSPSDITAE 455
QY 412 GSPTKVQKWSFNDRTRFRPSLRLKSSQPKVIDADTALGTDVDEKCCQCDVSDVLT 471
Db 456 GSPTKVQKWSFNDRTRFRPSLRLKSSQPKVIDADTALGTDVDEKCCQCDVSDVLT 515

QY 472 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDVVKOVIROYISAGHLDMLCRIKSLQTRVDQIL 531
Db 516 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDVVKOVIROYISAGHLDMLCRIKSLQTRVDQIL 575
QY 532 GKGOITSDKSKREKITAHEHTTDDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKRGK 591
Db 576 GKGOITSDKSKREKITAHEHTTDDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKRGK 635
QY 592 ASALALASFOIPPPPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTPN 651
Db 636 ASALALASFOIPPPPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTPN 695
QY 652 EFSAQTFYALSPPTWHSQATQVPISQSDGSAVAATNTIANQINTAPKPAATTIQTIPPLP 711
Db 696 EFSAQTFYALSPPTWHSQATQVPISQSDGSAVAATNTIANQINTAPKPAATTIQTIPPLP 755
QY 712 AIKHLPRPETLHPNPAGLOESISDVTTCVLVASKENVQVQASNLTKDRSMRKSFDMGGETL 771
Db 756 AIKHLPRPETLHPNPAGLOESISDVTTCVLVASKENVQVQASNLTKDRSMRKSFDMGGETL 815
QY 772 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSGSGSQDFYPKWRKSLFITDEE 831
Db 816 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSGSGSQDFYPKWRKSLFITDEE 875
QY 832 VGPETETDTFDDAPOPAREAAAFASDLRTGRSSQSICKAGESTDALSPLHVKLK 888
Db 876 VGPETETDTFDDAPOPAREAAAFASDLRTGRSSQSICKAGESTDALSPLHVKLK 932

RESULT 9
US-10-661-629-7
; Sequence 7, Application US/10661629
; Publication NO. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTISCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNEL
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-629-7

Query Match 94.6%; Score 4300.5; DB 16; Length 854;
Best Local Similarity 98.8%; Pred. No. 1.1e-307;
Matches 841; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

QY 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRGKGARMSLLGKPLS 60
Db 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRGKGARMSLLGKPLS 60
QY 61 YTSQSCRRNVKRYRQVNYLVNLERPRGWAFIYHAFVFLVFGCLILSVFSTIPEHTKL 120
Db 61 YTSQSCRRNVKRYRQVNYLVNLERPRGWAFIYHAFVFLVFGCLILSVFSTIPEHTKL 120
QY 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRYRGWQGLRFPKPCFVIDTIVILASIA 180
Db 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRYRGWQGLRFPKPCFVIDTIVILASIA 180
QY 181 VVSATQGNIFATSALESRLRFLQILRMVMDRGGTWMKLLGSVVYAHSKELITAWYIGFL 240
Db 181 VVSATQGNIFATSALESRLRFLQILRMVMDRGGTWMKLLGSVVYAHSKELITAWYIGFL 240
QY 241 VLIFFSFLVYLVEKDANKFSTYADALWNGTITLTITIGYDKTPTLTWGLRLLSAGFALLG 300
Db 241 VLIFFSFLVYLVEKDANKFSTYADALWNGTITLTITIGYDKTPTLTWGLRLLSAGFALLG 300
QY 301 ISFFALPAGILGSGFALKVQEOHQHFKFRKRNPAANLIQCVRYSYAADKSVSTATWKP 360

301 ISFPALPAGILGSGFALKVQEQHQHFKHFKRRNPAANLIQCVWRSYAADKSVSIATWKP 360
361 HLKALHTCSPT-----NQKLSFKERVVRMASPRGQSIKRSQASVGDRRSSTDTAE 411
361 HLKALHTCSPTKKEQGEASQKLSFKERVVRMASPRGQSIKRSQASVGDRRSSTDTAE 420
412 GSPTKVKQKSFNDRTFRPSRLKSSQPKPVIDADTALGTDVDDVYDEKGCOCVSVEDLT 471
421 GSPTKVKQKSFNDRTFRPSRLKSSQPKPVIDADTALGTDVDDVYDEKGCOCVSVEDLT 480
472 PPLKTVIRAIRIMKHFVAKRKFETLRPYDKVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
481 PPLKTVIRAIRIMKHFVAKRKFETLRPYDKVIEQYSAGHLDMLCRIKSLQTRVDQIL 540
532 GKQITSDKSKREKITAETHETDLSMLGRVVKVQVQVQVQVQVQVQVQVQVQVQVQVQV 591
541 GKQITSDKSKREKITAETHETDLSMLGRVVKVQVQVQVQVQVQVQVQVQVQVQVQV 600
592 ASALALASFOIIPPECEQTSYQSPVDSKDLGSGAONSGCLSRSTSANSIRGLQFILTNP 651
601 ASALALASFOIIPPECEQTSYQSPVDSKDLGSGAONSGCLSRSTSANSIRGLQFILTNP 660
652 EFSAQTFYALSPTHMSQATQVPIQSQDGSAAVATNTIANQINTAPKPAAPTTLQIPPLP 711
661 EFSAQTFYALSPTHMSQATQVPIQSQDGSAAVATNTIANQINTAPKPAAPTTLQIPPLP 720
712 AIKHLPRPETHLPNAGLQSIQSVDTTCLVASKENVQVQVQVQVQVQVQVQVQVQVQVQV 771
721 AIKHLPRPETHLPNAGLQSIQSVDTTCLVASKENVQVQVQVQVQVQVQVQVQVQVQV 780
772 LSVCPMPVKDLGKSLVQNLIRSTEELNIQLSGSESSGSGSQDQFYPKWRKSLFITDEE 831
781 LSVCPMPVKDLGKSLVQNLIRSTEELNIQLSGSESSGSGSQDQFYPKWRKSLFITDEE 840
832 VGPEETETDTF 842
841 VGPEETETDTF 851

RESULT 10
US-09-866-020-31
; Sequence 31, Application US/09866020
; Publication No. US2002040000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 31
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-020-31

Query Match 43.7%; Score 1985; DB 9; Length 695;
Best Local Similarity 60.3%; Pred. No. 3.2e-137;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;
35 GGGGGLRESRGKQAGARMSLLGKPL-----SYTSSQSCRNVKVRVQNYL 80
37 GGGGSPR-----RLGLLGSPLPPGALPGGSGSGSACGQSSAAHKRYRLQNWV 87
81 YNVLERPRGNAFYTHAFVLLVFCCLLSVFTPIETHKLASSCLLILEFVMIIVVFGLEP 140

88 YNVLERPRGNAFYTHAFVLLVFCCLLSVFTPIETHKLASSCLLILEFVMIIVVFGLEP 147
141 IIRWSAGCCCRYGQGRRLRFARKPCFVIDITVLIASIAVSVAKTQGNIFATSALRSR 200
148 IVRWSAGCCCRYGQGRRLRFARKPCFVIDIFVVASVAVIAAGTQGNIFATSALRSR 207
201 FLOILRVRMDRRGGTWKLLGSSVYVAHSKELIITAWYIGFLVLPSSFLVIVLVDKANKEF 260
208 FLOILRVRMDRRGGTWKLLGSSVYVAHSKELIITAWYIGFLVLPSSFLVIVLVDKANKEF 267
261 STVADALWMTITLTTIGYGDKTPLTWLGRLLSAGFALLIGISFPALPAGILGSGFALKVQ 320
268 SSVADSLWMTITLTTIGYGDKTPLTWLGRVLAAGFALLIGISFPALPAGILGSGFALKVQ 327
321 EQRHQRHFKRRRPAANLIQCVWRSYAAD-EKSVSIATW----- 358
328 EQRHQRHFKRRRPAANLIQAAWRLYSTDMRAYLTATWYIYDLSILPSPRELALLFEHVQ 387
359 -----KPHLKALHT----- 388
388 RARNGGLRPLEVRAPVPDGPARYPPVATCHRPGSTSCFGESSRMGIKDIRMGSQR 447
389 QSIKSRQ--ASVGDRRSPSTDTITAEQ-SPTKVOKSWSFNDRTFRPSRLRLKSSQPKVID 445
448 RTGFSKQOLAPPTMPTSPSEQVEATSPTKVOKSWSFNDRTFRASRL-----KRTS 502
446 ADTALGTDDVYDRKGCQCVSDVDELTPPLKTVIRAIRIMKHFVAKRKFETLRPYDKV 505
503 AEDA-PSEEAEEKSYQCBELTVDDIMPVAVTIRISIRILKFLVAKRKFETLRPYDKV 561
506 IEQYSAGHLDMLCRIKSLQTRVDQILKGQITSDKKSRE---KITAEHTTDDLSMLGRV 562
562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKDGKPSDAEVVEISMGRV 619
563 VKVEKQVQSTESKLDCLDIYQVLRKGSALALASFOIIPPECEQTSYQSPVDSKDL 622
620 VKVEKQVQSTESKLDCLDIYQVLRKGSALALASFOIIPPECEQTSYQSPVDSKDL 622
623 SGSAQNSGCLSRSTSANI 640
678 SVSAQTLIS-ISRVSSTNM 694

RESULT 11
US-09-810-796-15
; Sequence 15, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human KCNQ4
US-09-810-796-15

Query Match 43.7%; Score 1985; DB 9; Length 695;
Best Local Similarity 60.3%; Pred. No. 3.2e-137;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;
35 GGGGGLRESRGKQAGARMSLLGKPL-----SYTSSQSCRNVKVRVQNYL 80

Db 37 GGGGSPR-----RLGLLSPPLPGAPLPQPGSGSGSACQORSSAAHKYRRLQNW 87
QY 81 YNVLPRGWAIFYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILFVWVVGLEF 140
Db 88 YNVLPRGWAIFYHAFVLLVFGCLILSVLSTIQEHQELANECCLLILFVWVVGLEY 147
QY 141 IIRWSAGCCCRVWGQRLRFARKPCFVIDTIVLSTAVSAKTOGNIATSLRSLR 200
Db 148 IIRWSAGCCCRVWGQRLRFARKPCFVIDTIVLSTAVSAKTOGNIATSLRSMR 207
QY 201 FLOILRMVDRRGTTWKLGLSVVYAHSKELITAWIGFLVLFSSFLVLYVEKANKEF 260
Db 208 FLOILRMVDRRGTTWKLGLSVVYAHSKELITAWIGFLVLFSSFLVLYVEKANSDF 267
QY 261 STYADALWGGTITLTITIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILSGFALKVQ 320
Db 268 SSYADSLWGGTITLTITIGYDGTPLTWLGRVLAAGFALLGISFPALPAGILSGFALKVQ 327
QY 321 EHQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW-----KPHLKALHT----- 358
Db 328 EHQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW-----KPHLKALHT----- 387
QY 359 -----KPHLKALHT-----KPHLKALHT-----KPHLKALHT----- 388
Db 388 RARNGGLRPLEVRAPVDPGAPSRYPVATCHRGSTSPGESSRMGKDIRMGSSOR 447
QY 389 QSIKSRQ--ASVGDRRSPSTDTITAE--SPTKVQKSWSFNDRTFRPSRLKSSQPKVID 445
Db 448 RTGSPKQOLAPPTMTSPSSQVGEATSPTKVQKSWSFNDRTFRASRL-----KPTS 502
QY 446 ADTALGTDDVDEKGCQCVSDEDLTPPLKTVIRAIRIMKHFHVAKFKETLAPYDKV 505
Db 503 AEDA-PSSEVAEAKSYQCELTVDIMPVAVTIRIRILKFLVAKKFKETLAPYDKV 561
QY 506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGOITSDDKKSRE---KITAEHETDLSMLGRV 562
Db 562 IEQYSAGHLDMLCRIKSLQTRVDQILGKGOITSDDKKSRE---KITAEHETDLSMLGRV 619
QY 563 VKVEQVQSIESKLDCLDIYQOVLKGSASALASPOIPPECEOTSDYQSPVDSKOL 622
Db 620 VKVEQVQSIESKLDCLDIYQOVLKGSASALASPOIPPECEOTSDYQSPVDSKOL 677
QY 623 SGASQNGCLSRSTSANI 640
Db 678 SVSAQTLIS-ISRVSSTNM 694

RESULT 12
US-10-353-690-56
; Sequence 56, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacqueline
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 53590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
; FILE REFERENCE: MP102-018PARNOMNIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; CURRENT FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-353-690-56

Query Match 43.7%; Score 1985; DB 15; Length 695;
Best Local Similarity 60.3%; Pred No. 3.2e-137;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;

QY 35 GGGGGLRBSRRKQGMRLSLKPL-----SYTSSQSCRRNVKVRQNYL 80
Db 37 GGGGSPR-----RLGLLSPPLPGAPLPQPGSGSGSACQORSSAAHKYRRLQNW 87
QY 81 YNVLPRGWAIFYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILFVWVVGLEF 140
Db 88 YNVLPRGWAIFYHAFVLLVFGCLILSVLSTIQEHQELANECCLLILFVWVVGLEY 147
QY 141 IIRWSAGCCCRVWGQRLRFARKPCFVIDTIVLSTAVSAKTOGNIATSLRSLR 200
Db 148 IIRWSAGCCCRVWGQRLRFARKPCFVIDTIVLSTAVSAKTOGNIATSLRSMR 207
QY 201 FLOILRMVDRRGTTWKLGLSVVYAHSKELITAWIGFLVLFSSFLVLYVEKANKEF 260
Db 208 FLOILRMVDRRGTTWKLGLSVVYAHSKELITAWIGFLVLFSSFLVLYVEKANSDF 267
QY 261 STYADALWGGTITLTITIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILSGFALKVQ 320
Db 268 SSYADSLWGGTITLTITIGYDGTPLTWLGRVLAAGFALLGISFPALPAGILSGFALKVQ 327
QY 321 EHQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW-----KPHLKALHT----- 358
Db 328 EHQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW-----KPHLKALHT----- 387
QY 359 -----KPHLKALHT-----KPHLKALHT-----KPHLKALHT----- 388
Db 388 RARNGGLRPLEVRAPVDPGAPSRYPVATCHRGSTSPGESSRMGKDIRMGSSOR 447
QY 389 QSIKSRQ--ASVGDRRSPSTDTITAE--SPTKVQKSWSFNDRTFRPSRLKSSQPKVID 445
Db 448 RTGSPKQOLAPPTMTSPSSQVGEATSPTKVQKSWSFNDRTFRASRL-----KPTS 502
QY 446 ADTALGTDDVDEKGCQCVSDEDLTPPLKTVIRAIRIMKHFHVAKFKETLAPYDKV 505
Db 503 AEDA-PSSEVAEAKSYQCELTVDIMPVAVTIRIRILKFLVAKKFKETLAPYDKV 561
QY 506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGOITSDDKKSRE---KITAEHETDLSMLGRV 562
Db 562 IEQYSAGHLDMLCRIKSLQTRVDQILGKGOITSDDKKSRE---KITAEHETDLSMLGRV 619


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||||| 620 VKVEKQVQSIEHKLDLLLFYSRCLSGTSA--SLGAVQVPLFDPDITSYHSPVDHEDI 677
QY 623 SGSAQNSGCLSRSTSANI 640
Db 678 SVSAQTLS-ISRVSSTNM 694

RESULT 15
US-10-948-493-31
; Sequence 31, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-493-31

Query Match 43.7%; Score 1985; DB 17; Length 695;
Best Local Similarity 60.3%; Pred. No. 3.2e-137; Indels 92; Gaps 13;
Matches 409; Conservative 76; Mismatches 101;

QY 35 GGGGLRESRRGKQAGMSLIGKPL-----SYTSSQSCRRNVKYRRVQNYL 80
Db 37 GGGGSPR-----RLGLLGSPLPGAPLPFGSGSGACGQSSAAHKRYRRLQNVV 87

QY 81 YNVLERPRGAFIYHAFVFLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVGLF 140
Db 88 YNVLERPRGAFVYHVFLLVFLVFCVLSVLSVTIQEHQELANECLILEFVMIVVGLF 147

QY 141 IIRWSAGCCCRYGWQGLRFARKPCFVIDTIVLIASIAVWSAKTOCNIFATSALRSLR 200
Db 148 IVRWWSAGCCCRYGWQGLRFARKPCFVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

QY 201 FLQILRMVMDRRGGTGWKLGSVVYVAHSHKELITAWYIGFLVLIFFSFLVYLVEKDANKEP 260
Db 208 FLQILRMVMDRRGGTGWKLGSVVYVAHSHKELITAWYIGFLVLIFFASFLVYLAEKDANSDF 267

QY 261 STYADALWNGTITLTITIGYDKTPTLWGLLSAGFALLGISFPALPAGILGSGFALKVQ 320
Db 268 SSYADSLWNGTITLTITIGYDKTPTLWGLVLAAGFALLGISFPALPAGILGSGFALKVQ 327

QY 321 EQRQKHKEKRNPAANLIQCVRSYAAD-EKSVSIATW----- 358
Db 328 EQRQKHKEKRNPAANLIQAARLYSTDMRSAYLATATWYVYDSITLPSFRELALLFEHVQ 387

QY 359 -----KPHLKALHT-----CSPTNQKLSFKERVMSAPRG 388
Db 388 RARNGGLRPLEVRRAPVDPGAPRYPPVATCPGSGTSFCPGESSRMGKIRIRMGSSQR 447

QY 389 QSIKSRQ--ASVGDRESPTDITAEQ-SPTKVQKSWSFNDRTRFRPSLRKSSQPKPID 445
Db 448 RTGPSKQQLAPPTMTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

QY 446 ADTALGTDDVDYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKHFVAKRKFKETLRPYDVKDV 505
Db 503 AEDA-PSEEVABEKSQCCLTVDDIMPAVKTVIRISIRILKFLVAKRKFKETLRPYDVKDV 561
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QY 506 IEQYSAGHLDMLCRKIKSLQTRVDQILKGQITSDKKSRE---KITAEHETDLSMLGRV 562
Db 562 IEQYSAGHLDMLGRKIKSLQTRVDQIVGRG--PGDRKAREKDGKPSDAEVDISMGRV 619

QY 563 VKVEKQVQSIESKLDCLLDIYQOVLKGSASALALASFOIPPPPECEOTSDYQSPVDSKDL 622
Db 620 VKVEKQVQSIIEHKLDLLLFYSRCLRSRTSA--SLGAVQVPLFDPDITSYHSPVDHEDI 677

QY 623 SGSAQNSGCLSRSTSANI 640
Db 678 SVSAQTLS-ISRVSSTNM 694

Search completed: April 8, 2005, 16:46:17
Job time : 155 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:32:30 ; Search time 50 Seconds
(without alignments)
1708.810 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVESGRGRVLNSAARG.....SICKAGESTDALSLPHVKLK 888

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: Pirl2:.*
3: Pirl3:.*
4: Pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1226.5	27.0	393	2 JC5275	voltage-gated pota
2	1226	27.0	744	2 T34116	voltage-gated pote
3	950	20.9	645	2 T27186	hypothetical prote
4	423.5	9.3	664	2 T28852	probable potassium
5	291.5	6.4	858	2 S31761	potassium channel
6	289	6.4	853	1 CHRT01	potassium channel
7	279	6.1	857	2 I56529	potassium channel
8	272	6.0	802	2 JH0595	potassium channel
9	248.5	5.5	528	2 T34417	delayed rectifier
10	248.5	5.5	924	2 B41359	potassium channel
11	245	5.4	484	2 T24238	hypothetical prote
12	245	5.4	581	2 S17150	potassium channel
13	242.5	5.3	490	2 T26983	potassium channel
14	242	5.3	613	2 A39402	hypothetical prote
15	242	5.3	624	2 S22703	potassium channel
16	241.5	5.3	344	2 E90564	voltage-gated pota
17	241	5.3	263	2 A12384	hypothetical prote
18	238	5.2	654	2 S11049	potassium channel
19	237	5.2	523	2 A38101	potassium channel
20	237	5.2	525	2 A43531	potassium channel
21	235.5	5.2	625	2 S13919	potassium channel
22	235.5	5.2	660	2 S24125	potassium channel
23	235	5.2	924	2 S12746	potassium channel
24	234	5.1	643	2 S00480	potassium channel
25	234	5.1	653	2 A39922	potassium channel
26	233.5	5.1	656	2 JH0133	potassium channel
27	232	5.1	528	2 I84205	potassium channel
28	231.5	5.1	769	2 I56546	Shaw type potassium
29	230	5.1	280	2 E75470	probable ion trans

30	230	5.1	495	2 B39113	potassium channel
31	229.5	5.0	495	2 I57680	potassium channel
32	228.5	5.0	511	2 A46020	potassium channel
33	228.5	5.0	511	2 S07095	potassium channel
34	228	5.0	651	2 A39372	potassium channel
35	227.5	5.0	630	2 JU0271	voltage-sensitive
36	226.5	5.0	558	2 T23991	hypothetical prote
37	226	5.0	495	2 A40090	potassium channel
38	225.5	5.0	585	2 A39395	delayed rectifier
39	224	4.9	679	2 A42073	potassium channel
40	223.5	4.9	602	2 JH0166	potassium voltage-
41	222.5	4.9	490	2 A35312	potassium channel
42	221.5	4.9	295	2 C72692	probable potassium
43	220.5	4.8	597	2 S51212	BAK5 protein - bov
44	219	4.8	361	2 S19552	potassium channel
45	215.5	4.7	460	2 T27759	hypothetical prote

ALIGNMENTS

RESULT 1

JC5275
voltage-gated potassium channel protein - human
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: JC5275
R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A:Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific
A:Reference number: JC5272; MUID:97191543; PMID:9039501
A:Contents: neuroblastoma cell
A:Accession: JC5275
A:Molecule type: mRNA
A:Residues: 1-393 <YOK>
A:Cross-references: UNIPROT:O43526; DDBJ:D82346; NID:g1841341; PIDN:BAA11557.1; PID:d101

Query Match 27.0%; Score 1226.5; DB 2; Length 393;
Best Local Similarity 69.2%; Pred. No. 2.1e-73;
Matches 238; Conservative 33; Mismatches 56; Indels 17; Gaps 4;

Qy	17	AARGDGLLLGTRAAATLGGGGGLRESRRKQKQARMSSLLGKPLSYTSSQSCRRNVKRRV	76
Db	34	STRDGALLIAGSPAK---RGSILSKPRAGAGA-----GKP-----PKRNAFRKL	77
Qy	77	QNYLYNVLPRGMAFYHAFVLLVFGCLILSVFSTIPBHTKLASSCLLILEFWMIVWF	136
Db	78	QNFLYNVLPRGMAFYHAYVLLVFSCLVLSVFSTIKEYEKSSECALVILEITVIVWF	137
Qy	137	GLEFIIRWSAGCCCRYRGHGRFARKPCVIDITVLIASTAVVSATQGNIFATSAL	196
Db	138	GVEYFVRWIAAGCCCRYRGWRGLKFAKPCVIDINVLIASTAVLAAGSQGNVATSAL	197
Qy	197	RSURFLQILRMVRDRGGTWKLLGSVVAHSEKLITAWYIGFLVLFSSFLVVLVEKDA	256
Db	198	RSURFLQILRMVRDRGGTWKLLGSVVAHSEKLITAWYIGFLCLILASFLVLAKEGE	257
Qy	257	NKEFSTYADALWAGTITLTITIGYDKTPTLWGLRLSAGFALLGISFPALPAGILSGGFA	316
Db	258	NDHFDIVADALWGLITLTITIGYDKYQPTWNGRLLAATFTLIGVSFFALPAGILSGGFA	317
Qy	317	LKVOEQRHQHFERRNPANLIQCWRSYAADEKSVSI-ATWK	359
Db	318	LKVQEQHRQHFERRNPAAGLIQSAWRFYATNLRSITDLHSTWQ	361

RESULT 2

T34116
voltage-gated potassium channel klq-1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T34116
R;Wilcox, L.

submitted to the EMBL Data Library, December 1995
 A;Description: The sequence of C. elegans cosmid C25B8.
 A;Reference number: Z21479
 A;Accession: T34116
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-744 <WIL>
 A;Cross-references: EMBL:U41556; PIDN:AAC70874.1; GSPDB:GN00028; CESP:C25B8.1
 A;Experimental source: strain Bristol N2; clone C25B8
 C;Genetics:
 A;Gene: klg-1; CESP:C25B8.1
 A;Map position: X
 A;Introns: 31/3; 64/1; 81/3; 131/2; 161/3; 204/1; 262/3; 304/3; 341/3; 402/2; 426/1; 477

Query Match	27.0%;	Score	1226;	DB 2;	Length	744;
Best Local Similarity	41.1%;	Pred. No.	5.9e-73;			
Matches	276;	Conservative	121;	Mismatches	184;	Indels
					90;	Gaps
					17;	

QY 40 LRESRGKQARMSLLGKPLSYTSQSCRRNVYRRVONLYNVLERPRGW-AFIYHAFV 98
 DB 77 LHDSEGNR--KMSLVGKPLTY---KNYRQDQFRMQRNQHFLERPRGWKAATYHLAV 131
 QY 99 FLLVFGCLILSVSTPEHTKLASSCLLILEFVMVVFLEFIIRWSAGCCCRVGRWGQ 158
 DB 132 LFWLMCLALSVFSTPDPFVNATVLYLEIVFVIMLATEYICRVMSAGCRVGRGISG 191
 QY 159 RLRFARPCFVIDIVLIASIAVSAKTQGNIFATSALRSIRFLOILRMVRMDRRGTWK 218
 DB 192 RIRFATSAYCVIDIIVILASITVLCIGATGVFAASAIRGLRFFQILRLMLRIDRRAGTWK 251
 QY 219 LLGSVYVAHSELITAWYIGLVLFISFLVYVEKDANKEFSTYADALWNGTITLTIG 278
 DB 252 LLGSVVAHRELLTYVIGLVLFISFLVYVEKDANKEFSTYADALWNGTITLTIG 311
 QY 279 YGDKTPTLWGLRLSAGFALLIGFFPALPAGILSGFALKVQEOHROKHFEKRNPAANL 338
 DB 312 YGDKTPTWPGKIITAAFCALLIGSFFPALPAGILSGFALKVQEOHROKHILIRRVPAKL 371
 QY 339 TQCVRSYAADKESYATWPKPHLK-----ALHTCSPTNOKLSFKERVRMASPRGSIK 392
 DB 372 IOCLRHRYSAAPESTSLATWIKHLARELPPIVKLTPNGSNATGLINLRQSTKRTPLN 431
 QY 393 SRQASVGRDRS-----PSTDITAGSPTKVQKSWNSNDTRFRPSLR-- 434
 DB 432 NQNLAVNSQATSKNLSVPRVHDITSLVSTSDISEIQLGALGSLGWKSKSYGSGKAT 491
 QY 435 -----LKSOPKV-----IDADTALGDDVYDEKGCQCVSDLPPLKTVIRAIRMKFH 487
 DB 492 DDSVLQSRMLAPSNALDEEEAVG---YQPG-----TIEFTPALKNVCVRAIRIQLL 541
 QY 488 VAKRKFKEITRPYVDKVDIEQYSAGHLDMLCRIKSLQTRVDQIILGKGQITSDKKSREKIT 547
 DB 542 VAKRKFKEALKYVDKVDIEQYSAGHLDMLCRIKSLQTRVDQIILGKGQITSDKKSREKIT 593
 QY 548 ABHETDLDLSMGRVVKVEKQVQSTESKLDCLLDIYQOVLKGSASALAFQIPPEEC 607
 DB 594 PK-----ISMETRIATLETTVGKMDKKLDLVMELM-----GROASQVFSQNTSP--- 639
 QY 608 EQTSDYQSPVDSKOLGSAQNGCLSRSTSANISRGLOFILTPNEFSQATFVALSPTMHS 667
 DB 640 ---RGFESEPTSAQ-----DLTRRSRSMVSTDMEM-----YTARSH---SPGVYHG 679
 QY 668 QATQVPIQSQD 678
 DB 680 DARPI-IAQID 689

RESULT 3
 T27186
 hypothetical protein Y54G9A.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T27186

R;Smyle, R.
 submitted to the EMBL Data Library, October 1998
 A;Reference number: Z20324
 A;Accession: T27186
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-645 <WIL>
 A;Cross-references: UNIPROT:Q9XWG9; EMBL:AL032648; PIDN:CAA21699.1; GSPDB:GN00020; CESP:
 A;Experimental source: clone Y54G9A
 C;Genetics:
 A;Gene: CESP:Y54G9A.3
 A;Map position: 2
 A;Introns: 56/3; 100/2; 148/1; 411/2; 541/2; 575/3

Query Match	20.9%;	Score	950;	DB 2;	Length	645;
Best Local Similarity	36.2%;	Pred. No.	8.2e-55;			
Matches	247;	Conservative	92;	Mismatches	175;	Indels
					168;	Gaps
					22;	

QY 73 YRVQNYLVNLERPRGW-AFIYHAFVFLVFGCLILSVSTPEHTKLASSCLLILEFV 131
 DB 3 YRAM---IYNCLERPTGKCFYHFSVFLVILICLILSVLSTVEESHSHFAELLYILEIV 59
 QY 132 MIVVFGLEFIIRWSAGCCCRVGRWGRLRFARPCFVI----- 170
 DB 60 LVVFFSVFIVRLMSAGCRSKYGVYGLKFKVRKPIITLIGRGRHLQLIRDLMLRHGGPS 119
 QY 171 -----DTI-----VLIASIAVVS--AKTQGNIFATSA-----L 196
 DB 120 FCGKRDAGDTVSADSEADPRRSAGWHMVEIRISKPIEFKSLKIGIFKNFANWFOF 179
 QY 197 RSLRFLOILR----- 230
 DB 180 RXLEFSKILKKNLGRVHWGSATPSSGDPDLVCCFPKLHLQLASFRLLGSLVVFIRHQE 239
 QY 231 LITAWYIGLVLFISFLVYVEK-----DANKEFSTYADALWNGTITLTIGYDKTPTL 285
 DB 240 LITLYIGLVLFISFYVFLAEKDHIGVDGRQAFTSYADALWNGVITMTTIGYDVVPQ 299
 QY 286 TWGLRLSAGFALLIGSFPALPAGILSGFALKVQEOHROKHFEKRNPAANLIOCVMRS 345
 DB 300 TWGLRIVASCFSIPALSFALPAGILSGFALKVQEOHROKHFNQIPAAATLIQCLWRC 359
 QY 346 YAADEKSVGIATWKPHLKAL-HTCSPTNOKLSFKERVRMAS---PRGOSIKSRQASVGD- 400
 DB 360 HAA-EKVS-ATWNAHIDPLAHETKETHWNGKKEASMSDNNLTKRQLFKKQSLVNT 417
 QY 401 ---RRSPSTDITAGSPTKVQKSWNSNDTRFRPSLRKSSQPKVIDADTALGTD-- 454
 DB 418 FRKKGSPSTDV-----EMGELQOERLLRHNSDITDDEKR 452
 QY 455 VYDEKGCQCDVSVB-----DLTPPLKTVIRAIRIMKFKRKFKE 496
 DB 453 IY-RVGADIEIDVETEEPTTPRPOGHIHVCELTDAHNAIRAIRRVKYFVARRRFOQA 511
 QY 497 LRPYDKVDIEQYSAGHLDMLCRIKSLQTRVDQIILGKGQITSDKKSREKITAHEHTDDL 556
 DB 512 RPYDVRDIEQYSQGHLMNVMVRIKELQRLDQTLGKPGYDGKSRK---GHPVT--- 564
 QY 557 SMLGRVVKVEKQVQSTESKLD-----CLLDIYQOVLKSG---SASALALASFOIPPECE 608
 DB 565 -IGSRLSRLQWSSLDKRVESNRNTNIALYRLMADRNSLTISPSPALISRPVSPAACL 623
 QY 609 QTSYQSPVDSKDLGSAQNSG 630
 DB 624 SPRDQLSPT-----SISQSRSG 640

RESULT 4
 T28852
 probable potassium channel - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
 C;Accession: T28852

CHRTD1

CANADA
potassium channel protein drkl - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
R:Accession: S05448; A44838
R:Frech, G.C.; VanDongen, A.M.J.; Schuster, G.; Brown, A.M.; Joho, R.H.
Nature 340, 642-645, 1989
A:Title: A novel potassium channel with delayed rectifier properties isolated from rat B
A:Reference number: S05448; MUID:89365157; PMID:2770868
A:Accession: S05448
A:Molecule type: mRNA
A:Residues: 1-853 <PRE>
A:A/Cross-references: UNIPROT:P15387; EMBL:X16476; NID:g57785; PID:g57786
A>Note: it is uncertain whether Met-1 or Met-17 is the initiator
R:Drewe, J.A.; Verma, S.; Frech, G.; Joho, R.H.
J. Neurosci. 12, 538-548, 1992
A:Title: Distinct spatial and temporal expression patterns of K+ channel mRNAs from diff
A:Reference number: A44838; MUID:92156897; PMID:1740650
A:Accession: A44838
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'MPAG', 1-571 <DRE>
A:A/Cross-references: GB:M81783; NID:g205038
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIP:81768)
C:Genetics:
A:Gene: drkl
C:Superfamily: potassium channel protein drkl
C:Keywords: glycoprotein; ion channel; phosphoprotein; potassium channel; transmembrane
F:1-182/Domain: intracellular #status predicted <INT1>
F:183-204/Domain: transmembrane #status predicted <TM1>
F:225-245/Domain: transmembrane #status predicted <TM2>
F:256-276/Domain: transmembrane #status predicted <TM3>
F:291-312/Domain: transmembrane #status predicted <TM4>
F:327-348/Domain: transmembrane #status predicted <TM5>
F:369-410/Domain: transmembrane #status predicted <TM6>
F:411-853/Domain: intracellular #status predicted <INT2>
F:279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	6.4%	Score 289	DB 1	Length 853	
Best Local Similarity	19.7%	Pred. No. 5.8e-11			
Matches 176	Conservative 134	Mismatches 269	Indels 316	Gaps 37	
QY	80	LYNVLERPRGWA---FIYHAFVLLVFGCLILSVFSTIPEHTKL-----ASSCLILILE	129		
DB	171	LWDLLEKSNSSVAAKILAILISIMFIVLSTIALSL-NTLPQLQSLDFEQGSTNDPQLARHE	229		
QY	130	FVMIVVFGLEPIIRIWSAGCCRYRGWGGRURFARKPCFVDTITVLTIASIAVWSAKTQGN	189		
DB	230	AVCTAWFTMEVLLFELSP-----KKW---KPFKGPLNAIDLLAILPYV-----T	272		
QY	190	IPATSAURLS-----RFLQILRVMWRDRGGTWKLIQSVVYAHSKEL-ITAW	235		
DB	273	IFLTESNKSVLQFQNVREVVQIPRIMILIRILKLAHSGTGQSLGFTLRSSYNELGILLIL	332		
QY	236	YIGFLAVLIFSSFLVVLVEKDA-NKEFSTYADALWMGTITLTIGYGDKTPTITWGLRLISA	294		
DB	333	FLAMGIMLPSS-LVFFAEKDEDDTKFSIPASFWWATITMTVGVGDIVPTKLLGKIVGG	391		
QY	295	GFALLGISFFALPAGILSGSPALKVQEOHQKHFKERNPAANLIQCVRVSYAADERSVS	354		
DB	392	LCCTAGVLVIALPIPIIIVNNFSEFYKQKROEKAIKRR-----	429		
QY	355	IATWKPHLKALHTCSPTNQKLSFKERVRMASPRGOSIKRSQASVGDRRSPSTDITAEOSP	414		
DB	430	-----EALERAKNGSGIV-----	442		
QY	415	TKVQKSWGFNDTRFRPSIRLKKSSQPKVIDADTALGTDDVYDEKGCQCVSDLTPLPL	474		
DB	443	-----SNMKDKDAFARSIEM-----MDIVVEKNG-----	465		
QY	475	KTVIRAIRIMKPHVAKRFKETLRPYDVKQDVIEQYSAGHDLMLCRISLQTRVDQILGKG	534		

[illegible]

QY 213 RGGTWKLLGSSVVAHNSKELITAWYIGFLVLIFSSFLVYLVEKO-ANKEFSTYADALWGT 271
Db 393 FSSGLQTFGTMQSQKQLQWMTIVLLTGVVFFSTMIYFLEKDEGTFPTSIPAAVWCI 452
QY 272 ITLTTCIGVGTPLTWLGRLLSAGFALLGTSFPALPAGILSGFALKVQHQKHFEXR 331
Db 453 VTMTTGVGDAVPATTWTKIIASAAIMCGVLVLTPIITIVDNF-IKVADEQQAEOQKN 511
QY 332 RNPAANL 338
Db 512 DQSQEQL 518

RESULT 10
B41359
potassium channel protein ehbab1 - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 16-Feb-1997
C:Accession: B41359
R:Butler, A.; Wei, A.; Baker, K.; Salkoff, L.
Science 243, 943-947, 1989
A:Title: A family of putative potassium channel genes in *Drosophila*.
A:Reference number: A41359; MUID:89146139; PMID:2493160
A:Accession: B41359
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-924 <BUT>
A:Cross-references: FlyBase:FBgn0003383
C:Superfamily: potassium channel protein drk1

Query Match 5.5%; Score 248.5; DB 2; Length 924;
Best Local Similarity 26.2%; Pred. No. 3.1e-08;
Matches 98; Conservative 70; Mismatches 153; Indels 53; Gaps 15;

QY 72 KYRRVQNYLVNLERP-----RGWAFIYHAFVLLVFGCLILSVFSTIPE-----HTK 119
Db 413 KFSEYQKYLWELKEKPTSPAARVIAVISILFVL-----STIALTLNLPQLQHDNGTP 468
QY 120 LASSCLLILFVNVVFLGIPIIRWSAGCCRYRGWQGRRLRPARKPFCVIDIVLIA-S 178
Db 469 QDNPLQAMVAVCITFTWLYILRFSS-----PDKWKFKGGLNIDLLALPYF 519
QY 179 IAVVSATQGNIFATSALRSL-----RFLQILRMVMDRRRGTKWKLGSVVVAHNSKEL 231
Db 520 VSLFLEETKN--ATDQFQVRRVQVFRIMRLVRLKLAHSTGLQSLGFTLNSYKEL 577
QY 232 -ITAWYIGFLVLIFSSFLVYLVEKO-ANKEFSTYADALWGTITLTITTYGDKTPTLWLG 289
Db 578 GLEMLFLAMGVLLIFSS-LAYFAEKDEKDTKFSVSIPEAFWAGITMTTVGIRDICPTTALG 636
QY 290 RLISAGFALLGTSFPALPAGILSGFALKVQHQKHFEXR-----PAANLIQCVWRS 345
Db 637 KVTGTVCICGVIALVPIPIVNNFAEFYKNQMRREKALKRREHSIVPSGRGQHCLLPS 696
QY 346 YAADE---KSVSTATWPKHLKALHTCPTNOKLSFKERVMSAPR-GOSIKSQASVGDR 401
Db 697 YQSERSFAKSNMLID-----VIVDTGKQTN--VVHPGKRGKQSTENIGRQTLVDQSAAPHN 749
QY 402 RSPSTDITAEQSPT 415
Db 750 LSQTDGNSTEGEST 763

RESULT 11
T24238
hypothetical protein R186.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24238
R:Barlow, K.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19861

A:Accession: T24238

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-484 <WIL>

A:Cross-references: UNIPROT:Q22012; EMBL:Z78016; PIDN:CAB01442.1; GSPDB:GN00023; CESP:R186

A:Experimental source: clone R186

C:Genetics:

A:Gene: CESP:R186.5

A:Map position: 5

A:Introns: 30/2; 65/2; 85/3; 128/3; 235/3; 370/3; 409/3; 446/1

C:Superfamily: potassium channel protein drk1

Query Match 5.4%; Score 245; DB 2; Length 484;

Best Local Similarity 24.2%; Pred. No. 2e-08;

Matches 72; Conservative 59; Mismatches 117; Indels 50; Gaps 8;

QY 73 YRRVQNYLVNLERP---RGWAFIYHAFVLLVFGCLI-----LSVFSTIPE 116

Db 148 WQIKPRIMWLPDEPNSSRSQAFAISVFFLITAIIVFCLKTHPLRIPELAPFGNFSR 207

QY 117 HTKLASS-----CLLILEFVNVVFGLEFIIRWSAGCCRYRGWQ 158

Db 208 NHRSTSRHPAQINIDKANSRPHPTFMVETICNIWFTIEIL-----ARFSSCPS 258

QY 159 RLRFARKPCFVIDITVILIASIAVVSATQGNIFATSALRSLRFLQILRMVMDRRRGTK 218

Db 259 RPEYLAPVNIID---IVATLTFYIDLLSSMFGATADLEFFSIIRWLFKTHNSGLK 315

QY 219 LLGSVVVAHNSKEL-ITAWYIGFLVLIFSSFLVYL--VEKDANKEFSTYADALWGTITLT 275

Db 316 ILMHTFRAGAKELMLLVFLVGVVVASLYVAERVESNEDNQFVSIPIGLWAIWVMT 375

QY 276 TIGYGDTPLTWLGRLSAGFALLGISFPALPAGILSGFALKVQ- OHRQKHFEXR 332

Db 376 TIGYGDITHTYLGRLIGSICALAGVLTIALPVPVIVSNFAMFYSHQAKSKMPKRR 433

RESULT 12

S17150

potassium channel protein - rat

C:Species: *Rattus norvegicus* (Norway rat)

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Feb-2001

C:Accession: S17150

R:Luneau, C.; Wiedmann, R.; Smith, J.S.; Williams, J.B.

FEBS Lett. 288, 163-167, 1991

A:Title: Shaw-like rat brain potassium channel cDNA's with divergent 3' ends.

A:Reference number: S17150; MUID:91348257; PMID:1879548

A:Molecule type: DNA

A:Residues: 1-581 <LUN>

C:Superfamily: potassium channel protein drk1

Query Match 5.4%; Score 245; DB 2; Length 581;

Best Local Similarity 23.3%; Pred. No. 2.6e-08;

Matches 94; Conservative 79; Mismatches 138; Indels 92; Gaps 17;

QY 35 GGGGGLRESRGQKQARMSL-----LGKPLSYTSSQCRNVKRYRVQNYLVNLERP-- 87

Db 176 GGDGDEDLGGK---RLGIEDAAGLGGPDG-----KSGRWKLQPRMWFALFDPYS 224

QY 88 -RGWAFIYHAFVLLVFG---CL-----ILSVFSTIPEHTKLASSCLLI 127

Db 225 SRAARFIAFASLFFILVSITTFCLTHEAFNIVKNKTEPVINGTSVAVLQVEIETDPALTY 284

QY 128 LEFVMIVVFGLEPIIRWSAGCCRYRGWQGRRLRPARKPFCVIDITVLI-----ASTAVV 182

Db 285 VEGCVVWTFEFLVRIVFS-----PNKLEFIKNLNIIDFVAILLPFYLEVGLSGL 335

QY 183 SAKTQGNIFATSALRSLRFLQILRMVMDRRRGTKWKLGSVVVAHNSKEL-LITAWYIGFLV 241

Db 336 SSKAAKDVLL--GFLRVVRFRILIRIKLTHFVGLRVGLGTLRASTNEFLLLIFLALGV 393

QY 242 LIPSSFLVYLVEK-----DANKEFSTYADALWNGTITLTITIGYGDKTPLTWLGRL 291
Db 394 LIPAT-MIYAERVGAQNDPSASEHTQFNKPIPGFWAVVTMTTLGYGDMYPQWGSML 452
QY 292 LSAGFALLGISFFALPAGIL-----GSGFALKVQEQ-----HRQKH 331
Db 453 VGALCALAGVLTITAMPVPVIVNFMGYSLAMAKQKLPKRKKHIPPAPLASSPTFCCKTE 512
QY 332 RNPAANIQ---CWMRYAADEKSVSIATWPKPHKALHTCSPT 371
Db 513 LNMACNSTQSDTCILGKRNLEHNRVAS---TLEPMESTSQT 552

RESULT 13
T26983
hypothetical protein Y48A6B.6 - Caenorhabditis elegans
A;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Accession: T26983
R;Gardner, A.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z20295
A;Accession: T26983
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-490 <WIL>
A;Cross-references: UNIPROT:Q9XXD1; EMBL:AL023844; PIDN:CAA19530.1; GSPDB:GN00021; CESP:
A;Experimental source: clone Y48A6B
C;Genetics:
A;Gene: CESP:Y48A6B.6
A;Map position: 3
A;Introns: 34/2; 94/1; 138/1; 175/3; 256/1; 282/1; 365/3; 410/2; 419/1; 429/1; 452/3
C;Superfamily: potassium channel protein drk1

Query Match 5.3%; Score 242.5; DB 2; Length 490;
Best Local Similarity 27.1%; Pred. No. 3e-08;
Matches 76; Conservative 63; Mismatches 110; Indels 31; Gaps 10;

QY 69 RNKYRRVQVLYNVLERP-----RGWAFIYHAFVFLV-FGCLLSVFTSTPEHTKLASS 123
Db 192 KTLRFGBIRRCWNIIEBPASSGKAQAFVCSVVFLISISGLVGLPELQVATKQRNN 251
QY 124 -----CLLILEFMIIVFGLFIIRIWSAGCCCRVKGQRLR-----FARKP 166
Db 252 LTGSEFTMEPMPTLGIYEVYCIWFTMEYGLKMLVS--AERSKTFRQLNLIIDLLAILP 309
QY 167 FCVIDTIVLIASIAVVSAGTKQGNIFATSLRSLRFLQILRMVRMDRGGTWKLGSVVYA 226
Db 310 F-IEMLLIFGISTEQRLDKGAPL--VIRILRVIRVLKGRYSSGLQMPGKTLKA 366
QY 227 HSKELITAWYIGFLVLFISFVLYLVEKD--ANKEFSTYADALWNGTITLTITIGYGDKTP 284
Db 367 SFRQLGMWMMVMTGVIFSTLVLYLEKDEPASK-FHSIPAAQWCVITMTVGYGDLTP 425
QY 285 LTWIGRLLSAGFALLGISFPALPAGIISGSGFALKVQEQHR 324
Db 426 VTPVPGKLVGATACGVLLALPITIIVDNE-MKVAETER 464

RESULT 14
A39402
potassium channel protein IIRIA form 1, shaker-type - rat
A;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
A;Accession: A39402
R;McCormack, T.; Vega-Saenz de Miera, E.C.; Rudy, B.
Proc. Natl. Acad. Sci. U.S.A. 88, 4060, 1991
A;Reference number: A39402; MUID:91219512; PMID:2023956
A;Contents: erratum
A;Accession: A39402
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-613 <CC>
A;Cross-references: UNIPROT:P22462; CB:M34052; NID:G206913; PIDN:AAA42142.1; PID:G206914
C;Superfamily: potassium channel protein drk1

Query Match 5.3%; Score 242; DB 2; Length 613;
Best Local Similarity 24.1%; Pred. No. 4.5e-08;
Matches 83; Conservative 70; Mismatches 117; Indels 74; Gaps 14;

QY 35 GGGGLRESRRRGQAGMSL-----LGKPLSYTSSQSCRNVKRYRVQVLYNVLERP-- 87
Db 176 GGDPGDDEDLGGK---RLGIEDAAAGLGGPDG-----KSGRWKLPQRMWALFEDPYS 224
QY 88 -RGWAFIYHAFVFLVFG---CL-----ILSVFSTPEHTKLASSCLLI 127
Db 225 SRAARFIAPASLFFILVISITTFCTHEAFNIVKNTEPVINGTSVAVLQEIETDPALTY 284
QY 128 LEFVMIVVFGLEPIIRIWSAGCCCRVKGQRLRFAKPFCDITIVLI-----ASIAVV 182
Db 285 VEGCVVWFTFELVRIVFS-----PNKLEFIKNLNIIDFVAILPFYLEVGLSGL 335
QY 183 SAKTQGNIFATSLRSLRFLQILRMVRMDRGGTWKLGSVVVAHSKE-LITAWYIGFLV 241
Db 336 SSRAAKDVL--GFLRVVRFVRIILRIFKLTFRHFGVLGRLTASTNEFLLIIFLALGV 393
QY 242 LIPSSFLVYLVEK-----DANKEFSTYADALWNGTITLTITIGYGDKTPLTWLGRL 291
Db 394 LIPAT-MIYAERVGAQNDPSASEHTQFNKPIPGFWAVVTMTTLGYGDMYPQWGSML 452
QY 292 LSAGFALLGISFFALPAGIL-----GSGFALKVQEQ-----HRQKH 327
Db 453 VGALCALAGVLTITAMPVPVIVNFMGYSLAMAKQKLPKRKKH 496

RESULT 15
S22703
voltage-gated potassium channel protein Rawl - rat
A;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-2001
C;Accession: S22703; A45292; S19099
R;Rettig, J.; Wunder, F.; Stocker, M.; Lichtinghagen, R.; Mastiaux, F.; Beckh, S.; Kues,
EMBO J. 11, 2473-2486, 1992
A;Title: Characterization of a shaw-related potassium channel family in rat brain.
A;Reference number: S22702; MUID:92331599; PMID:1378392
A;Accession: S22703
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-624 <RET>
R;Rudy, B.; Kentros, C.; Weiser, M.; Fruhling, D.; Serodio, P.; Vega-Saenz de Miera, E.;
Proc. Natl. Acad. Sci. U.S.A. 89, 4603-4607, 1992
A;Title: Region-specific expression of a K⁺ channel gene in brain.
A;Reference number: A45292; MUID:92262488; PMID:1374908
A;Accession: A45292
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 594-624 <RUD>
A;Note: sequence extracted from NCBI backbone (NCBIN:102300, NCBIPI:102305)
C;Superfamily: potassium channel protein drk1
C;Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein
F;230-248/Domain: transmembrane #status predicted <TM1>
F;282-303/Domain: transmembrane #status predicted <TM2>
F;315-335/Domain: transmembrane #status predicted <TM3>
F;347-365/Domain: transmembrane #status predicted <TM4>
F;382-401/Domain: transmembrane #status predicted <TM5>
F;452-473/Domain: transmembrane #status predicted <TM6>

Query Match 5.3%; Score 242; DB 2; Length 624;
Best Local Similarity 24.1%; Pred. No. 4.6e-08;
Matches 83; Conservative 70; Mismatches 117; Indels 74; Gaps 14;

QY 35 GGGGLRESRRRGQAGMSL-----LGKPLSYTSSQSCRNVKRYRVQVLYNVLERP-- 87
Db 176 GGDPGDDEDLGGK---RLGIEDAAAGLGGPDG-----KSGRWKLPQRMWALFEDPYS 224

88	QY	-RGWAFIYHAFVLLVFG----	CL-----	ILSVFSTIPBHTKLASSCLLI	127
225	Db	SRAARFAFASLFTILSVITTT	FCLEHAEFNIKVNKTEPVINGTS	SAVLQGYETDPALTY	284
128	QY	LEFWMIVFGLFEFTIRIWSAGCC	CCRYRGWGRLFARFKPCFVIDT	LVLT-----	ASIAVV 182
285	Db	VEGVCVWVTFTEFLVRIFS-----	PNKLEFIKNLNIIDFVAILPFV	LEVGLSGL	335
183	QY	SAKTOGNIFATSALRSURFLFOL	ILRMVRMDRGRTKLLGVVYAH	SKKE-LITAWYIGFV	241
336	Db	SSKAAKDVL--GFLRVRFVRIL	RIFKLTRHFVGLRVLGHTR	LSASNEFLLIIIFALQV	393
242	QY	LIFSLSFLVLEK-----	DANKEFSTYADALMWGTITL	TTTIGYGDTPLTWLGR	291
394	Db	LIPAT-MIYAEVRCAQNPDS	ASEHTQFNPIGFWWAVVTT	LLGYGDMYPOITWSGML	452
292	QY	LSAGFALIGISFPA	PAGIL-----	GSGFALKVQEQ----	HRQXH 327
453	Db	VGALCALAGVLTIAMP	VPVIVNNFGMYSLAMAKOKL	PRKRKH	496

Search completed: April 8, 2005, 16:42:50
Job time : 54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:24:15 ; Search time 187 Seconds
(without alignments)
2431.692 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVESGRGVILNSAAARG.....SICKAGESTDALSPHVKLK 888

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4527.5	99.6	897	1 CIQ5_HUMAN	Q9nr82 homo sapien
2	4227.5	93.0	878	1 CIQ5_MOUSE	Q9jk45 mus musculu
3	2655.5	58.4	572	2 Q8BSF6	Q8bsf6 mus musculu
4	1985	43.7	695	1 CIQ4_HUMAN	P56696 homo sapien
5	1930	42.4	427	2 Q86W40	Q86w40 homo sapien
6	1803.5	39.7	852	1 CIQ2_RAT	Q88943 rattus norv
7	1799.5	39.6	870	2 Q8R498	Q8r498 mus musculu
8	1783	39.2	872	1 CIQ2_HUMAN	Q43526 homo sapien
9	1754	38.6	759	1 CIQ2_MOUSE	Q9z351 mus musculu
10	1587.5	34.9	872	1 CIQ3_HUMAN	Q43525 homo sapien
11	1556.5	34.2	866	1 CIQ3_BOVIN	P58126 bos taurus
12	1556.5	34.2	873	2 Q8K3F6	Q8k3f6 mus musculu
13	1555.5	34.2	873	1 CIQ3_RAT	Q88944 rattus norv
14	1525.5	33.5	523	2 Q8C9F6	Q8c9f6 mus musculu
15	1364.5	30.0	840	2 Q8IGU8	Q8iguh drosophila
16	1354	29.8	807	2 Q9V5H6	Q9v5h6 drosophila
17	1329.5	29.2	649	2 Q8IT87	Q8it87 drosophila
18	1321.5	29.1	992	2 Q9V5H7	Q9v5h7 drosophila
19	1226	27.0	692	2 Q967F8	Q967f8 caenorhabdi
20	1226	27.0	740	2 Q8MQC5	Q8mqc5 caenorhabdi
21	1198.5	26.4	459	2 Q7PP97	Q7pp97 anopheles g
22	1181	26.0	409	2 Q9BX08	Q9bx08 homo sapien
23	1145	25.2	621	2 Q9XWG9	Q9xwg9 caenorhabdi
24	1106.5	24.3	512	2 Q7QHB3	Q7qhb3 anopheles g
25	1102	24.2	676	1 CIQ1_HUMAN	P51787 homo sapien
26	1100.5	24.2	668	1 CIQ1_MOUSE	P37414 mus musculu
27	1097.5	24.1	669	1 CIQ1_RAT	Q9z0n7 rattus norv
28	1083.5	23.8	660	1 CIQ1_SQUAC	Q73925 squalus aca
29	1064.5	23.4	294	2 Q9BX07	Q9bx07 homo sapien
30	957.5	21.1	612	2 Q8K3P3	Q8k3p3 rattus norv
31	910.5	20.0	440	2 Q8CJG2	Q8cjg2 mus musculu

32	899.5	19.8	377	1	CIQ1_XENLA	P70057 xenopus lae
33	716	15.7	236	2	Q6DAP7	Q6dkp7 cavia porce
34	702	15.4	284	2	Q6DKP6	Q6dkp6 cavia porce
35	647	14.2	276	1	CIQ4_MOUSE	Q9jk97 mus musculu
36	591.5	13.0	172	1	CIQ1_FELCA	O97531 felis silve
37	549.5	12.1	392	2	Q96A19	Q96a19 homo sapien
38	538.5	11.8	169	1	CIQ1_CAVPO	O70344 cavia porce
39	486.5	10.7	155	1	CIQ1_RABIT	Q9my86 oryctolagus
40	452.5	10.0	363	2	Q9BQU4	Q9bqu4 homo sapien
41	446.5	9.8	168	1	CIQ4_RAT	Q9jk96 rattus norv
42	441	9.7	145	2	Q6DKQ1	Q6dkq1 cavia porce
43	437	9.6	97	2	Q9CTU2	Q9ctu2 mus musculu
44	430	9.5	675	2	Q9GYM8	O9gym8 caenorhabdi
45	424.5	9.3	399	2	Q9BQU5	Q9bqu5 homo sapien

ALIGNMENTS

RESULT 1

ID	CIQ5_HUMAN	STANDARD;	PRT;	897 AA.
AC	Q9NR82; Q9NRN0; Q9NYA6;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	03-JUN-2004 (Rel. 44, Last annotation update)			
DE	Potassium voltage-gated channel subfamily KQT member 5 (Voltage-gated potassium channel subunit Kv7.5) (Potassium channel alpha subunit KvLQT5) (KQT-like 5).			
DE	Name=KCNQ5;			
GN	Homo sapiens (Human)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Brain;			
RX	MEDLINE=20357367; PubMed=10787416; DOI=10.1074/jbc.M002378200;			
RA	Lerche C., Scherer C.R., Seebohm G., Derst C., Wei A.D., Busch A.E., Steinmeyer K.;			
RA	"Molecular cloning and functional expression of KCNQ5, a potassium channel subunit that may contribute to neuronal M-current diversity."			
RL	J. Biol. Chem. 275:22395-22400(2000).			
[2]				
RN	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).			
RP	TISSUE=Brain;			
RC	TISSUE=Brain;			
RX	MEDLINE=20379054; PubMed=10816588; DOI=10.1074/jbc.M003245200;			
RA	Schroeder B.C., Hechenberger M., Weinreich F., Kubisch C., Jentsch T.J.;			
RA	"KCNQ5, a novel potassium channel broadly expressed in brain, mediates M-type currents."			
RL	J. Biol. Chem. 275:24089-24095(2000).			
[3]				
RN	SEQUENCE FROM N.A.			
RP	Kananura C., Bivert B., Hechenberger M., Engels H., Steinlein O.K.;			
RA	"The new voltage gated potassium channel KCNQ5 and early infantile convulsions."			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			
[4]				
RN	SEQUENCE OF 37-897 FROM N.A. (ISOFORM 1).			
RP	TISSUE=Brain, and Retina;			
RC	Kniazeva M., Han M.;			
RA	"A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5, is a candidate gene for retinal disorders."			
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
[5]				
RN	CHARACTERIZATION, AND ACTIVATION BY RETICABINE.			
RP	MEDLINE=21095345; PubMed=11159685;			
RX	Wickenden A.D., Zou A., Wagoner P.K., Jegla T.;			
RA	"Characterization of KCNQ5/Q3 potassium channels expressed in mammalian cells."			
RL	Br. J. Pharmacol. 132:381-384(2001).			
CC	-I- FUNCTION: Probably important in the regulation of neuronal			


```

Db 661 EFSAQTFVALSPTHMSQATQVPISSDGSAAVAANTIANQINTAPKPAATTLQIPPLP 720
Qy 712 AIKHLPRPETHLPNPAQLESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDWGSETL 771
Db 721 AIKHLPRPETHLPNPAQLESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDWGSETL 780
Qy 772 LSVCPMPVKDLGKSLVQNLIRSTRTEELNIQLSGSESSGRSQDPYFKWRKSLFITDEE 831
Db 781 LSVCPMPVKDLGKSLVQNLIRSTRTEELNIQLSGSESSGRSQDPYFKWRKSLFITDEE 840
Qy 832 VGPETETDTFDAAPQAPAREAAAFASDSLRTGRSSSSOSICKAGESTDALSPLPHVKLK 888
Db 841 VGPETETDTFDAAPQAPAREAAAFASDSLRTGRSSSSOSICKAGESTDALSPLPHVKLK 897

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RESULT 2

```

C1Q5 MOUSE ID_C1Q5_MOUSE STANDARD; PRT; 878 AA.
AC O9JK45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 5 (Voltage-gated
DE potassium channel subunit Kv7.5) (Potassium channel alpha subunit
DE Kv7.5) (KQT-like 5) (Fragment).
GN Name=Kcnq5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RA Knaizeva M., Han M.;
RT "A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5,
RT is a candidate gene for retinal disorders."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ3 to form a potassium channel
CC which contributes to m-type current, a slowly activating and
CC deactivating potassium conductance which plays a critical role in
CC determining the subthreshold electrical excitability of neurons.
CC May contribute, with other potassium channels, to the molecular
CC diversity of an heterogeneous population of M-channels, varying in
CC kinetic and pharmacological properties, which underly this
CC physiologically important current (By similarity).
CC -1- SUBUNIT: Heteromultimer with KCNQ3 (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position (By similarity).
CC -1- SIMILARITY: Belongs to the potassium channel family. KQT
CC subfamily.

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DR EMBL; AF263836; AAF73447.1; -.
DR HSSP; Q54397; 1JVM.
DR MGd; MG1:1924937; Kcnq5.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR003091; K channel.
DR InterPro; IPR003937; KCNQ channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF03520; KCNQ_channel; 1.

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DR PRINTS; PR00169; KCHANNEL.
KW Ion transport; Ionic channel; Multigene family; Potassium;
KW Potassium channel; Potassium transport; Transmembrane; Transport;
KW Voltage-gated channel.
FT NON_TER 1 1
FT TRANSMEM 72 92 Segment S1 (Potential).
FT TRANSMEM 103 123 Segment S2 (Potential).
FT TRANSMEM 147 167 Segment S3 (Potential).
FT TRANSMEM 176 198 Segment S4 (Potential).
FT TRANSMEM 213 233 Segment S5 (Potential).
FT TRANSMEM 272 292 Segment S6 (Potential).
FT DOMAIN 245 265 Segment H5 (pore-forming) (Potential).
FT SITE 257 262 Selectivity filter (By similarity).
SQ SEQUENCE 878 AA; 97029 MW; 3579F9C7D630F55 CRC64;

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Query Match 93.0%; Score 4227.5; DB 1; Length 878;
Best Local Similarity 94.3%; Pred. No. 4.4e-227;
Matches 827; Conservative 14; Mismatches 27; Indels 9; Gaps 1;

Qy 20 GDGLLLGTRAAVTGGGGGLRESRRKQKQARMSSLLGKPLSYTSSQSCRNVKRRVQNY 79
Db 1 GDGLLLGTRAAALGGGGGLRESRRKQKQARMSSLLGKPLSYTSSQSCRNVKRRVQNY 60
Qy 80 LYNVLERPRGWAFTYHAFVLLVFGCLLSVFSTIPEHTKLASSCLLILFVMIIVFGLE 139
Db 61 LYNVLERPRGWAFTYHAFVLLVFGCLLSVFSTIPEHTKLASSCLLILFVMIIVFGLE 120
Qy 140 FIIRWSAGCCCRYRGQGRLEFARKPFVVIDIVILIASIAVVSATQGNIFATSALRSL 199
Db 121 FIIRWSAGCCCRYRGQGRLEFARKPFVVIDIVILIASIAVVSATQGNIFATSALRSL 180
Qy 200 RFLQILRMVMDRRGGTGWLLGSSVVAHAKSELITAMVIGFLVLIFFSFLVLYVEKDANKE 259
Db 181 RFLQILRMVMDRRGGTGWLLGSSVVAHAKSELITAMVIGFLVLIFFSFLVLYVEKDANKE 240
Qy 260 FSTYADALMWGTTTLTTIGVGDKTPLTWLGRLLSAGFALLIGISFFALLXAGIXGSGFALKV 319
Db 241 FSTYADALMWGTTTLTTIGVGDKTPLTWLGRLLSAGFALLIGISFFALLXAGIXGSGFALKV 300
Qy 320 QEHRQKHFKERNPAANLIQCVRSYAADKSVSIATWPKHLKALHATCSPT----- 371
Db 301 QEHRQKHFKERNPAANLIQCVRSYAADKSVSIATWPKHLKALHATCSPTKKEQGEAS 360
Qy 372 -NOKLSFKERVRVASPRGQSIKRSQASVGRDRSPSTDITAEQSPTKVKQKSWFNDRTRFR 430
Db 361 SSQKLSFKERVRVASPRGQSIKRSQASVGRDRSPSTDITAEQSPTKVKQKSWFNDRTRFR 420
Qy 431 PSURLKSSQPKVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKHVAK 490
Db 421 PSURLKSSQPKVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKHVAK 480
Qy 491 RPKETLRPYDVKDVIQESAGHLDMLCRIKSLQTRVDQILGKQITSDKKSREKITAHEH 550
Db 481 RPKETLRPYDVKDVIQESAGHLDMLCRIKSLQTRVDQILGKQITSDKKSREKITAHEH 540
Qy 551 ETTDDLSMLGRVVKVKEQVQSIKESKLDCLLDIYQOVLKGSASALALASQIIPPFCEQT 610
Db 541 ETTDDPSMLARVVVKVKEQVQSIKESKLDCLLDIYQOVLKGSASALALASQIIPPFCEQT 600
Qy 611 SDYQSPVDSKDLGSGSAQNSCLSRSTANISRGLOFTLTNEFSQAOTFYALSPTMHQAOT 670
Db 601 SDYQSPVDSKDLGSGSAQNSCLSRSTANISRGLOFTLTNEFSQAOTFYALSPTMHQAOT 660
Qy 671 QVPISQSGSAVAATNTIANQINTAPKPAATTLQIPPLPAIKHPRPETHLPNPAQGL 730
Db 661 QVPMSQNDGSSVVAATNIAQISAAKPAATTLQIPPLSAIKHLSRPEPLLSNPTGLQ 720
Qy 731 ESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDWGSETLLSVCPMPVKDLGKSLVQ 790
Db 721 ESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDWGSETLLSVCPMPVKDLGKSLVQ 780
Qy 791 LIRSTEELNIQLSGSESSGRSQDPYFKWRKSLFITDEEVPETETDTFDAAPAR 850

```


DE KvLOT4 (KQT-like 4).

GN Name=KCNQ4;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT DFNA2 SER-285.

RC TISSUE=Retina;

RX MEDLINE=99148276; PubMed=10025409; DOI=10.1016/S0092-8674(00)80556-5;

RA Kubisch C., Schroeder B.C., Friedrich T., Luetjohann B.,

RA El-Amraoui A., Marlin S., Petit C., Jentsch T.J.;

RT "KCNQ4, a novel potassium channel expressed in sensory outer hair

RT cells, is mutated in dominant deafness.";

RL Cell 96:437-446(1999).

RN [2]

RP INHIBITION BY M1 MUSCARINIC RECEPTORS.

RX MEDLINE=20178300; PubMed=10713961;

RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,

RA Brown D.A.;

RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells

RT via M1 muscarinic acetylcholine receptors.";

RL J. Physiol. (Lond.) 522:349-355(2000).

RN [3]

RP PHARMACOLOGICAL CHARACTERIZATION, AND POSSIBLE FUNCTION.

RX MEDLINE=21143874; PubMed=11245603;

RA Soegaard R., Ljungstrom T., Pedersen K.A., Olesen S.-P.,

RA Jensen B.S.;

RT "KCNQ4 channels expressed in mammalian cells: functional

RT characteristics and pharmacology.";

RL Am. J. Physiol. 280:C859-C866(2001).

RN [4]

RP VARIANTS DFNA2 SER-276; CVS-285 AND SER-321.

RX MEDLINE=99299248; PubMed=10369879; DOI=10.1093/hmg/8.7.1321;

RA Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schattman I.,

RA Van Velzen D., Meyers J., Ensink R.J., Verstreken M., Declau P.,

RA Marres H., Kastury K., Bhasin S., McGuirt W.T., Smith R.J.H.,

RA Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.,

RA Van Camp G.;

RT "Mutations in the KCNQ4 gene are responsible for autosomal dominant

RT deafness in four DFNA2 families.";

RL Hum. Mol. Genet. 8:1321-1328(1999).

RN [5]

RP VARIANT DFNA2 SER-281.

RX MEDLINE=20040027; PubMed=10571947;

RA DOI=10.1002/(SICI)1098-1004(199912)14:6<493::AID-HUMUS>3.0.CO;2-P;

RA Talebizadeh Z., Kelley P.M., Askew J.W., Beisel K.W., Smith S.D.;

RT "Novel mutation in the KCNQ4 gene in a large kindred with dominant

RT progressive hearing loss.";

RL Hum. Mutat. 14:493-501(1999).

RN [6]

RP VARIANT DFNA2 HIS-274.

RX MEDLINE=20388752; PubMed=10925378;

RA DOI=10.1002/1096-8628(20000731)93:3<184::AID-AJMG4>3.0.CO;2-5;

RA Van Hauwe P., Coucke P.J., Ensink R.J., Huygen P., Cremers C.W.R.J.,

RA Van Camp G.;

RT "Mutations in the KCNQ4 K+ channel gene, responsible for autosomal

RT dominant hearing loss, cluster in the channel pore region.";

RL Am. J. Med. Genet. 93:184-187(2000).

CC -1- FUNCTION: Probably important in the regulation of neuronal

CC excitability. May underlie a potassium current involved in

CC regulating the excitability of sensory cells of the cochlea. KCNQ4

CC channels are blocked by linopirdin, XE991 and bepridil, whereas

CC clofilium is without significant effect. Muscarinic agonist

CC oxotremorine-M strongly suppress KCNQ4 current in CHO cells in

CC which cloned KCNQ4 channels were coexpressed with M1 muscarinic

CC receptors.

CC -1- SUBUNIT: May form heteromultimers with KCNQ3.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Situated at the

CC basal membrane of cochlear outer hair cells (By similarity).

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC

CC Name=1;

CC IsoId=PS56696-1; Sequence=Displayed;

CC Name=2;

CC IsoId=PS56696-2; Sequence=VSP_001013;

CC TISSUE SPECIFICITY: Expressed in the outer, but not the inner,

CC sensory hair cells of the cochlea. Slightly expressed in heart,

CC brain and skeletal muscle.

CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is

CC characterized by a series of positively charged amino acids at

CC every third position (By similarity).

CC -1- DISEASE: Defects in KCNQ4 are a cause of nonsyndromic

CC sensorineural deafness type 2 (DFNA2) [MIM:600101], an autosomal

CC dominant form of progressive hearing loss.

CC -1- MISCELLANEOUS: Mutagenesis experiments were carried out by

CC expressing in Xenopus oocytes KCNQ4 mutants either individually

CC (homomultimers) or in combination with wild-type KCNQ4 (mut/wt

CC homomultimers) in a ratio of 1:1, to mimic the situation in a

CC heterozygous DFNA2 patient.

CC -1- SIMILARITY: Belongs to the potassium channel family. KQT

CC subfamily.

CC -1- DATABASE: NAME=Hereditary hearing loss homepage; NOTE=Gene page;

CC WWW="http://www.uia.ac.be/dnalab/hhh/".

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see http://www.isb-sib.ch/announce/

CC or send an email to license@isb-sib.ch).

CC

CC EMBL; AF105202; AAD14680.1; -

CC EMBL; AF105216; AAD14681.1; -

CC EMBL; AF105203; AAD14681.1; JOINED.

CC EMBL; AF105204; AAD14681.1; JOINED.

CC EMBL; AF105205; AAD14681.1; JOINED.

CC EMBL; AF105206; AAD14681.1; JOINED.

CC EMBL; AF105207; AAD14681.1; JOINED.

CC EMBL; AF105208; AAD14681.1; JOINED.

CC EMBL; AF105209; AAD14681.1; JOINED.

CC EMBL; AF105210; AAD14681.1; JOINED.

CC EMBL; AF105211; AAD14681.1; JOINED.

CC EMBL; AF105212; AAD14681.1; JOINED.

CC EMBL; AF105213; AAD14681.1; JOINED.

CC EMBL; AF105214; AAD14681.1; JOINED.

CC EMBL; AF105215; AAD14681.1; JOINED.

CC HSP; Q54397; IJVM.

CC Genew; HGNC:6298; KCNQ4.

CC MIM; 603537; -

CC MIM; 600101; -

CC GO; GO:0005267; P:potassium channel activity; TAS.

CC GO; GO:0007605; P:perception of sound; TAS.

CC GO; GO:0006813; P:potassium ion transport; TAS.

CC InterPro; IPR005821; Ion trans.

CC InterPro; IPR001622; K-channel_pore.

CC InterPro; IPR003091; K-channel.

CC InterPro; IPR003937; KCNQ channel.

CC InterPro; IPR005820; M-channel_rlg.

CC Pfam; PF00520; Ion trans; 1.

CC Pfam; PF03520; KCNQ channel; 1.

CC PRINTS; PR00169; KCHANNEL.

CC Alternative splicing; Deafness; Disease mutation; Ion transport;

CC Ionic channel; Multigene family; Potassium; Potassium channel;

CC Potassium transport; Transmembrane; Transport; Voltage-gated channel.

CC TRANSMEM 98 118 Segment S1 (Potential).

CC TRANSMEM 132 152 Segment S2 (Potential).

CC TRANSMEM 173 193 Segment S3 (Potential).

CC TRANSMEM 202 224 Segment S4 (Potential).

CC TRANSMEM 238 258 Segment S5 (Potential).

CC TRANSMEM 297 317 Segment S6 (Potential).

CC DOMAIN 271 292 Segment H5 (pore-forming) (Potential).

CC SITE 283 288 Selectivity filter (By similarity).

CC VARSPLIC 378 431 Missing (in isoform 2).

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FT VARIANT 274 274 /FTID=VSP_001013.
FT L -> H (in DFN2).
FT /FTID=VAR_010936.
FT VARIANT 276 276 W -> S (in DFN2).
FT /FTID=VAR_008726.
FT VARIANT 281 281 L -> S (in DFN2).
FT /FTID=VAR_010937.
FT VARIANT 285 285 G -> C (in DFN2); loss of potassium
FT selectivity of the pore.
FT /FTID=VAR_008727.
FT VARIANT 285 285 G -> S (in DFN2).
FT /FTID=VAR_001547.
FT VARIANT 321 321 G -> S (in DFN2).
FT /FTID=VAR_008728.
FT MUTAGEN 285 285 G-S: No current (homomultimers). 90% wt
FT current reduction (mu/wt homomultimers).
FT /FTID=VAR_008729.
SQ SEQUENCE 695 AA; 77091 MW; A58737BD845E1A3A CRC64;

Query Match 43.7%; Score 1985; DB 1; Length 695;
Best Local Similarity 60.3%; Pred. No. 2.6e-102; Indels 92; Gaps 13;
Matches 409; Conservative 76; Mismatches 101;

QY 35 GGGGLRESRRGKQAGMRLGKPL-----SYTSQSCRNVKRRVQNYL 80
DB 37 GGGGSPR-----RLGLGSLPPGAPLPGSGSGSACGORSAAHKRYRRLQNVV 87

QY 81 YNVLEPRGWAIFYHAFVFLVFGCLLSVFSSTIPETHTKLASSCLLLEFVMIVFGLEF 140
DB 88 YNVLEPRGWAIFYHAFVFLVFGCLLSVFSSTIPETHTKLASSCLLLEFVMIVFGLEF 147

QY 141 IIRIWSAGCCRCRGMQGRLEFARKPCFVIDIIVLIASIAVSAKTQGNIFATSALRSR 200
DB 148 IIRIWSAGCCRCRGMQGRLEFARKPCFVIDIIVLIASIAVSAKTQGNIFATSALRSR 207

QY 201 FLQILRMVMDRGCTWKLGSVYVYHAKELITAWYIGFVLVFPSSFLVLEKDKANER 260
DB 208 FLQILRMVMDRGCTWKLGSVYVYHAKELITAWYIGFVLVFPSSFLVLEKDKANER 267

QY 261 STYADALWNGTITITIGYDKTPTLWGLRLSAGFALLGISFPALPAGILGSGFALKVQ 320
DB 268 STYADALWNGTITITIGYDKTPTLWGLRLSAGFALLGISFPALPAGILGSGFALKVQ 327

QY 321 EHQHROKHFKEKRRNPANLIQCVWRSYAAD-EKSVSIATW----- 358
DB 328 EHQHROKHFKEKRRNPANLIQCVWRSYAAD-EKSVSIATW----- 387

QY 359 -----KPHLKALHT-----CSPTNOKLSFKERVMSAPRG 388
DB 388 RARNGGLRPLEVRRAPVDPGAPSRYPVATCPGTSFCPCGSRRMGKIDRIWGSQR 447

QY 389 QSIKSRQ--ASVGDRRSPSTDTAEG-SPTKVQKSWSFNDRTRFRPSLRKSSQPKPID 445
DB 448 RTGPKQQLAPTMTPTSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPTS 502

QY 446 ADTALGTDDVDYDEKQCQCVSDVEDTTPPLKVIRAIRIMKHFVAKRKETLRYDVYKDV 505
DB 503 AEDA-PSEVEAEKSYQCELTVDDIMPVAVKTVIRSIRILKFLVAKRKETLRYDVYKDV 561

QY 506 IEQYSAGHLDMLCRKLSLQTRVDQILGKQITSDKKSR-----KITAHEHTTDLISMLGRV 562
DB 562 IEQYSAGHLDMLGRKLSLQTRVDQILGKQITSDKKSR-----KITAHEHTTDLISMLGRV 619

QY 563 VKVEKQVQSIKSLDCLLDIYQOVLKSGSALALASFQIPPECEQTSQYSPVDSKDL 622
DB 620 VKVEKQVQSIKSLDCLLDIYQOVLKSGSALALASFQIPPECEQTSQYSPVDSKDL 677

QY 623 SGSAQNSGCLSRSTSANI 640
DB 678 SVSAQTLN-ISRVSSTNM 694
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RESULT 5
Q86W40

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ID Q86W40 PRELIMINARY; PRT; 427 AA.
AC Q86W40;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC050689; AAH50689.1; -.
RA HSSP; Q54397; IJ95.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005249; P:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:potassium ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003947; KCNQ2 channel.
DR InterPro; IPR003937; KCNQ2 channel.
DR InterPro; IPR003091; K channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01461; KCNQ2CHANNEL.
DR PRINTS; PR01459; KCNQCHANNEL.
DR KW Hypothetical protein; Ion transport; Ionic channel; Transmembrane;
KW Transport.
SQ SEQUENCE 427 AA; 46942 MW; 175F91B7BB48836B CRC64;

Query Match 42.4%; Score 1930; DB 2; Length 427;
Best Local Similarity 99.2%; Pred. No. 1.6e-99;
Matches 371; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDVESGRVLLNSAARGDGLLLGTRAAATGGGGGLRERKQAGMRLGKPLS 60
DB 36 MKDVESGRVLLNSAARGDGLLLGTRAAATGGGGGLRERKQAGMRLGKPLS 95

QY 61 YTSQSCRNVKRRVQNYLYNVLEPRGWAIFYHAFVFLVFGCLLSVFSSTIPETHTKL 120
DB 96 YTSQSCRNVKRRVQNYLYNVLEPRGWAIFYHAFVFLVFGCLLSVFSSTIPETHTKL 155

QY 121 ASSCLLILEFVMIVFGLEFIIRWSAGCCRCRGMQGRLEFARKPCFVIDIIVLIASIA 180
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Db 156 ASSCLLLEFWMVVGLEFIIRWSAGCCRRGMRGRPFARKPCVDTIVILASIA 215
Qy 181 VVSAKTQGNIFATSALRSRPLQLRMRVDRRGTTWKLGSVVVYAHSKELITAWYIGFL 240
Db 216 VVSAKTQGNIFATSALRSRPLQLRMRVDRRGTTWKLGSVVVYAHSKELITAWYIGFL 275
Qy 241 VLIFFSFLVYLVEKDANKSESTYADALWNGTITLTITTYGDKTPTLWGLLSAGFALLG 300
Db 276 VLIFFSFLVYLVEKDANKSESTYADALWNGTITLTITTYGDKTPTLWGLLSAGFALLG 335
Qy 301 ISFFALPAGILGSGFALKVQEHQKHFEKRRNPAANLIOCVRWSYAADKSVSIATWKP 360
Db 336 ISFFALPAGILGSGFALKVQEHQKHFEKRRNPAANLIOCVRWSYAADKSVSIATWKP 395
Qy 361 HLKALHTCSPNTQK 374
Db 396 HLKALHTCSPNTKE 409

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RESULT 6

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C1Q2 RAT STANDARD; PRT; 852 AA.
AC O88943;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 2 (Voltage-gated
DE potassium channel subunit Kv7.2) (Potassium channel alpha subunit
DE KvLOT2) (KQT-like 2).
GN Name=Kcnq2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RA Derst C., Preisig-Mueller R., Hennighausen A., Daut J.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=20493350; PubMed=11038262; DOI=10.1016/S0169-328X(00)00146-7;
RA Jow F., Wang K.-W.;
RT "Cloning and functional expression of rKCNQ2 K(+) channel from rat
RL brain.";
RL Brain Res. Mol. Brain Res. 80:269-278(2000).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Sympathetic ganglion;
RX MEDLINE=21154288; PubMed=11230508;
RA Pan Z., Selyanko A.A., Hadley J.K., Brown D.A., Dixon J.E.,
RA McKinnon D.;
RT "Alternative splicing of KCNQ2 potassium channel transcripts
RT contributes to the functional diversity of M-currents.";
RL J. Physiol. (Lond.) 531:347-358(2001).
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=99055398; PubMed=9836639; DOI=10.1126/science.282.5395.1890;
RA Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RA Dixon J.E., McKinnon D.;
RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
RT the M-channel.";
RL Science 282:1890-1893(1998).
CC -I- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ3 to form a potassium channel
CC with essentially identical properties to the channel underlying
CC the native M-current, a slowly activating and deactivating
CC potassium conductance which plays a critical role in determining
CC the subthreshold electrical excitability of neurons as well as the
CC responsiveness to synaptic inputs. KCNQ2 current is blocked by
CC barium and tetraethylammonium whereas 4-aminopyridine and

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CC charybdotoxin have no effect on KCNQ2 current. Tyrosine kinase
CC inhibitors genistein or herbimycin a markedly down-regulate KCNQ2
CC current. Muscarinic agonist oxotremorine-M suppress KCNQ2/KCNQ3
CC current in CHO cells in which cloned KCNQ2/KCNQ3 channels were
CC coexpressed with human M1 muscarinic receptors.
CC -I- SUBUNIT: Heteromultimer with KCNQ3.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=9;
CC Comment=Splice isoforms fell into three classes, those that
CC contain an in frame exon 16 (isoforms A-I) those that contain an
CC out-of-frame exon 16 due to an alternative splice junction in
CC exon 14 and those that terminate prematurely to exon 16. Only
CC the forms containing an in frame exon 16 are able to form
CC functional channels. A similar splice pattern is also produced
CC for splice variants that contain an out-of-frame exon 16. A wide
CC variety of different truncated isoforms were isolated for splice
CC variants that terminate prematurely to exon 16;
CC Name=A;
CC IsoId=O88943-1; Sequence=Displayed;
CC Name=B;
CC IsoId=O88943-2; Sequence=VSP_001009, VSP_001011;
CC Name=C;
CC IsoId=O88943-3; Sequence=VSP_001007;
CC Name=D;
CC IsoId=O88943-4; Sequence=VSP_001008, VSP_001010;
CC Name=E;
CC IsoId=O88943-5; Sequence=VSP_001008;
CC Name=F;
CC IsoId=O88943-6; Sequence=VSP_001007, VSP_001008, VSP_001010;
CC Name=G;
CC IsoId=O88943-7; Sequence=VSP_001011;
CC Name=H;
CC IsoId=O88943-8; Sequence=VSP_001007, VSP_001008;
CC Name=I;
CC IsoId=O88943-9; Sequence=VSP_001010;
CC -I- TISSUE SPECIFICITY: Expressed in brain and sympathetic ganglia. In
CC brain, expressed in cortex, hippocampus, and cerebellum. In
CC sympathetic ganglia, expressed at lower levels in celiac ganglia
CC and superior mesenteric ganglia than in superior cervical ganglia.
CC -I- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position (By similarity).
CC -I- MISCELLANEOUS: When coexpressed with KCNQ3 subunit in CHO cells or
CC Xenopus oocytes, isoform B was found to have significantly
CC different deactivation-activation kinetics. The kinetics was 2.5
CC times more slowly than the kinetics of other isoforms. The
CC presence of exon 15a in isoform B accounts for the slow
CC deactivation-activation kinetics. Alternative splicing of the
CC KCNQ2 gene may contribute to the variation in M-current kinetics
CC seen in vivo.
CC -I- SIMILARITY: Belongs to the potassium channel family. KQT
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF087453; AAC36722.1; -.
CC HSSP; Q54397; IJVM.
CC RGD; 621504; Kcnq2.
CC InterPro; IPR005821; Ion trans.
CC InterPro; IPR01622; K+channel_pore.
CC InterPro; IPR003091; K channel.
CC InterPro; IPR003937; KCNQ channel.
CC InterPro; IPR005820; M+channel_nlg.
CC Pfam; PF00520; Ion trans; 1.
CC Pfam; PF03520; KCNQ channel; 1.
CC PRINTS; PR00169; KCHANNEL.

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KW Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW Phosphorylation; Potassium; Potassium channel; Potassium transport;
KW Transmembrane; Transport; Voltage-gated channel;
FT TRANSMEM 92 112 Segment S1 (Potential).
FT TRANSMEM 123 143 Segment S2 (Potential).
FT TRANSMEM 167 187 Segment S3 (Potential).
FT TRANSMEM 198 221 Segment S4 (Potential).
FT TRANSMEM 232 252 Segment S5 (Potential).
FT TRANSMEM 292 312 Segment S6 (Potential).
FT DOMAIN 265 285 Segment H5 (pore-forming) (Potential).
FT SITE 277 282 Selectivity filter (By similarity).
FT MOD_RES 52 52 Phosphoserine (by PKA) (By similarity).
FT VARSPPLIC 373 382 Missing (in isoform C, isoform F and isoform H).
FT VARSPPLIC 416 416 S -> SKGRFCRCGLCGCRPHSS (in isoform D, isoform E, isoform F and isoform H).
FT VARSPPLIC 417 428 /FTid=VSP_001008.
FT VARSPPLIC 491 491 Missing (in isoform B).
FT VARSPPLIC 491 491 /FTid=VSP_001009.
FT VARSPPLIC 571 571 Missing (in isoform D, isoform F and isoform I).
FT VARSPPLIC 571 571 /FTid=VSP_001010.
FT VARSPPLIC 571 571 R -> RIDMIVGPPPPPTPRHKKYKPKGTPAPRSPPQVSP
FT VARSPPLIC 571 571 R (in isoform B and isoform G).
FT VARSPPLIC 571 571 /FTid=VSP_001011.
SQ SEQUENCE 852 AA; 93949 MW; 82A5PE42A5F259A CRC64;
Query Match 39.7%; Score 1803.5; DB 1; Length 852;
Best Local Similarity 49.0%; Pred. No. 4.4e-92;
Matches 413; Conservative 96; Mismatches 193; Indels 141; Gaps 22;
QY 17 AARGDGLLLGTRATLGGGGGLRSRRGKQGRMSLLGKPLSYTSSQSCRNVKRV 76
DB 34 STRDGALLIAGEAPK--RGSVLSKPTGAGA-----GKP-----PKENAFYRKL 77
QY 77 QNYLYNVLERPRGWAFTYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILFVMIWVF 136
DB 78 QNFLYNVLERPRGWAFTYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILFVMIWVF 137
QY 137 GLEFIIRIWSAGCCCRYRGQGRRLRFAKPFQVIDITVILIASIVAVSAKTQGNIFATSAL 196
DB 138 GVEYFVRIWAAGCCCRYRGQGRRLRFAKPFQVIDITVILIASIVAVSAKTQGNIFATSAL 197
QY 197 RSLRFLQILRMVDRGGTWKLGSVVYAHSEKELITAWYIGFVLVIFSSFLVYVEKDA 256
DB 198 RSLRFLQILRMVDRGGTWKLGSVVYAHSEKELITAWYIGFVLVIFSSFLVYVEKDA 257
QY 257 NKEPSTVADALWGGTITLTITIGYGDYKVPQTWNGRLAATFTLIGVSPFALPAGILGSGFA 316
DB 258 NDHFDTVADALWGGTITLTITIGYGDYKVPQTWNGRLAATFTLIGVSPFALPAGILGSGFA 317
QY 317 LKVOEQHROKHFKERRRPAANLICOVRSVADEKSVSI-ATWK----- 359
DB 318 LKVOEQHROKHFKERRRPAANLICOVRSVADEKSVSI-ATWK----- 377
QY 360 -----PHLKALHTC-----SPTNQKLSFKERVMASSPRGOSIK 392
DB 378 TYGASRLIPPLNQLMLRNLKSKSLTFRKEPQPEPSP-SQKVSLLKDRV-FSSPRGVAAK 435
QY 393 SRQASVGD--RRSPSTDIABGSPTKVOKSFSFNDRTRFRPSLRKLSKSPKFPVIDATDAL 450
DB 436 GKGSPQAQTVRRSPSADQSLDSSPKVPSKWSFGDRSRARQAFRIKGAASRQNSEASLP 495
QY 451 GTDDVYDEKGCQDVSDVETLPPKLTIVIRIRIMKFFHAKKFKETLRPYDVKDVIROY 510
DB 496 GEDIVEDNKSNCHEFVETLIPGLKVSIRAVCVWRFLVSKKFKESLRPYDMDVIEQYS 555
QY 511 AGHLDMLCRIKSLQTRVDQILKGQITSDKKSREKITAETHETDLDLMLGRVWVKQVQ 570
DB 556 AGHLDMLCRIKSLQTRVDQILKGQITSDKKSREKITAETHETDLDLMLGRVWVKQVQ 614
QY 571 SIESKLDCLLDIYQOVLKGSASALASAFQIPPEF-----BQTSYQSPVDSKD 621

DB 615 SMEKKDLFLVSIYTO--RMG-----IPPAETAYFGAKEPEPAPPVHSPEDSKD 661
QY 622 LSGSAQNSGC---LSRSTSANISRGLOFILTNEFSAQTFFVALSPTHMSQATQVPIQSOD 678
DB 662 ---HADKHCIIKIVRSISS-----TGORKYAAPPVM--PPAECPPSTS- 700
QY 679 GSAVAATNTIANQINATPKPAATTLLQIPPPPLPAIKHLPRPETLHPNPAGLOESISDVTT 738
DB 701 -----WQSHQRHGTSPVGDHGSLSVRIPPP-----PAH-ERSLSAYSG 737
QY 739 CLIVASKENVQAQSNLTK--DRSMKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIIRSTE 796
DB 738 GNRASTEFLURGTGTPACRPSEALRDS-----DTSISIPSDVDEHLERSFSGFSISQSK 792
QY 797 ELN 799
DB 793 NLN 795
RESULT 7
Q8R498 PRELIMINARY; PRT; 870 AA.
ID Q8R498
AC Q8R498; 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Potassium channel KCNQ2.
GN Name=Kcnq2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=12233552;
RA Wen H., Levitan I.B.;
RT "Calmodulin Is an Auxiliary Subunit of KCNQ2/3 Potassium Channels."
RL J. Neurosci., 22:7991-8001 (2002).
DR EMBL; AF490773; AAM09696.1; --
DR HSSP; Q54397; 1J95.
DR MGD; MGI:1309503; Kcnq2.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003947; KCNQ2 channel.
DR InterPro; IPR003937; KCNQ channel.
DR InterPro; IPR003091; K channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF03520; KCNQ channel; 1.
DR PRINTS; PR0169; KCHANNEL.
DR PRINTS; PR01461; KCNQ2CHANNEL.
DR PRINTS; PR01459; KCNQCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 870 AA; 95741 MW; 9C6106C27C70C5F CRC64;
Query Match 39.6%; Score 1799.5; DB 2; Length 870;
Best Local Similarity 47.9%; Pred. No. 7.5e-92;
Matches 408; Conservative 96; Mismatches 195; Indels 153; Gaps 21;
QY 17 AARGDGLLLGTRATLGGGGGLRSRRGKQGRMSLLGKPLSYTSSQSCRNVKRV 76
DB 34 STRDGALLIAGEAPK--RGSVLSKPTGAGA-----GKP-----PKENAFYRKL 77
QY 77 QNYLYNVLERPRGWAFTYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILFVMIWVF 136
DB 78 QNFLYNVLERPRGWAFTYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILFVMIWVF 137
QY 137 GLEFIIRIWSAGCCCRYRGQGRRLRFAKPFQVIDITVILIASIVAVSAKTQGNIFATSAL 196
DB 138 GVEYFVRIWAAGCCCRYRGQGRRLRFAKPFQVIDITVILIASIVAVSAKTQGNIFATSAL 197

197 RSLRFLQILVMDRGGTCKLLGSSVYAHKSLITAWYIGFLVLFSSFLVLYVEKDA 256
198 RSLRFLQILVMDRGGTCKLLGSSVYAHKSLITAWYIGFLVLFSSFLVLYVEKGE 257
257 NKFSFTYADALWMTITLTITIGYDKTPTLWGLRLSAGFALLGISFPALPAGILGSGFA 316
258 NDHEDTYADALWGLTITLTITIGYDKTPTWNGELLAAATTLTGVSFPALPAGILGSGFA 317
317 LKVOEQRHQHFKEKRNPAANLQCVWRSYAAD-----EKSYSIATW----- 358
318 LKVOEQRHQHFKEKRNPAAGLIQSAWRFYATNLSRDLHSTWYERTVTPVMSQQTQ 377
359 -----KHLKALHTCSP---TNOKL 375
378 TYGASRLIPINOLELRLNLSKSLGLTRKEPOPEPSKGRPCGLCCGCCGHSSQKV 437
376 SFKERVMAFPRGOSIKRSQASVGD--RRSPFSDITTAEGSPTKVQKSWFNDTRFRPSL 433
438 SLKDRV-FSSPRGMAAKGSPQAQTVRRSPADQSLDPSFKVPSWFGDRSRTRQAF 496
434 RLKSSQPKVIDADLTGTDVDEKGCQCDVSVEDLTPLKTVIRAIRIMKHFVAKRKF 493
497 RIKGAASRQNSEASLPGEDIVEDNKSNCNCFVTEDLTPGLKVSIRAVCVMRFLVSKRF 556
494 KETLRPYDVNDVIEQYSAGHLMCRISLQTRVDQILGQITSDKKSREKITAHEHTT 553
557 KESLRPYDVNDVIEQYSAGHLMCRISLQTRVDQIVGRGPTTD-KORTKGPAAETELP 615
554 DLSMLGRVVKVEKQVQSIKSLDCLDIYQVLRKGSASALALASFOIPPFEC----- 607
616 EDSMGRGLKVEKQVLSMEKLDLFLVSIYQ--RMG-----IPASTEAYFGA 662
608 ---EOTSQYSPVDSKDLSSAQNCGC---LSRSTSANISRGQLFILTNPFEQAQTFYAL 661
663 KEPEPAPYHSPEDSRD---HADKHGCIKIVRSTSS-----TGQRNYAA 704
662 SPTMHSQATQVPSQSOGSAVAATNTIANQINTAPKPAATTIQLIPPLFA----- 712
705 PPA-----IPPAQCPS--TSWQSHQHRGTSFVGDHGLSVLRIPPP-PAHERSLSAYG 754
713 -----IKHLRPETLHPNAGLOESIDVTTCVLVASKENVQVQASNLTKDRSMKSF 764
755 GGNRASTEFRLGTPACRPFSEALRSDTSISIPSV-DHEELERSFGFSISQS-KENL 812
765 DMCGETLLSVCP 776
813 DALGSCVAAP 824

RESULT 8
C1Q2_HUMAN STANDARD; PRT; 872 AA.
AC O43526; O43796; O75580; O95845; Q96J59; Q99454;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 2 (Voltage-gated
DE potassium channel subunit Kv7.2) (Neuroblastoma-specific potassium
DE channel alpha subunit KvLQT2) (KQT-like 2).
GN Name=KCNQ2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RC TISSUE=Neuroblastoma;
RX MEDLINE=97191543; PubMed=9039501;
RA Yokoyama M., Nishi Y., Yoshii J., Okubo K., Matsubara K.;
RT "Identification and cloning of neuroblastoma-specific and nerve
RT tissue-specific genes through compiled expression profiles.";
RL DNA Res. 3:311-320(1996).

[2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS BPNC1 CYS-284 AND
RP THR-306.
RC TISSUE=Brain, Fetal brain, and Temporal cortex;
RX MEDLINE=9805864; PubMed=9425895;
RA Singh N.A., Charlier C., Stauffer D., DuPont B.R., Leach R.J.,
RA Melis R., Ronen G.M., Bjerre I., Quattlebaum T., Murphy J.V.,
RA McHarg M.L., Gagnon D., Rosales T.O., Peiffer A., Anderson V.E.,
RA Leppert M.;
RT "A novel potassium channel gene, KCNQ2, is mutated in an inherited
RT epilepsy of newborns.";
RL Nat. Genet. 18:25-29(1998).
[3]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=fetal brain;
RX MEDLINE=98092527; PubMed=9430594; DOI=10.1126/science.279.5349.403;
RA Biervert C., Schroeder B.C., Kubisch C., Berkovic S.F., Propping P.,
RA Jentsch T.J., Steinlein O.K.;
RT "A potassium channel mutation in neonatal human epilepsy.";
RL Science 279:403-406(1998).
[4]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RX MEDLINE=99055398; PubMed=9836639; DOI=10.1126/science.282.5395.1890;
RA Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RA Dixon J.E., McKinnon D.;
RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
RT the M-channel.";
RL Science 282:1890-1893(1998).
[5]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 5).
RX MEDLINE=99043242; PubMed=9827540; DOI=10.1016/S0014-5793(98)01296-4;
RA Tinel N., Lauritzen I., Chouabe C., Lazdunski M., Borsotto M.;
RT "The KCNQ2 potassium channel: splice variants, functional and
RT developmental expression. Brain localization and comparison with
RT KCNQ3.";
RL FEBS Lett. 438:171-176(1998).
[6]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Brain, and Fetal brain;
RX MEDLINE=98344027; PubMed=9677360; DOI=10.1074/jbc.273.31.19419;
RA Yang W.-P., Levesque P.C., Little W.A., Conder M.L., Ramakrishnan P.,
RA Neubauer M.G., Blamar M.A.;
RT "Functional expression of two KvLQT1-related potassium channels
RT responsible for an inherited idiopathic epilepsy.";
RL J. Biol. Chem. 273:19419-19423(1998).
[7]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=21114072; PubMed=11160379;
RA Smith J.S., Iannotti C.A., Dargatzis P.G., Christian E.P., Aiyar J.;
RT "Differential expression of KCNQ2 splice variants: implications to M
RT current function during neuronal development.";
RL J. Neurosci. 21:1096-1103(2001).
[8]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klatschke R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[9]
RN
RP MUTAGENESIS OF SER-52; GY-279 AND TYR-284.
RX MEDLINE=99087323; PubMed=9872318; DOI=10.1038/25367;
RA Schroeder B.C., Kubisch C., Stein V., Jentsch T.J.;
RT "Moderate loss of function of cyclic-AMP-modulated KCNQ2/KCNQ3 K+
RL channels causes epilepsy.";
RL Nature 396:687-690(1998).
[10]
RN
RP INVOLVEMENT IN M-LIKE CURRENT.
RX MEDLINE=99410758; PubMed=10479678;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Delmas P.,
RA Buckley N.J., London B., Brown D.A.;
RT "Two types of K(+) channel subunit, Erg1 and KCNQ2/3, contribute to
RL the M-like current in a mammalian neuronal cell.";
RL J. Neurosci. 19:7742-7756(1999).
[11]
RN
RP ASSOCIATION WITH KCNE2.
RX MEDLINE=20487128; PubMed=11034315; DOI=10.1016/S0014-5793(00)01918-9;
RA Tinel N., Diochet S., Lauritzen I., Barhanin J., Lazdunski M.,
RA Borsotto M.;
RT "M-type KCNQ2-KCNQ3 potassium channels are modulated by the KCNE2
RL subunit.";
RL FEBS Lett. 480:137-141(2000).
[12]
RN
RP SURFACE EXPRESSION OF HETEROMERS.
RX MEDLINE=20250883; PubMed=10788442; DOI=10.1074/jbc.275.18.13343;
RA Schwake M., Pusch M., Kharkovets T., Jentsch T.J.;
RT "Surface expression and single channel properties of KCNQ2/KCNQ3, M-
RL type K+ channels involved in epilepsy.";
RL J. Biol. Chem. 275:13343-13348(2000).
[13]
RN
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20150152; PubMed=10684873;
RA Shapiro M.S., Roche J.P., Kaftan E.J., Cruzblanca H., Mackie K.,
RA Hille B.;
RT "Reconstitution of muscarinic modulation of the KCNQ2/KCNQ3 K(+)
RL channels that underlie the neuronal M current.";
RL J. Neurosci. 20:1710-1721(2000).
[14]
RN
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20178300; PubMed=10713961;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
RA Brown D.A.;
RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
RL via M1 muscarinic acetylcholine receptors.";
RL J. Physiol. (Lond.) 522:349-355(2000).
[15]
RN
RP ACTIVATION BY RETIGABINE.
RX MEDLINE=20368587; PubMed=10908292;
RA Main M.J., Cryan J.E., Dupure J.R., Cox B., Clare J.J., Burbidge S.A.;
RT "Modulation of KCNQ2/3 potassium channels by the novel anticonvulsant
RL retigabine.";
RL Mol. Pharmacol. 58:253-262(2000).
[16]
RN
RP ACTIVATION BY RETIGABINE.
RX MEDLINE=20411474; PubMed=10953053;
RA Wickenden A.D., Yu W., Zou A., Jegla T., Wagoner P.K.;
RT "Retigabine, a novel anti-convulsant, enhances activation of KCNQ2/Q3
RL potassium channels.";
RL Mol. Pharmacol. 58:591-600(2000).
[17]
RN
RP ACTIVATION BY RETIGABINE.
RX MEDLINE=20180045; PubMed=10713399; DOI=10.1016/S0304-3940(00)00866-1;
RA Rundfeldt C., Netzer R.;
RT "The novel anticonvulsant retigabine activates M-currents in Chinese
RL hamster ovary-cells transfected with human KCNQ2/3 subunits.";
RL Neurosci. Lett. 282:73-76(2000).
[18]
RN
RP TISSUE DISTRIBUTION, AND BIOCHEMICAL CHARACTERIZATION.
RX MEDLINE=20243795; PubMed=10781098; DOI=10.1073/pnas.090092797;
RA Cooper E.C., Aldape K.D., Abosch A., Barbaro N.M., Berger M.S.,
RA Peacock W.S., Jan Y.N., Jan L.Y.;
RT "Colocalization and coassembly of two human brain M-type potassium
RL channel subunits that are mutated in epilepsy.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4914-4919(2000).
[19]
RN
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
[20]
RN
RP VARIANT THR-780.
RX MEDLINE=99254826; PubMed=10323247;
RA Biervet C., Steinlein O.K.;
RT "Structural and mutational analysis of KCNQ2, the major gene locus for
RL benign familial neonatal convulsions.";
RL Hum. Genet. 104:234-240(1999).
[21]
RN
RP VARIANT BFNC1 TRP-214.
RX MEDLINE=21037661; PubMed=11175290; DOI=10.1038/sj.ejhg.5200570;
RA Miraglia del Giudice E., Coppola G., Scuccimarra G., Cirillo G.,
RA Bellini G., Pascotto A.;
RT "Benign familial neonatal convulsions (BFNC) resulting from mutation
RL of the KCNQ2 voltage sensor.";
RL Eur. J. Hum. Genet. 8:994-997(2000).
CC -!- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ3 to form a potassium channel
CC with essentially identical properties to the channel underlying
CC the native M-current, a slowly activating and deactivating
CC potassium conductance which plays a critical role in determining
CC the subthreshold electrical excitability of neurons as well as the


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QY 494 KETLRPYDVXVBOYQISAGHLDMLCRKLSQTRVDQILKGQITSDKKSREKTAEBHETT 553
D 556 KESLRPYDVXVBOYQISAGHLDMLSRKLSQTRVDQILKGQITSDKKSREKTAEBHETT 614
QY 554 DDLRLMLGVVKEQVQOSIESKLDCLLDIYQOVLKRGKSASALASQIIPPFEC----- 607
D 615 EDPSMGRGLKVEQVLSMEKKLDLFLVNIYQO-----RMG-----IPPTTEAVFGA 661
QY 608 ---EQTSYOSPVDSKDLGSAQNGCLSRSTGSANISRGILQFILTNPFEQAOTFYALSPT 664
D 662 KEPEPAPPYHSPEDSRE---HVDHGGCIKVIKVRSSSTG-----QKNFSAPP--AAPP- 709
QY 665 MHSQATQVPIQS-----DGSAAVATNTIANQINTAPKPAAPPTLIQI----- 706
D 710 ----VQCPPESTWQPSQHPRGHGTSPVGDHGLVLRIPPPPAHERSLRAYGGGNRASME 764
QY 707 -----PP-----PLPAIKHLPRPETHLPNAGLQSSISDVTTCVLVASK 744
D 765 FLQEDTPGCRPPGPNURSDTSISIPVDH-----EELERSFSGF--SISQ-----SK 811
QY 745 ENVOVAQS 752
D 812 ENLDALNS 819

RESULT 9
ID_C1Q2 MOUSE STANDARD; PRT: 759 AA.
AC Q92351; Q9QWN9; Q92342; Q92343; Q92344; Q92345; Q92346; Q92347;
AC Q92348; Q92349; Q92350;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 2 (Voltage-gated
DE potassium channel subunit Kv7.2) (Potassium channel alpha subunit
DE Kv1Q2) (KQT-like 2).
GN Name=Kcnq2; Synonyms=Kqt2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9; 10 AND 11).
RP TISSUE=Brain;
RX MEDLINE=98330948; PubMed=9666519;
RA Nakamura M., Watanabe H., Kubo Y., Yokoyama M., Matsumoto T.,
RA Sasaki H., Nishi Y.;
RT "KQT2, a new putative potassium channel family produced by alternative
RT splicing. Isolation, genomic structure, and alternative splicing of
RT the putative potassium channels."
RL Recept. Channels 5:255-271(1998).
RN [2]
RP ROLE IN NEURAL HYPEREXCITABILITY.
RX MEDLINE=20312851; PubMed=10854243;
RA Watanabe H., Nagata E., Kosakai A., Nakamura M., Yokoyama M.,
RA Tanaka K., Sasaki H.;
RT "Disruption of the epilepsy KCNQ2 gene results in neural
RT hyperexcitability."
RL J. Neurochem. 75:28-33(2000).
CC -1- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ3 to form a potassium channel
CC with essentially identical properties to the channel underlying
CC the native M-current, a slowly activating and deactivating
CC potassium conductance which plays a critical role in determining
CC the subthreshold electrical excitability of neurons as well as the
CC responsiveness to synaptic inputs.
CC -1- SUBUNIT: Heteromultimer with KCNQ3.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=11;
CC Name=1; Synonyms=KQT2.1;
CC IsoId=Q92351-1; Sequence=Displayed;

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CC Name=2; Synonyms=MKQT2.2;
CC IsoId=Q92351-2; Sequence=VSP_001001;
CC Name=3; Synonyms=MKQT2.3;
CC IsoId=Q92351-3; Sequence=VSP_001000;
CC Name=4; Synonyms=MKQT2.4;
CC IsoId=Q92351-4; Sequence=VSP_001002;
CC Name=5; Synonyms=MKQT2.5;
CC IsoId=Q92351-5; Sequence=VSP_001003; VSP_001004;
CC Name=6; Synonyms=MKQT2.6;
CC IsoId=Q92351-6; Sequence=VSP_001005; VSP_001006;
CC Name=7; Synonyms=MKQT2.7;
CC IsoId=Q92351-7; Sequence=VSP_000997; VSP_000998; VSP_000999;
CC Name=8; Synonyms=MKQT2.8;
CC IsoId=Q92351-8; Sequence=VSP_000998; VSP_000999;
CC Name=9; Synonyms=MKQT2.9;
CC IsoId=Q92351-9; Sequence=VSP_000993; VSP_000994;
CC Name=10; Synonyms=MKQT2.10;
CC IsoId=Q92351-10; Sequence=VSP_000995; VSP_000996;
CC Name=11; Synonyms=MKQT2.11;
CC IsoId=Q92351-11; Sequence=VSP_000991; VSP_000992;
CC -1- TISSUE SPECIFICITY: Exclusively expressed in the brain. Expressed
CC in every neuron-containing regions of the central nervous system
CC examined, such as the cerebellum, cerebral cortex, occipital pole,
CC substantia nigra, amygdala, caudate nucleus, hippocampus and
CC thalamus. Also detected in the cochlea.
CC -1- DEVELOPMENTAL STAGE: Detected at day 11, 15 and 17 of the
CC embryonic development. Expression increases by a factor of 2.5 at
CC 1 week after birth. Then the expression level remains stable until
CC the adult stage. The mRNAs for shorter forms (isoforms 9, 10 and
CC 11) are specifically expressed in an embryo on the 11th day after
CC gestation.
CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position (By similarity).
CC -1- SIMILARITY: Belongs to the potassium channel family. KQT
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB000494; BAA37156.1; -
CC EMBL; AB000495; BAA37157.1; -
CC EMBL; AB000496; BAA37158.1; -
CC EMBL; AB000497; BAA37159.1; -
CC EMBL; AB000498; BAA37160.1; -
CC EMBL; AB000499; BAA37161.1; -
CC EMBL; AB000500; BAA37162.1; -
CC EMBL; AB000501; BAA37163.1; -
CC EMBL; AB000502; BAA37164.1; -
CC EMBL; AB000503; BAA37165.1; -
CC EMBL; AB000504; BAA37166.1; -
CC MGD; MGI:1309503; Kcnq2.
CC InterPro; IPR005821; Ion trans.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR003091; K+channel.
CC InterPro; IPR003937; KCNQ_channel.
CC Pfam; PF00520; Ion trans; 1.
CC Pfam; PF03520; KCNQ_channel; 1.
CC PRINTS; PR00169; KCHANNEL.
CC Alternative splicing; Ion transport; Ionic channel; Multigene family;
CC Phosphorylation; Potassium; Potassium channel; Potassium transport;
CC Transmembrane; Transport; Voltage-gated channel.
CC TRANSMEM 92 112 Segment S1 (Potential).
CC TRANSMEM 123 143 Segment S2 (Potential).
CC TRANSMEM 167 187 Segment S3 (Potential).
CC TRANSMEM 198 221 Segment S4 (Potential).
CC TRANSMEM 232 252 Segment S5 (Potential).

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TRANSNEM	292	312	Segment S6 (Potential).	
FT DOMAIN	265	285	Segment H5 (pore-forming) (Potential).	
FT SITE	277	282	Selectivity filter (By similarity).	
FT MOD RES	52	52	Phosphoserine (By PKA) (By similarity).	
FT VARSPLIC	310	338	GILGSGFALKVQSRPKPKFKERPNPAAG -> VSPAHLPT LEMLGVLEAPKAWPWPCTCEL (in isoform 11).	
FT			/FtId=vsp_000991.	
FT VARSPLIC	339	759	Missing (in isoform 11).	
FT			/FtId=vsp_000992.	
FT VARSPLIC	342	349	SAWRFYAT -> GQVRCAGH (in isoform 9).	
FT			/FtId=vsp_000993.	
FT VARSPLIC	350	759	Missing (in isoform 9).	
FT			/FtId=vsp_000994.	
FT VARSPLIC	342	347	SAWRFY -> VSLSPC (in isoform 10).	
FT			/FtId=vsp_000995.	
FT VARSPLIC	348	759	Missing (in isoform 10).	
FT			/FtId=vsp_000996.	
FT VARSPLIC	372	372	Y -> YSSQTQYGAS (in isoform 7).	
FT			/FtId=vsp_000997.	
FT VARSPLIC	406	463	SQVSLKDRYFESSPRGMAAKGSGPQAQTVRRSPSADQSLD DSRSKVPKSGFDRSR -> RSVPPASRPVGCCTHLALL SLCIHVSGWRATMGPCVFCYVQOVTVCPGTPRVTSQL (in isoform 7 and isoform 8).	
FT			/FtId=vsp_000998.	
FT VARSPLIC	464	759	Missing (in isoform 7 and isoform 8).	
FT			/FtId=vsp_000999.	
FT VARSPLIC	407	418	Missing (in isoform 3).	
FT			/FtId=vsp_001000.	
FT VARSPLIC	562	596	IDMTVGGPPESTPRDKKYPKGTPTAPSRSPQVSP -> QE PLPVQSGHEQPPQGNQAWKHGQGLGD (in isoform 2).	
FT			/FtId=vsp_001001.	
FT VARSPLIC	562	597	Missing (in isoform 4).	
FT			/FtId=vsp_001002.	
FT VARSPLIC	562	570	IDMTVGGPPP -> SCDWRGVLA (in isoform 5).	
FT			/FtId=vsp_001003.	
FT VARSPLIC	571	759	Missing (in isoform 5).	
FT			/FtId=vsp_001004.	
FT VARSPLIC	562	623	IDMTVGGPPESTPRDKKYPKGTPTAPSRSPQVSPRVDTIV GRGTITDKRTKGPATELP -> QSLPVQSGHEQGPQG QNAWHKHGQGLGRCACQGGYQVWRSPLTLLASCCLLCP HTVCF (in isoform 6).	
FT			/FtId=vsp_001005.	
FT VARSPLIC	624	759	Missing (in isoform 6).	
FT			/FtId=vsp_001006.	
FT CONFLICT	125	125	A -> P (in Ref. 1; BAA37161).	
FT CONFLICT	326	326	P -> Q (in Ref. 1; BAA37160/BAA37165).	
FT SEQUENCE	759 AA; 84450 MW; 84450 MW; CID12DBFF3979D3P CRC64;			
Query Match	38.6%;	Score 1754;	DB 1; Length 759;	
Best Local Similarity	51.9%;	Pred. No. 2.1e-89;		
Matches	387;	Conservative 73;	Mismatches 149;	Indels 136; Gaps 18;
QY	17	AARGDGLLLGTRATLGGGGGLRESRRGQGRMSLLGLPLSYTSQSCRNVKRRV 76		
Db	34	STRDGLLIAGSEAPK-----RGSVLSKPRTGAGA-----GKP-----PKRNAFYRKL 77		
QY	77	QNYLYNVLERPGWAFIYHAFVFLVFCGLIILSVFTEPTHTKLASSCLLILEFVMIWVF 136		
Db	78	QNYLYNVLERPGWAFIYHAFVFLVFCGLIILSVFTEPTHTKLASSCLLILEFVMIWVF 137		
QY	137	GLEFIIRIWSAGCCRYRGWQGRLFARKPCFVIDTIVLIASIVASAKTQGNIFATSAL 196		
Db	138	GVEYFVRIWAAGCCRYRGWGRGLFARKPCFVIDIMVLIASIVLAAGSQGNVAFATSAL 197		
QY	197	RSRLFQILIRVMDRGGTGWKLSGVVYHASKELITAWYIGFLVLIIPSSFLVYLVEKDA 256		
Db	198	RSRLFQILIRVMDRGGTGWKLSGVVYHASKELITAWYIGFLVLIIPSSFLVYLVEKGE 257		
QY	257	NKEFSTYADALWMTITLTIGYGDKTPLTWLGRLLISAGFALLGISFFPAGILGSGFA 316		
Db	258	NHFDITYADALWMLITLTIGYGDYKYPQWNGRLLAATFTLIGVSFFPAGILGSGFA 317		

QY	317	LKVOEHQROKHFEKRRNPAAANLIQCVWRSYAAD-----EKSVSIATWK--PH 361		
Db	318	LKVOEHQRPKHFEXRRNPAAAGLIQSAWRFYATNLSETDLHSTWQYERTVTVPYRLIPP 377		
QY	362	LKALHTC-----SPTNOKLSFKERVRMASPRGOSIKSRQASVGD-- 400		
Db	378	LNQLELLNLKSKSLGTLFRKEPQPEPSP-SQVSLKDRV-FSSPRGMAAKGSGPQAQTV 435		
QY	401	RRSPSTDTITARGSPTKVQKWSFNDRTRFRPSRLKSKSQPKPVIDADTALGTDDVDYDEKG 460		
Db	436	RRSPADQSLDSDSGKVPKWSFGDRSTRQAFRIKGAASRQNSEASLPGEDIVEDNKS 495		
QY	461	CQCDSVEDLTPPLKTVIRAIRIMKFHVAKFKETLRPYDKVDVIEQYSAGHLDMLCRI 520		
Db	496	CNCEPVTEDLTPLGLKVSIRAVCWRFVLSKFKESLRPYDMDVMDVIEQYSAGHLDMLSRI 555		
QY	521	KSLQT-----RVDQILGKGQITSDKKGRE 544		
Db	556	KSLQSRIDMIVGPPPPPTPRDKKYPKGTPTAPSRSPQVSPRVDHIVRGFTID-KDRT 614		
QY	545	KITAEHETTDLLSMLGRVVKVEKQVOSIESKLDCLLDIYQVLRKGSASALALASFOIPP 604		
Db	615	KGPATELPEDPSMMGLKVEKQVLSMEKKLDFLVSITQ--RMG-----IPP 661		
QY	605	FEC-----EQTSYQSPVDSKDLSGSAQNSC-----LSRSTSANISRGLOFILTPE 652		
Db	662	AETAYFGAKPEPAPPYHSPEDSRD---HADKHGCIIVKIRSTSS----- 704		
QY	653	FSAQTFYALSPTMHSAQTQVPIQSQ 677		
Db	705	-TGQRNYAAPAI--PPAQCPPESTS 726		
RESULT 10				
C1Q3_HUMAN STANDARD; PRT; 872 AA.				
ID	C1Q3_HUMAN			
AC	O43525;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Potassium voltage-gated channel subfamily KQT member 3 (Voltage-gated potassium channel subunit Kv7.3) (Potassium channel alpha subunit KvLQT3) (KQT-like 3).			
DE	Name=KCNQ3;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., CHARACTERIZATION OF VARIANT BFNC2 VAL-310, AND MUTAGENESIS OF GLY-318.			
RC	TISSUE=Brain;			
RC	MEDLINE=99087323; PubMed=9872318; DOI=10.1038/25367;			
RA	Schroeder B.C., Kubisch C., Stein V., Jentsch T.J.;			
RT	"Moderate loss of function of cyclic-AMP-modulated KCNQ2/KCNQ3 K+ channels causes epilepsy.";			
RL	Nature 396:687-690(1998).			
RN	[2]			
RP	SEQUENCE OF 48-872 FROM N.A., AND VARIANT BFNC2 VAL-310.			
RC	TISSUE=Brain;			
RC	MEDLINE=9805869; PubMed=9425900;			
RA	Charlier C., Singh N.A., Ryan S.G., Lewis T.B., Reus B.E., Leach R.J., Leppert M.;			
RT	"A pore mutation in a novel KQT-like potassium channel gene in an idiopathic epilepsy family.";			
RL	Nat. Genet. 18:53-55(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. AND CHARACTERIZATION.			
RC	TISSUE=Brain, and Fetal brain;			
RC	MEDLINE=98344027; PubMed=9677360; DOI=10.1074/jbc.273.31.19419;			
RA	Yang W.-P., Levesque P.C., Little W.A., Conder M.L., Ramakrishnan P., Neubauer M.G., Blamnar M.A.;			
RT	"Functional expression of two KvLQT1-related potassium channels			

RT responsible for an inherited idiopathic epilepsy.";
J. Biol. Chem. 273:19419-19423(1998).
[4]
RP INVOLVEMENT IN M-LIKE CURRENT.
RX MEDLINE=99410758; PubMed=10479678;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Delmas P.,
RA Buckley N.J., London B., Brown D.A.:
RT "Two types of K(+) channel subunit, Erg1 and KCNQ2/3, contribute to
RT the M-like current in a mammalian neuronal cell.";
J. Neurosci. 19:7742-7756(1999).
[5]
RP ASSOCIATION WITH KCNE2.
RX MEDLINE=20487128; PubMed=11034315; DOI=10.1016/S0014-5793(00)01918-9;
RA Tinel N., Diocot S., Lauritzen I., Barhanin J., Lazdunski M.,
RA Borsotto M.:
RT "M-type KCNQ2-KCNQ3 potassium channels are modulated by the KCNE2
RT subunit.";
FEBS Lett. 480:137-141(2000).
[6]
RP SURFACE EXPRESSION OF HETEROMERS.
RX MEDLINE=20250883; PubMed=10786442; DOI=10.1074/jbc.275.18.13343;
RA Schwake M., Pusch M., Kharkovets T., Jentsch T.J.:
RT "Surface expression and single channel properties of KCNQ2/KCNQ3, M-
RT type K+ channels involved in epilepsy.";
J. Biol. Chem. 275:13343-13348(2000).
[7]
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20150152; PubMed=10694873;
RA Shapiro M.S., Roche J.P., Kaftan E.J., Cruzblanca H., Mackie K.,
RA Hille B.:
RT "Reconstitution of muscarinic modulation of the KCNQ2/KCNQ3 K(+) channels that underlie the neuronal M current.";
J. Neurosci. 20:1710-1721(2000).
[8]
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20178300; PubMed=10713961;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
RA Brown D.A.:
RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
RT via M1 muscarinic acetylcholine receptors.";
J. Physiol. (Lond.) 522:349-355(2000).
[9]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20368587; PubMed=10908282;
RA Main M.J., Cryan J.E., Dupre J.R., Cox B., Clare J.J., Burbidge S.A.:
RT "Modulation of KCNQ2/3 potassium channels by the novel anticonvulsant
RT retigabine.";
Mol. Pharmacol. 58:253-262(2000).
[10]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20411474; PubMed=10953053;
RA Wickenden A.D., Yu W., Zou A., Jegla T., Wagoner P.K.:
RT "Retigabine, a novel anti-convulsant, enhances activation of KCNQ2/Q3
RT potassium channels.";
Mol. Pharmacol. 58:591-600(2000).
[11]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20180045; PubMed=10713399; DOI=10.1016/S0304-3940(00)00866-1;
RA Rundfeldt C., Netzer R.:
RT "The novel anticonvulsant retigabine activates M-currents in Chinese
RT hamster ovary-cells transfected with human KCNQ2/3 subunits.";
Neurosci. Lett. 282:73-76(2000).
[12]
RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
RX MEDLINE=21095345; PubMed=11159685;
RA Wickenden A.D., Zou A., Wagoner P.K., Jegla T.:
RT "Characterization of KCNQ5/Q3 potassium channels expressed in
RT mammalian cells.";
Br. J. Pharmacol. 132:381-384(2001).
[13]
RP VARIANT BFNC2 ARG-309.
RX MEDLINE=20309392; PubMed=10852552;
DOI=10.1002/1531-8249(200006)47:6<822::AID-ANAL9>3.3.CO;2-O;

RA Hirose S., Zenri F., Akiyoshi H., Fukuma G., Iwata H., Inoue T.,
RA Yonekani M., Tsutsumi A.:
RT "A novel mutation of KCNQ3 (c.925T-->C) in a Japanese family with
RT benign familial neonatal convulsions.";
Ann. Neurol. 47:822-826(2000).
CC -I- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ2 or KCNQ5 to form a potassium
CC channel with essentially identical properties to the channel
CC underlying the native M-current, a slowly activating and
CC deactivating potassium conductance which plays a critical role in
CC determining the subthreshold electrical excitability of neurons as
CC well as the responsiveness to synaptic inputs.
CC -I- SUBUNIT: Heteromultimer with KCNQ2 or KCNQ5. May associate with
CC KCNE2.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Predominantly expressed in brain.
CC -I- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position (By similarity).
CC -I- DISEASE: Defects in KCNQ3 are the cause of benign familial
CC neonatal convulsions type 2 (BFNC2) [MIM:121201]; also known as
CC epilepsy, benign neonatal type 2 (BFN2). BFNC2 is an autosomal
CC dominant form of epilepsy in the newborn that clears spontaneously
CC after a few weeks and is followed by normal psychomotor
CC development.
CC -I- MISCELLANEOUS: Mutagenesis experiments were carried out in Xenopus
CC oocytes by coexpression of either KCNQ3(mut) and KCNQ2 at the
CC ratio of 1:1, or of KCNQ3(mut), KCNQ3(wt) and KCNQ2 at the ratio
CC of 1:1:2, to mimic the situation in a heterozygous patient with
CC BFNC2 disease.
CC -I- SIMILARITY: Belongs to the potassium channel family. KQT
CC subfamily.

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CC EMBL; AF071491; AAC96101.1; -
CC EMBL; AF071478; AAC96101.1; JOINED.
CC EMBL; AF071479; AAC96101.1; JOINED.
CC EMBL; AF071480; AAC96101.1; JOINED.
CC EMBL; AF071481; AAC96101.1; JOINED.
CC EMBL; AF071482; AAC96101.1; JOINED.
CC EMBL; AF071483; AAC96101.1; JOINED.
CC EMBL; AF071484; AAC96101.1; JOINED.
CC EMBL; AF071485; AAC96101.1; JOINED.
CC EMBL; AF071486; AAC96101.1; JOINED.
CC EMBL; AF071487; AAC96101.1; JOINED.
CC EMBL; AF071488; AAC96101.1; JOINED.
CC EMBL; AF071489; AAC96101.1; JOINED.
CC EMBL; AF071490; AAC96101.1; JOINED.
CC HSSP; Q54397; IJVM.
CC Genew; HGNC:6297; KCNQ3.
CC MIM; 602232; -
CC MIM; 121201; -
CC GO; GO:0008076; C:voltage-gated potassium channel complex; TAS.
CC GO; GO:0005249; F:voltage-gated potassium channel activity; TAS.
CC GO; GO:0006813; P:potassium ion transport; TAS.
CC GO; GO:0007268; P:synaptic transmission; TAS.
CC InterPro; IPR005821; Ion trans.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR003091; K+channel.
CC InterPro; IPR003937; KCNQ channel.
CC InterPro; IPR005820; M+channel_nlg.
CC Pfam; PF00520; Ion trans; 1.
CC Pfam; PF03520; KCNQ channel; 1.
CC PRINTS; PR00169; KCHANNEL.

Disease mutation; Epilepsy; Ion transport; Ionic channel;
Multigene family; Potassium; Potassium channel; Potassium transport;
Transmembrane; Transport; Voltage-gated channel.
TRANSMEM 122 142 Segment S1 (Potential).
TRANSMEM 153 173 Segment S2 (Potential).
TRANSMEM 197 217 Segment S3 (Potential).
TRANSMEM 226 247 Segment S4 (Potential).
TRANSMEM 262 282 Segment S5 (Potential).
TRANSMEM 331 351 Segment S6 (Potential).
TRANSMEM 304 324 Segment S5 (pore-forming) (Potential).
DOMAIN 13 24 Poly-Gly.
SITE 316 321 Selectivity filter (By similarity).
VARIANT 309 309 W -> R (in BFN2).
VARIANT 310 310 G -> V (in BFN2; about 50% reduction of wild-type heteromeric current; ratio of

Query Match 34.9%; Score 1587.5; DB 1; Length 872;
Best Local Similarity 42.8%; Pred. No. 4.8e-80;
Matches 386; Conservative 106; Mismatches 244; Indels 165; Gaps 28;

QY 3 DVESGRVLLNSAARGDGLILGTTAAATLGGGGGLRESRGKOGARMSLLGK-PLSY 61
DB 49 DVEQ---VTALGAGADKDGTL---EGGDEGGRTPQG--IGLLAKTPLSR 95
QY 62 TSSQSCRRNVKRYRQVLYNVLPRGMAFIHAFVFLVFGCLILSVFSTIPEHTKLA 121
DB 96 PVK---RNNAKYRIQIYDALERPGWALLYHALVFLVGLCLILAVLTTFKEYETVS 152
QY 122 SSCILLIEFVMVVGLEFIIRIWSAGCCRYRGWQRLRPARKPFCVIITVILIASIV 181
DB 153 GDWLLLETFEFAIFGAFAIRLWAAGCCRYGWRGLRFPARKPLCMLDFVLIASVPV 212
QY 182 VSATQGNIFATSLRSIFLOILRMVMDRRGTWKLGSVVVAHSEKILITAWYIGFLV 241
DB 213 VAVNGQNVLIATS--LRSIRFLQILRMMDRRGTWKLGSALCAHSEKILITAWYIGFLT 271
QY 242 LIFSSFLVYLVEKDA-----NKEFSTYDALMWGITITLTIGYDKTFLTWLGR 291
DB 272 LILSSFLVYLVEKDVPEVDAQGBEMKEFEFYDALMWGITLTATIGYDKTPTWEGRL 331
QY 292 LSAGFALLIGTFPAPALGILSGFALKVQEHQKHEKERNPAANILQCVWSYAADEK 351
DB 332 IAAATFSLIGVSFFPALGILSGFALKVQEHQKHEKERNPAANILQCVWSYAADEK 391
QY 352 SVS-IATWK-----PHLKALTCSTNOKLSFKERVMASPRGQSIKSROASVGDRR 402
DB 392 RIDIVATWRFVESVVSFPFFKKEQLAASSQKGLLDRLVLSNPRGSNTK-----OKLF 445
QY 403 SPSTDTITAGSPPTKVQKSWSFNDRTRFRPSLRK-----SSQPKVIDADTALGTDDVY 456
DB 446 TPLNVDAIEESPSKEPKPVGLNNKRFRTAPMKAYAFQSSSE-----DAGTG---DPMA 497
QY 457 DEKGQCDVSVEDLTPPLKTVIRAIKMHVAKKETLRPYDVKDVIQYQYSGHLD 516
DB 498 EDRGYNDFPIEDIMPTLKAIRAVRILQFLRYKKFKETLRPYDVKDVIQYQYSGHLD 557
QY 517 LCRIKSLQTRVDQILGKQITSDKKSR-----EKITABHETT--DDLS 557
DB 558 LSRKYLQTRIDMFTFPPTTPKHKSQKSAFTFPSPQSPRNPVYVAPSTSEIEDQS 617
QY 558 MLGRVVKVEKQVQIESKCLDCLDIYQVQLR-----KGSASALALASFOIPIPF 605
DB 618 MWGRFVKVERQVDMGKGLDPLVDMHMQHMERLQVQVTEYYPTKGTSS-----PA 667
QY 606 ECEQTSQVPSVDSKDLGSAQNSCLSRSSANISRLGLQILTPNFFSAOTFFVALSPTM 665
DB 668 EAERKEDNRYSS-DUKTIICNSETGPPPPYFHH-----QVITDKVSPGVGFADHP-- 717
QY 666 HSQATQVPIQSDGSAVAATNTIANQINATPKPAAPTTLQIPPLPAIKHLPRPETLHPN 725
DB 718 ----VNLPRGGSSGKVQAT-----PPSSATTVERPTVLTILTLLDSRVSGH-S 762

QY 726 PAGLQESISDVTTCLVASKENVQVQASNLTKDRSMRKSFGDMGGETILLSVCVMPVKDLGKS 785
DB 763 QADLQCPYS-----RISPRQ-----RSITRSDTFLSL----- 792
QY 786 LSVQNLIRSTEELNQLSGSSSGSGSQDFYP-----KWRESKLITDEEVGPEETETDT 841
DB 793 MSVNH-----EELERSPSGFSISQDRDDVYVFGPNGGSSWMREKRYLAE--GETDTIDP 844
QY 842 F 842
DB 845 F 845

RESULT 11
C1Q3_BOVIN STANDARD; PRT; 866 AA.
AC P58126;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 3 (Voltage-gated
DE Potassium channel subunit Kv7.3) (Potassium channel alpha subunit
DE KvLQT3) (KQT-like 3).
GN Name=KCNQ3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rae J.L.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ2 to form a potassium channel
CC with essentially identical properties to the channel underlying
CC the native M-current, a slowly activating and deactivating
CC potassium conductance which plays a critical role in determining
CC the subthreshold electrical excitability of neurons as well as the
CC responsiveness to synaptic inputs.
CC -!- SUBUNIT: Heteromultimer with KCNQ2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position (By similarity).
CC -!- SIMILARITY: Belongs to the potassium channel family. KQT
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR HESB; AF325548; AAK11221.1; -.
DR HSPB; Q54397; 1JVM.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001632; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003937; KCNQ_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF03520; KCNQ channel; 1.
DR PRINTS; PR00169; KCHANNEL.
DR Ion transport; Ionic channel; Multigene family; Potassium;
KW Potassium channel; Potassium transport; Transmembrane; Transport;
KW Voltage-gated channel.
FT TRANSMEM 122 142 Segment S1 (Potential).
FT TRANSMEM 153 173 Segment S2 (Potential).
FT TRANSMEM 197 217 Segment S3 (Potential).
FT TRANSMEM 226 247 Segment S4 (Potential).


```

Db 393 RDLVATWRYESVSPFPFRKQLEAAASQKGLLDRVLSNPRGSNTK-----GKLF 446
Qy 403 SPSTDITAEGSPYTKVQKSMFNDRTFRPSLRUK-----SSQPKVVIDADTALGTDDVY 456
Db 447 TPLNDAIEBSPKPKPGLNKKRFRFTAFRMKAYAFWQSS-----DAGTG---DPMA 498
Qy 457 DEKGCQDVSDVETLTPPLKTVIRAIRIMKPHVAKRPFKTLRVDYDKVIEQVSAGHLDM 516
Db 499 EDRGYGNDFLIEDIMFTLKAARAVRILQPLRYKKKFKETLRBYDVKDVIEQVSAGHLDM 558
Qy 517 LCRIKSLQTRVDQITLKGQITSDKKGREK-----ITAHEHTDDLS 557
Db 559 LSRKYLQTRIDMLFTPGPSTPKHKKSQKSGSAFTVPSQSPRNEPVVARAATSETDQS 618
Qy 558 MLGRVVKVQKQVIESKLCCLDITVQVLRKGSASALASQIIPPFCEQTSQSDQSPV 617
Db 619 MMGRFVKVERQVDMGKKLFLVDMHQMHER-----LQVHVTEYPTKGAASSFA 668
Qy 618 D-----SKDLGSAQNSGCLSRSTANISRGLOFILTP-NEPSAQTFFVALSPTMHSQATQVP 673
Db 669 EGEKKENRNSDLKTIICINSETGPPDPYPSFQVPIIDRVGPYGFPAHD-----VK 720
Qy 674 ISQDGSAAVATNTIANQINTAPKAAPTTLQIPPLPAIKHLPRPETLHPNPAQLOESI 733
Db 721 LTRGSPSSTKAQNLPS-----SGSTVAERPTVLPILTLDDSCVSVH-----762
Qy 734 SDVTCLVASKENVOVAQSNLTKDRSMKSFDMGGETLLSVCPMPVKDLGKSLSVQNLIR 793
Db 763 -----SQTELQGYPSDHISPR-QRRSITRSDTPLSL-----MSVNH---798
Qy 794 STEELNIQLSGSESGSRGSDQFYP-----KWRESKLFITDEEVGPEETETDTF 842
Db 799 --EELERSPGFSISQDRDDYVFGPSGSSWMREKRYLAE---GETDITDTPF 846

RESULT 13
C103 RAT
ID C103 RAT STANDARD; PRV; 873 AA.
AC O88944; Q82240;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 3 (Voltage-gated
DE potassium channel subunit Kv7.3) (Potassium channel alpha subunit
DE Kv1QT3) (KQT-like 3).
GN Name=Kcnq3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Derst C., Preisig-Mueller R., Hennighausen A., Daut J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=99055398; PubMed=9836339; DOI=10.1126/science.282.5395.1890;
RA Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RA Dixon J.E., McKinnon D.;
RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
RT the M-channel.";
RL Science 282:1890-1893 (1998).
CC
CC -!- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ2 to form a potassium channel
CC with essentially identical properties to the channel underlying
CC the native M-current, a slowly activating and deactivating
CC potassium conductance which plays a critical role in determining
CC the subthreshold electrical excitability of neurons as well as the
CC responsiveness to synaptic inputs.
CC -!- SUBUNIT: Heteromultimer with KCNQ2.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

```

```

CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O88944-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O88944-2; Sequence=VSP_001012;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Expressed in brain and sympathetic ganglia. In
CC brain, expressed in cortex, hippocampus and at much lower levels
CC in cerebellum. In sympathetic ganglia, expressed at approximately
CC equal levels in both superior cervical ganglia and prevertebral
CC ganglia.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position (By similarity).
CC -!- SIMILARITY: Belongs to the potassium channel family. KQT
CC subfamily.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF087454; AAC36723.2; -;
CC EMBL; AF091247; AAC79846.1; -;
CC HSSP; O54397; 1JVM.
CC RGD; 69222; Kcnq3.
CC InterPro; IPR005821; Ion trans.
CC InterPro; IPR001622; K-channel_pore.
CC InterPro; IPR003091; K channel.
CC InterPro; IPR003937; KCNQ channel.
CC InterPro; IPR005820; M-channel_nlg.
CC Pfam; PF00520; Ion trans; 1.
CC Pfam; PF03520; KCNQ channel; 1.
CC PRINTS; PR00169; KCHANNEL.
CC KW Alternative splicing; Ion transport; Ionic channel; Multigene family;
CC Potassium; Potassium channel; Potassium transport; Transmembrane;
CC Transport; Voltage-gated channel.
CC TRANSMEM 123 143 Segment S1 (Potential).
CC TRANSMEM 154 174 Segment S2 (Potential).
CC TRANSMEM 198 218 Segment S3 (Potential).
CC TRANSMEM 227 248 Segment S4 (Potential).
CC TRANSMEM 263 283 Segment S5 (Potential).
CC TRANSMEM 332 352 Segment S6 (Potential).
CC DOMAIN 305 325 Segment H5 (pore-forming) (Potential).
CC DOMAIN 13 25 Poly-Gly.
CC SITE 317 322 Selectivity filter (By similarity).
CC VARSPLIC 1 83 MGLKARRAAGAGGGGGGGGGGAGNANPAGDSAVAGDEE
CC RKVGLAPGDVEQVTLALGTADKDGTLLEGGREGGQRT
CC P -> MALEFPGQLQPPPPRPTPSAPSSRSSSGEGEAPSG
CC /FTId=VSP_001012.
CC CONFLICT 654 654 H -> R (in Ref. 2).
CC SEQUENCE 873 AA; 96897 MW; D77AF808051E15 CRC64;
CC
CC Query Match 34.2%; Score 1555.5; DB 1; Length 873;
CC Best Local Similarity 42.1%; Pred. No. 2.9e-78;
CC Matches 376; Conservative 106; Mismatches 262; Indels 149; Gaps 25;
CC
Qy 3 DVESGRGVLLNSAARGDGLLILGTAAATLGGGGGLRESREGKQARMSLQK-PLSY 61
Db 50 DVEQ---VTIALGTGADKDGTLLE-----EGGREGGQRTPG--IGLLAKTPLSR 96
Qy 62 TSSQSCRNKVRVQVLYNVLPRGWAFIYHAFVLLVFLGCLILSVFSTPIEHTKLA 121
Db 97 PVK---RNNAKYRIQTLIYDALERPGWALLYHALVFLVGLCLILAVLTTFKEVETS 153
Qy 122 SSCLLILEFVMIYVVGLEFIIRIWSAGCCCRYGWQGLRFAFKPCFVIDTIVILASIV 181
Db 154 GDWLLILETFAIFGAEFALRIWAAGCCCRYGWGRGLKFAFKPKLCMLDIFVLIASVPV 213

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QY 182 VSAKTOGNIATFATSLRSLRFLQILRLMVRMDRGCTWKLGLGSSVVYAHASKELITAWYIGFLV 241
Db 214 VAVNQGNVLATS-LRSLRFLQILRLMVRMDRGCTWKLGLGSAICAHASKELITAWYIGFLT 272
QY 242 LIFSSFLVYLVEKDA-----NKEFFSYADALMWGTTITLTIGYGDKTPLTWLGR 291
Db 273 LILSSFLVYLVEKDVPEMDAQGEEMKEFEFYADALMWGLITLTIYGYDKTPKWEGR 332
QY 292 LSGAFALLGTSFPALPAGILGSGFALKVQSHQKQKHEKRNPAANIQCWRSYAADEK 351
Db 333 IAATFSLIGVSFFALPAGILGSGFALKVQSHQKQKHEKRNPAANIQAARYYATNP 392
QY 352 SVS-IATWK-----PHLKALHTCPTNKLKSFKEVRMASPRGQSIKSRQASVCDRR 402
Db 393 RLDLVATWRYESVVSFFPKRQLEAAASQKGLLDRVLSNPRGSNTK-----GKLF 446
QY 403 SPSTDIATAGSPKTKVQKSWFNDRTRPRSLRLK-----SSQPKVIDADTALGTDDVY 456
Db 447 TPLNVDIAIESPSKEPKVPGLNKKERTAFRMKAYAFWQSSE-----DAGTG---DPMT 498
QY 457 DEKGCQCDVSDVDTPLPKTVIRAIRIMKHFVAKRKPETLRPYDVKDVIEQVSAGHLDM 516
Db 499 EDGRYGNDFLIEDMPTLKAAIRAVRILQFLRYLKKFKETLRPYDVKDVIEQVSAGHLDM 558
QY 517 LCRIKSLQTRVDQILGKQITSDKSKREK-----ITAHEHTTDL 557
Db 559 LSRILYQTRIDMIFTGPGSTPKHKKSQKSGAFTYPSQSPRNPVYVARAATSETEDQS 618
QY 558 MLGRVVRKVEQVQSIKSLCLDIYQVLRKSGSALALASFOIPPECEQTSYQSPV 617
Db 619 MNGKFKVVRQVDMGKGLFLVDMHMHMER-----LQVHVTYPPYKGSPPA 668
QY 618 D-----SKDLSGSAQNSGCLSRSTANSIRGQFILTLP-NEFSAQTFYALSTPMHSQATQVP 673
Db 669 EGEKKEDNRYSDLKTIIICNYSSEGPDPYPYSHQVPIRVPYGFPAHDP-----VK 720
QY 674 ISQSDGSAVATNTIANQINTAPKPAAPTTLQIPPLPAIKHLPRPTLHPNAGLOESI 733
Db 721 LTRGGPSTQAQNLPS-----SGSTYAEPTVLPIITLLDSCVSYH-----762
QY 734 SDVTTCLVASKENVQVAQSNLTKDRSMRKGFDMGGETLLSCVPMVPRKDLKSLSVQNLIR 793
Db 763 -----SQTELQGYPSHISPR-ORRISITRSDSTPLSL-----MSVNH---798
QY 794 STEELNQLSGSSSGSRGSDQFYP-----KWRESKLPITDEEVGPEETDTDF 842
Db 799 --EELERSPSGFSISQDRDDVFGSPGSSWMREKRYLAE--GETDITDTPF 846

RESULT 14
Q8C9Y6 PRELIMINARY; PRT; 523 AA.
AC Q8C9Y6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A43007521 product:potassium voltage-gated channel,
DE subfamily Q, member 4, full insert sequence. (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
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RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK040190; BAC30534.1; -.
DR HSPB; Q54397; IJ95.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003937; KCNQ_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR005820; M+channel_mlg.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01459; KCNOCHANNEL.
DR Ion transport; Ionic channel; Transmembrane; Transport.
KW NON_TER 1
FT NON_TER 523
SQ SEQUENCE 523 AA; 58016 MW; A9D3C67024F84C18 CRC64;

Query Match 33.5%; Score 1525.5; DB 2; Length 523;
Best Local Similarity 58.3%; Pred. No. 7.1e-77;
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Matches 308; Conservative 59; Mismatches 70; Indels 91; Gaps 9;
Qy 35 GGGGLRESRGQAGMSLLGKPL-----SYTSSQSRNKKVRYVQNY 79
Db 14 GGGGSPR-----RLGLGSLPPGAPLPDGGSGSACGGQSSAAQKRYRLQNW 64
Qy 80 LYNVLERPRGWAFTYHAFVFLVFGCLILSVFTSTPEHTKLASSCLLILEFVMIVVFGLE 139
Db 65 VYNVLERPRGWAFTYHAFVFLVFGCLILSVFTSTPEHTKLASSCLLILEFVMIVVFGLE 124
Qy 140 FIIRWAGCCCRVGRGQRLRFARPCFVIDTIVLIASIAVSVAKTQGNIFATSLRSL 199
Db 125 YIIRWAGCCCRVGRGQRLRFARPCFVIDTIVLIASIAVSVAKTQGNIFATSLRSL 184
Qy 200 RFQILRMVMDRGGTGWKLLGSVVVAHSEKLTATWYIGFLVLI FSSFLVLYEKDANKE 259
Db 185 RFQILRMVMDRGGTGWKLLGSVVVAHSEKLTATWYIGFLVLI FSSFLVLYEKDANSD 244
Qy 260 FSTYADALWAGTTITLTIGYDKTPTLWGLRLSAGFALIGISFFALPAGILSGFALKV 319
Db 245 FSSYADSLWAGTTITLTIGYDKTPTLWGLRLSAGFALIGISFFALPAGILSGFALKV 304
Qy 320 QEOHQKHFKEKRRNPAANLIQCVWRSYAAD-EKSVSIATW----- 358
Db 305 QEOHQKHFKEKRRNPAANLIQAAWRLYSTDTSRAYLTATWYIYDSILPSPRELALLFEHI 364
Qy 359 -----KPHLKALHT-----CSPNOKLSFKERVMA SPR 387
Db 365 QRARNGGLRLEVVRAPVPGAPSRYPVATCHRPGSASFPGESSRMGKDIRIRISSQ 424
Qy 388 GQSISRSQ--ASVGDRSPSDITAE--GSPTKVQKSWFNDTRFRPSLRK---SSQPK 441
Db 425 KRTGPSKQLAPPPIPTSPSEQGEASSPSKVQKSWFNDTRFRASLRKPRCSAEEG 484
Qy 442 PVIDADTALGDDVDYDKGQCQDVSDVDELTPPLKTVIRAIRMKFVA 489
Db 485 P-----SEEAEEKSYQCELTVDVDMVPAKSVIRSVRIKFLVA 523

RESULT 15
Q8IGU8
ID Q8IGU8 PRELIMINARY; PRT; 840 AA.
AC Q8IGU8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RE26469P (Fragment).
GN Name=KCNQ;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo K., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celnikier S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT001588; AAN71343.1; -.
DR HSSP; Q54397; 1BL8.
DR FlyBase; FBgn0033494; KCNQ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
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DR InterPro; IPR003937; KCNQ_channel.
DR InterPro; IPR003091; K channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF03220; KCNQ_channel; 1.
DR PRINTS; PR00169; KCNCHANNEL.
DR PRINTS; PR01459; KCNQCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON TER 1
SQ SEQUENCE 840 AA; 95154 MW; C1813B33F528588A CRC64;

Query Match 30.0%; Score 1364.5; DB 2; Length 840;
Best Local Similarity 38.9%; Pred. No. 1.2e-67;
Matches 333; Conservative 112; Mismatches 247; Indels 165; Gaps 23;

Qy 51 RMSLLGKPLSYTSSQSRNKKVRYVQNYLYNVLERPRG-WAFIVHAFVFLVFGCLILS 109
Db 66 RMSLLGKPLNY--NRTRDVRYYRRLQSLRYNLFPRGLHAFVHVMVFLVMTCLALS 123
Qy 110 VFSTPEHTKLASSCLLILEFVMIVVFGLEFIIIRWAGCCCRVGRGQRLRFARPCFV 169
Db 124 VFSTIKEYEEDAVYILFRMELVWTFWTFEGCARLWSSGCRGYQCLGRKFVKRPF 183
Qy 170 IDTIVLIASIAVSVAKTQGNIFATSLRSLRFLOILRMVMDRGGTGWKLLGSVVVAH 229
Db 184 IDIVTILASIVVLGMSGTQGVFATSLRSLRGLRPFQILRMVMDRGGTGWKLLGSVV 243
Qy 230 ELITAWYIGFLVLI FSSFLVLYEKDANKEFSTYADALWAGTTITLTIGYDKTPTLW 289
Db 244 ELITWYIGFLGLIFASFLVYWEKDVNDKFSNFAQALWAGVITLCTVGYGDMVPIT 303
Qy 290 RLISAGFALLGISFFALPAGILSGFALKVQBOHQKHFKEKRRNPAANLIQCVWRSYA 349
Db 304 KLIASCCALLGISFFALPAGILSGFALKVQOQOKHMIRRRQPAATLIQAWRCYAA 363
Qy 350 EKSVSITATWPKHLKALHTCSPNOKLSFKERVMA SPRQSISKRSQASVGDRESPT 409
Db 364 EHSVSIVATWNIHRVALPSPASRASSSFKHNT-----SFVARLPTIRRHKSQT 415
Qy 410 AEGSPTKVOK-SWSFNDRTRFRPSLRKSSQPKPVIDADTALGTDVDYDEKGCQCQDV 468
Db 416 GGGDGGGVSKPGSSRASTRYTTIR-----DINASVENLDEEPRC-----T 459
Qy 469 DLTPPLKTVIRAIRIMKFWAKKFKETLRPDYDKVIEQYAGHLDMLCRIKSLQTRVD 528
Db 460 QLTNRHKTATIRFKLYFARRKFKALKPYDKVDMEQYAGHVDLLGRVKMLHLRLD 519
Qy 529 QILKGQITSDKKSREKITAETHETDLSMLGRVVKVQVQSIKSLDCLLDIYQQVLR 588
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Db 565 -----MEDRD-----RFLA 573
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Db 574 LP-----LPAPKIHSTISPSHKPLHHAHLNLAIDVMKRTAALSVPHPQVTTPLN 625
Qy 699 AAP-----TTLQIP-----PPLPAIKHL--PRPETHPNPAGLQ-ESISD 735
Db 626 SAPDSSELRLATQTPPTTTTDAIATQTPMPHVQHTATNTKSSVLNSYOLGSEKQOHN 685
Qy 736 VTTCLVASKENVQVQASNLTKDSMRKSP-----DMGGETLLSVCPMVPKDLGKS 785
Db 686 V---FWTELENRTKRVTLSLHRSTSEPYSKQEQRIIIPDEGADSLDSSAKTPPDSSI 742
Qy 786 LSVQNLRSTFEELNIQLSGSESGSGSQDFYKPKWRESKLFITDEEVEGPE-ETETTFDA 844
Db 743 LIDYEDDFEEDLNCE-----GEMDHFTWE-----IDSDIGVEVDVADADGD 786
Qy 845 AQPAREAAFAFASDSLRT 861
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Db 787 CDESTEDTALLQCART 803

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Job time : 192 secs

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